

OM protein - protein search, using sw model
 Run on: July 27, 2006, 11:54:57 ; Search time 198 Seconds
 (without alignments)
 1380.886 Million cell updates/sec

Title: US-10-677-669-69
 Perfect score: 3135
 Sequence: 1 MCSRVPLLLPLLLALLPGP.....PLMGFGPGGLQSPHLAKPYI 598
 Scoring table: BLOSUM62

Searched: Gapop 10.0 , Gapext 0.5
 Total number of hits satisfying chosen parameters: 2589679
 Minimum DB seq length: 0
 Maximum DB seq length: 2000000000
 Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 1500 summaries

Database :
 A Geneseq 8:
 1: geneseqp1980s:*
 2: geneseqp1990s:*
 3: geneseqp2000s:*
 4: geneseqp2001s:*
 5: geneseqp2002s:*
 6: geneseqp2003as:*
 7: geneseqp2003bs:*
 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Match Length	DB ID	Description
RESULT 1				
ID	AA06484	standard; protein; 598 AA.		
DE	Human tumour-associated protein PRO357.			
PN	WO9935170-A2.			
PD	15-JUL-1999.			
PA	(GETH) GENENTECH INC.			
Query Match	100.0%;	Score 3135; DB 2;	Length 598;	
Best Local Similarity	100.0%;	Pred. No. 4e-190;		
RESULT 2				
ID	AA01322	standard; protein; 598 AA.		
DE	Human PRO357 polypeptide.			
PN	WO200032776-A2.			
PD	08-JUN-2000.			
PA	(GETH) GENENTECH INC.			
Query Match	100.0%;	Score 3135; DB 3;	Length 598;	
Best Local Similarity	100.0%;	Pred. No. 4e-190;		
RESULT 3				
ID	AA93691	standard; protein; 598 AA.		
DE	Amino acid sequence of novel polypeptide PRO357.			
PN	WO200037640-A2.			
PD	29-JUN-2000.			
PA	(GETH) GENENTECH INC.			
Query Match	100.0%;	Score 3135; DB 3;	Length 598;	
Best Local Similarity	100.0%;	Pred. No. 4e-190;		
RESULT 4				
ID	AA083643	standard; protein; 598 AA.		
DE	Human PRO protein, Seq ID No 104.			
PN	WO200208288-A2.			
PD	31-JAN-2002.			
PA	(GETH) GENENTECH INC.			
Query Match	100.0%;	Score 3135; DB 5;	Length 598;	
Best Local Similarity	100.0%;	Pred. No. 4e-190;		
RESULT 5				
ID	ADY31844	standard; protein; 598 AA.		
DE	Novel human secreted and transmembrane protein PRO357.			
PN	WO200193983-A1.			
PD	13-DEC-2001.			
PA	(GETH) GENENTECH INC.			
Query Match	100.0%;	Score 3135; DB 5;	Length 598;	
Best Local Similarity	100.0%;	Pred. No. 4e-190;		
RESULT 6				
ID	ABU55931	standard; protein; 598 AA.		
DE	Human secreted/transmembrane protein PRO357.			

PN US2002142959-A1.
 PD 03-OCT-2002.
 PA (GETH) GENENTECH INC.
 Query Match
 Best Local Similarity 100.0%; Score 3135; DB 6; Length 598;
 RESULT 7
 ID ABU0790 standard; protein; 598 AA.
 DE Human PRO polypeptide #52.
 PN US2003036635-A1.
 PD 20-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match
 Best Local Similarity 100.0%; Score 3135; DB 6; Length 598;
 RESULT 8
 ID ABO33756 standard; protein; 598 AA.
 DE Novel human secreted and transmembrane protein PRO357.
 PN US2003045687-A1.
 PD 06-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match
 Best Local Similarity 100.0%; Score 3135; DB 6; Length 598;
 RESULT 9
 ID ABU60241 standard; protein; 598 AA.
 DE Human PRO polypeptide #12.
 PN US2002132768-A1.
 PD 19-SEP-2002.
 PA (GETH) GENENTECH INC.
 Query Match
 Best Local Similarity 100.0%; Score 3135; DB 6; Length 598;
 RESULT 10
 ID ABU64927 standard; protein; 598 AA.
 DE Human secreted/transmembrane protein PRO357.
 PN US2002173463-A1.
 PD 21-NOV-2002.
 PA (GETH) GENENTECH INC.
 Query Match
 Best Local Similarity 100.0%; Score 3135; DB 6; Length 598;
 RESULT 11
 ID ABU58361 standard; protein; 598 AA.
 DE Novel human secreted protein PRO357.
 PN US2002150976-A1.
 PD 17-OCT-2002.
 PA (GETH) GENENTECH INC.
 Query Match
 Best Local Similarity 100.0%; Score 3135; DB 6; Length 598;
 RESULT 12
 ID ABU57247 standard; protein; 598 AA.
 DE Human PRO357 protein.
 PN US2002142958-A1.
 PD 03-OCT-2002.
 PA (GETH) GENENTECH INC.
 Query Match
 Best Local Similarity 100.0%; Score 3135; DB 6; Length 598;
 RESULT 13
 ID ABU56312 standard; protein; 598 AA.
 DE Human secreted/transmembrane protein, PRO357.
 PN US2002132981-A1.
 PD 19-SEP-2002.
 PA (GETH) GENENTECH INC.
 Query Match
 Best Local Similarity 100.0%; Score 3135; DB 6; Length 598;
 RESULT 14
 ID ABU60352 standard; protein; 598 AA.
 DE Novel human secreted and transmembrane protein PRO357.
 PN US2002168715-A1.
 PD 14-NOV-2002.
 PA (GETH) GENENTECH INC.
 Query Match
 Best Local Similarity 100.0%; Score 3135; DB 6; Length 598;
 RESULT 15
 ID ABU82099 standard; protein; 598 AA.
 DE Novel human secreted and transmembrane protein PRO357.
 PN US2003088063-A1.

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PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 3135; DB 6; Length 598;
  Best Local Similarity 100.0%; Pred. No. 4e-190;
RESULT 16
ID ABUL1313 standard; protein; 598 AA.
DE Human pro357 protein sequence.
PN US2002127643-A1.
PD 12-SEP-2002.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 3135; DB 6; Length 598;
  Best Local Similarity 100.0%; Pred. No. 4e-190;
RESULT 17
ID ABU67132 standard; protein; 598 AA.
DE Human PRO polypeptide #12.
PN US2002165143-A1.
PD 07-NOV-2002.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 3135; DB 6; Length 598;
  Best Local Similarity 100.0%; Pred. No. 4e-190;
RESULT 18
ID ABU72279 standard; protein; 598 AA.
DE Human PRO357 protein.
PN US2003050448-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 3135; DB 6; Length 598;
  Best Local Similarity 100.0%; Pred. No. 4e-190;
RESULT 19
ID ABJ72407 standard; protein; 598 AA.
DE Human PRO357 protein.
PN US2003027988-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 3135; DB 6; Length 598;
  Best Local Similarity 100.0%; Pred. No. 4e-190;
RESULT 20
ID ABO34302 standard; protein; 598 AA.
DE Human secreted/transmembrane polypeptide PRO 357.
PN US2003044934-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 3135; DB 6; Length 598;
  Best Local Similarity 100.0%; Pred. No. 4e-190;
RESULT 21
ID ABJ72109 standard; protein; 598 AA.
DE Human membrane bound receptor/protein PRO357 amino acid sequence.
PN US2003065147-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 3135; DB 7; Length 598;
  Best Local Similarity 100.0%; Pred. No. 4e-190;
RESULT 22
ID ADB83594 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003073814-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 3135; DB 7; Length 598;
  Best Local Similarity 100.0%; Pred. No. 4e-190;
RESULT 23
ID ADB80700 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003088068-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 3135; DB 7; Length 598;
  Best Local Similarity 100.0%; Pred. No. 4e-190;
RESULT 24
ID ADB73241 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003096968-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 3135; DB 7; Length 598;
  Best Local Similarity 100.0%; Pred. No. 4e-190;
RESULT 25
ID ADB78323 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003092889-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 3135; DB 7; Length 598;
  Best Local Similarity 100.0%; Pred. No. 4e-190;
RESULT 26
ID ADB84971 standard; protein; 598 AA.
DE Human PRO polypeptide #52.
PN US2003073817-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 3135; DB 7; Length 598;
  Best Local Similarity 100.0%; Pred. No. 4e-190;
RESULT 27
ID ADB78077 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003092886-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 3135; DB 7; Length 598;
  Best Local Similarity 100.0%; Pred. No. 4e-190;
RESULT 28
ID ADB87143 standard; protein; 598 AA.
DE Human PRO polypeptide #52.
PN US2003088067-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 3135; DB 7; Length 598;
  Best Local Similarity 100.0%; Pred. No. 4e-190;
RESULT 29
ID ADB84725 standard; protein; 598 AA.
DE Human PRO polypeptide #52.
PN US2003092890-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 3135; DB 7; Length 598;
  Best Local Similarity 100.0%; Pred. No. 4e-190;
RESULT 30
ID ADB83840 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003069397-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 3135; DB 7; Length 598;
  Best Local Similarity 100.0%; Pred. No. 4e-190;
RESULT 31
ID ADB72995 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003092887-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 3135; DB 7; Length 598;
  Best Local Similarity 100.0%; Pred. No. 4e-190;
RESULT 32
ID ADC25825 standard; protein; 598 AA.
DE Human secreted/transmembrane PRO polypeptide #12.
PN US2002142419-A1.
PD 03-OCT-2002.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 3135; DB 7; Length 598;
  Best Local Similarity 100.0%; Pred. No. 4e-190;
RESULT 33
ID ADC25583 standard; protein; 598 AA.
DE Human secreted/transmembrane PRO polypeptide #12.
PN US2002156004-A1.
PD 24-OCT-2002.
PA (GETH ) GENENTECH INC.
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Query Match
Best Local Similarity 100.0%; Score 3135; DB 7; Length 598;
RESULT 34
ID ADC25704 standard; protein; 598 AA.
DE Human secreted/transmembrane PRO polypeptide #12.
PN US2003077698-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3135; DB 7; Length 598;
RESULT 35
ID ADC36833 standard; protein; 598 AA.
DE Human PRO polypeptide #52.
PN US2003088065-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3135; DB 7; Length 598;
RESULT 36
ID ADC21823 standard; protein; 598 AA.
DE Human PRO polypeptide #52.
PN US2003096969-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3135; DB 7; Length 598;
RESULT 37
ID ADC49854 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003088064-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3135; DB 7; Length 598;
RESULT 38
ID ADC49053 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003088070-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3135; DB 7; Length 598;
RESULT 39
ID ADC49570 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003088071-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3135; DB 7; Length 598;
RESULT 40
ID ADC47431 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003088072-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3135; DB 7; Length 598;
RESULT 41
ID ADC47176 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003105288-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3135; DB 7; Length 598;
RESULT 42
ID ADC78051 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003096972-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3135; DB 7; Length 598;

Best Local Similarity 100.0%; Pred. No. 4e-190;
RESULT 43
ID ADD06286 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003073816-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3135; DB 7; Length 598;
RESULT 44
ID ADC77805 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003088066-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3135; DB 7; Length 598;
RESULT 45
ID ADD50768 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003105291-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3135; DB 7; Length 598;
RESULT 46
ID ADD51014 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003105290-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3135; DB 7; Length 598;
RESULT 47
ID ADD50495 standard; protein; 598 AA.
DE Human PRO polypeptide #52.
PN US2003096971-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3135; DB 7; Length 598;
RESULT 48
ID ADD50249 standard; protein; 598 AA.
DE Human PRO polypeptide #52.
PN US2003096970-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3135; DB 7; Length 598;
RESULT 49
ID ADD51260 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003105289-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3135; DB 7; Length 598;
RESULT 50
ID ADH27489 standard; protein; 598 AA.
DE Human secreted/transmembrane PRO polypeptide #12.
PN US2003083479-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3135; DB 7; Length 598;
RESULT 51
ID ADC48807 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003092888-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 4e-190;

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RESULT 52
ID ADE20978 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003100735-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 4e-190;
RESULT 53
ID ADE05822 standard; protein; 598 AA.
DE Human PRO polypeptide #52.
PN US2003100728-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 4e-190;
RESULT 54
ID ADD75051 standard; protein; 598 AA.
DE Human PRO polypeptide #52.
PN US2003100712-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 4e-190;
RESULT 55
ID ADD75797 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003100717-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 4e-190;
RESULT 56
ID ADD85029 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003100722-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 4e-190;
RESULT 57
ID ADD86855 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003100738-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 4e-190;
RESULT 58
ID ADE20732 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003100734-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 4e-190;
RESULT 59
ID ADE39029 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003096362-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 4e-190;
RESULT 60
ID ADE05576 standard; protein; 598 AA.
DE Human PRO polypeptide #52.
PN US2003100727-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 4e-190;
RESULT 61
ID ADE05535 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003100718-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 4e-190;
RESULT 62
ID ADD78401 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003100737-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 4e-190;
RESULT 63
ID ADE21224 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003100736-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 4e-190;
RESULT 64
ID ADD77339 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003100732-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 4e-190;
RESULT 65
ID ADE20486 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003100733-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 4e-190;
RESULT 66
ID ADD75551 standard; protein; 598 AA.
DE Human PRO polypeptide #52.
PN US2003100054-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 4e-190;
RESULT 67
ID ADD74067 standard; protein; 598 AA.
DE Human PRO polypeptide #52.
PN US2003100708-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 4e-190;
RESULT 68
ID ADD74313 standard; protein; 598 AA.
DE Human PRO polypeptide #52.
PN US2003100709-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 4e-190;
RESULT 69
ID ADD76043 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003100718-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 4e-190;
RESULT 70
ID ADD85535 standard; protein; 598 AA.
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DE Novel human secreted and transmembrane protein PRO357.
PN US2003100721-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 4e-190;
RESULT 71
ID ADE05084 standard; protein; 598 AA.
DE Human PRO polypeptide #52.
PN US2003100726-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 4e-190;
RESULT 72
ID ADD75297 standard; protein; 598 AA.
DE Human PRO polypeptide #52.
PN US2003100714-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 4e-190;
RESULT 73
ID ADD76841 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003100715-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 4e-190;
RESULT 74
ID ADD86609 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003100719-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 4e-190;
RESULT 75
ID ADD78077 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003100731-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 4e-190;
RESULT 76
ID ADE71538 standard; protein; 598 AA.
DE Human secreted/transmembrane PRO polypeptide #12.
PN US2003096742-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 4e-190;
RESULT 77
ID ADD77585 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003100729-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 4e-190;
RESULT 78
ID ADD77831 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003100730-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 4e-190;
RESULT 79
ID ADD85289 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003100725-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 4e-190;
RESULT 80
ID ADD73821 standard; protein; 598 AA.
DE Human PRO polypeptide #52.
PN US2003100710-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 4e-190;
RESULT 81
ID ADD74559 standard; protein; 598 AA.
DE Human PRO polypeptide #52.
PN US2003100713-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 4e-190;
RESULT 82
ID ADD77087 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003100716-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 4e-190;
RESULT 83
ID ADD85781 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003100720-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 4e-190;
RESULT 84
ID ADE05330 standard; protein; 598 AA.
DE Human PRO polypeptide #52.
PN US2003100723-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 4e-190;
RESULT 85
ID ADD74805 standard; protein; 598 AA.
DE Human PRO polypeptide #52.
PN US2003100724-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 4e-190;
RESULT 86
ID ADG05617 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003096959-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 4e-190;
RESULT 87
ID ADG27171 standard; protein; 598 AA.
DE Human PRO polypeptide #52.
PN US2003096962-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 4e-190;
RESULT 88
ID ADG11234 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003096967-A1.
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PD 22-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3135; DB 8; Length 598;
 Best Local Similarity 100.0%; Pred. No. 4e-190;
 RESULT 89
 ID ADG12013 standard; protein; 598 AA.
 DE Novel human secreted and transmembrane protein PRO357.
 PN US2003096963-A1.
 PD 22-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3135; DB 8; Length 598;
 Best Local Similarity 100.0%; Pred. No. 4e-190;
 RESULT 90
 ID ADF94570 standard; protein; 598 AA.
 DE Novel human secreted and transmembrane protein PRO357.
 PN US2003096964-A1.
 PD 22-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3135; DB 8; Length 598;
 Best Local Similarity 100.0%; Pred. No. 4e-190;
 RESULT 91
 ID ADG06666 standard; protein; 598 AA.
 DE Human PRO polypeptide #52.
 PN US2003096966-A1.
 PD 22-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3135; DB 8; Length 598;
 Best Local Similarity 100.0%; Pred. No. 4e-190;
 RESULT 92
 ID ADG63481 standard; protein; 598 AA.
 DE Human secreted/transmembrane PRO polypeptide #12.
 PN US2003211570-A1.
 PD 13-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3135; DB 8; Length 598;
 Best Local Similarity 100.0%; Pred. No. 4e-190;
 RESULT 93
 ID ADH39010 standard; protein; 598 AA.
 DE Novel human secreted and transmembrane protein PRO357.
 PN US2003096965-A1.
 PD 22-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3135; DB 8; Length 598;
 Best Local Similarity 100.0%; Pred. No. 4e-190;
 RESULT 94
 ID ADH43210 standard; protein; 598 AA.
 DE Human secreted/transmembrane PRO polypeptide #12.
 PN US2003207401-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3135; DB 8; Length 598;
 Best Local Similarity 100.0%; Pred. No. 4e-190;
 RESULT 95
 ID ADG34100 standard; protein; 598 AA.
 DE Novel human secreted and transmembrane protein PRO357.
 PN US2004006206-A1.
 PD 08-JAN-2004.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3135; DB 8; Length 598;
 Best Local Similarity 100.0%; Pred. No. 4e-190;
 RESULT 96
 ID ADI33570 standard; protein; 598 AA.
 DE Human PRO polypeptide #52.
 PN US2003096960-A1.
 PD 22-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3135; DB 8; Length 598;
 Best Local Similarity 100.0%; Pred. No. 4e-190;
 RESULT 97
 ID ADH69664 standard; protein; 598 AA.
 DE Human PRO polypeptide #52.
 PN US2004019183-A1.
 PD 29-JAN-2004.

PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3135; DB 8; Length 598;
 Best Local Similarity 100.0%; Pred. No. 4e-190;
 RESULT 98
 ID ADI29825 standard; protein; 598 AA.
 DE Novel human secreted and transmembrane protein PRO357.
 PN US2003096961-A1.
 PD 22-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3135; DB 8; Length 598;
 Best Local Similarity 100.0%; Pred. No. 4e-190;
 RESULT 99
 ID ADM27222 standard; protein; 598 AA.
 DE Novel human secreted and transmembrane protein PRO357.
 PN US2004044179-A1.
 PD 04-MAR-2004.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3135; DB 8; Length 598;
 Best Local Similarity 100.0%; Pred. No. 4e-190;
 RESULT 100
 ID ADK66580 standard; protein; 598 AA.
 DE Human PRO polypeptide #52.
 PN US2004044180-A1.
 PD 04-MAR-2004.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3135; DB 8; Length 598;
 Best Local Similarity 100.0%; Pred. No. 4e-190;
 RESULT 101
 ID ADN00448 standard; protein; 598 AA.
 DE Human secreted/transmembrane PRO polypeptide #12.
 PN US2004091972-A1.
 PD 13-MAY-2004.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3135; DB 8; Length 598;
 Best Local Similarity 100.0%; Pred. No. 4e-190;
 RESULT 102
 ID ADU25372 standard; protein; 598 AA.
 DE Human secreted/transmembrane PRO polypeptide #12.
 PN US2004220385-A1.
 PD 04-NOV-2004.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3135; DB 8; Length 598;
 Best Local Similarity 100.0%; Pred. No. 4e-190;
 RESULT 103
 ID ADY39535 standard; protein; 598 AA.
 DE Human insulin-like growth factor homolog PRO357 precursor protein.
 PN US2005048613-A1.
 PD 03-MAR-2005.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3135; DB 9; Length 598;
 Best Local Similarity 100.0%; Pred. No. 4e-190;
 RESULT 104
 ID ADY73816 standard; protein; 598 AA.
 DE Human PRO357 protein, SEQ ID NO: 69.
 PN US2005059115-A1.
 PD 17-MAR-2005.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3135; DB 9; Length 598;
 Best Local Similarity 100.0%; Pred. No. 4e-190;
 RESULT 105
 ID AAY17831 standard; protein; 598 AA.
 DE Human PRO357 protein sequence.
 PN WO9928462-A2.
 PD 10-JUN-1999.
 PA (GETH) GENENTECH INC.
 Query Match 99.7%; Score 3126; DB 2; Length 598;
 Best Local Similarity 99.8%; Pred. No. 1.5e-189;
 RESULT 106
 ID AAB07428 standard; protein; 673 AA.
 DE Amino acid sequence of a leucine-rich surface glycoprotein (LRSG).
 PN WO200042170-A1.
 PD 20-JUL-2000.
 PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.

Query Match
Best Local Similarity 98.4%; Score 3083.5; DB 3; Length 673;
RESULT 107
ID AAB87533 standard; protein; 673 AA.
DE Human PRO1282.
PN WO200116318-A2.
PD 08-MAR-2001.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 4; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 108
ID AAB65166 standard; protein; 673 AA.
DE Human PRO1282 (UNQ652) protein sequence SEQ ID NO:52.
PN WO200073454-A1.
PD 07-DEC-2000.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 4; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 109
ID AAU75266 standard; protein; 673 AA.
DE Human Slit-like protein #1.
PN WO200212346-A2.
PD 14-FEB-2002.
PA (PHAA) PHARMACIA CORP.
Query Match 98.4%; Score 3083.5; DB 5; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 110
ID ABG95858 standard; protein; 673 AA.
DE Human secreted/transmembrane protein PRO1282.
PN US2002119130-A1.
PD 29-AUG-2002.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 5; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 111
ID ABG78042 standard; protein; 673 AA.
DE Human leucine-rich surface glycoprotein (LRSG-1).
PN US2002072089-A1.
PD 13-JUN-2002.
PA (HOLT/) HOLTZMAN D A.
PA (MCCA/) MCCARTHY S A.
PA (MACB/) MACBETH K J.
PA (BUSF/) BUSFIELD S J.
PA (PANY/) PAN Y.
PA (WHIT/) WHITE D.
PA (KHOD/) KHODADOUST M M.
PA (GUWW/) GU W.
Query Match 98.4%; Score 3083.5; DB 5; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 112
ID ABUS7981 standard; protein; 673 AA.
DE Human PRO polypeptide #13.
PN US2003027163-A1.
PD 06-FEB-2003.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 113
ID ABUS9059 standard; protein; 673 AA.
DE Novel human secreted or transmembrane protein PRO1282.
PN US2002132252-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 114
ID ABUS2571 standard; protein; 673 AA.
DE Human secreted/transmembrane protein PRO1282.
PN US2003032023-A1.
PD 13-FEB-2003.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 115
ID ABU60490 standard; protein; 673 AA.

DE Human secreted/transmembrane protein, #19.
PN US2002160384-A1.
PD 31-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 116
ID ABU13872 standard; protein; 673 AA.
DE Human PRO1282 polypeptide.
PN US2002103125-A1.
PD 01-AUG-2002.
PA (GETH) GENENTECH LTD.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 117
ID ABU72457 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003003531-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 118
ID ABU90883 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003018173-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 119
ID ABO33942 standard; protein; 673 AA.
DE Human secreted/transmembrane protein PRO1282.
PN US2003009013-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 120
ID ABU71959 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003018183-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 121
ID ABU71513 standard; protein; 673 AA.
DE Human secreted polypeptide PRO1282.
PN US2003013855-A1.
PD 16-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 122
ID ABU72294 standard; protein; 673 AA.
DE Human PRO polypeptide #8.
PN US2002182638-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 123
ID ABU90967 standard; protein; 673 AA.
DE Human PRO polypeptide #8.
PN US2003018168-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 124
ID ABUS9206 standard; protein; 673 AA.
DE Human secreted/transmembrane protein, #19.

PN US2003027162-A1.
 PD 06-FEB-2003. 98.4%; Score 3083.5; DB 6; Length 673;
 Query Match 88.7%; Pred. No. 8.5e-187;
 Best Local Similarity 88.7%; Pred. No. 8.5e-187;
 RESULT 125
 ID ABO25903 standard; protein; 673 AA.
 DE Human PRO1282 polypeptide.
 PN US2002127576-A1.
 PD 12-SEP-2002.
 PA (GETH) GENENTECH INC.
 Query Match 98.4%; Score 3083.5; DB 6; Length 673;
 Best Local Similarity 88.7%; Pred. No. 8.5e-187;
 RESULT 126
 ID ABO27288 standard; protein; 673 AA.
 DE Human secreted/transmembrane polypeptide PRO1282.
 PN US2003009012-A1.
 PD 09-JAN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 98.4%; Score 3083.5; DB 6; Length 673;
 Best Local Similarity 88.7%; Pred. No. 8.5e-187;
 RESULT 127
 ID ABO92483 standard; protein; 673 AA.
 DE Human secreted/transmembrane protein PRO1282.
 PN US2003045684-A1.
 PD 06-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 98.4%; Score 3083.5; DB 6; Length 673;
 Best Local Similarity 88.7%; Pred. No. 8.5e-187;
 RESULT 128
 ID ABO81153 standard; protein; 673 AA.
 DE Human secreted polypeptide PRO1282.
 PN US2003027212-A1.
 PD 06-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 98.4%; Score 3083.5; DB 6; Length 673;
 Best Local Similarity 88.7%; Pred. No. 8.5e-187;
 RESULT 129
 ID ABO53268 standard; protein; 673 AA.
 DE Novel human secreted and transmembrane protein PRO1282.
 PN US2003027986-A1.
 PD 06-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 98.4%; Score 3083.5; DB 6; Length 673;
 Best Local Similarity 88.7%; Pred. No. 8.5e-187;
 RESULT 130
 ID ABO58912 standard; protein; 673 AA.
 DE Human secreted/transmembrane protein, #19.
 PN US2002142961-A1.
 PD 03-OCT-2002.
 PA (GETH) GENENTECH INC.
 Query Match 98.4%; Score 3083.5; DB 6; Length 673;
 Best Local Similarity 88.7%; Pred. No. 8.5e-187;
 RESULT 131
 ID ABO92290 standard; protein; 673 AA.
 DE Novel human secreted and transmembrane protein PRO1282.
 PN US2003022187-A1.
 PD 30-JAN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 98.4%; Score 3083.5; DB 6; Length 673;
 Best Local Similarity 88.7%; Pred. No. 8.5e-187;
 RESULT 132
 ID ABO59355 standard; protein; 673 AA.
 DE Novel human secreted or transmembrane protein PRO1282.
 PN US2003027985-A1.
 PD 06-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 98.4%; Score 3083.5; DB 6; Length 673;
 Best Local Similarity 88.7%; Pred. No. 8.5e-187;
 RESULT 133
 ID ABO98270 standard; protein; 673 AA.
 DE Novel human secreted and transmembrane protein PRO1282.
 PN US2002183493-A1.
 PD 05-DEC-2002.
 PA (GETH) GENENTECH INC.
 Query Match 98.4%; Score 3083.5; DB 6; Length 673;
 Best Local Similarity 88.7%; Pred. No. 8.5e-187;

Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 134
ID ABU89275 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003036634-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 135
ID ABU82482 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2002183494-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 136
ID ABU92121 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003017476-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 137
ID ABU96446 standard; protein; 673 AA.
DE Human PRO polypeptide #8.
PN US2003027993-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 138
ID ABUL0827 standard; protein; 673 AA.
DE Human PRO polypeptide #13.
PN US2002123463-A1.
PD 05-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 139
ID ABUH1579 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2002177164-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 140
ID ABUT2116 standard; protein; 673 AA.
DE Human PRO polypeptide #8.
PN US2003023042-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 141
ID ABUH8518 standard; protein; 673 AA.
DE Human secreted and transmembrane polypeptide PRO1282.
PN US2002197615-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 142
ID ABO34032 standard; protein; 673 AA.
DE Human PRO1282 polypeptide.
PN US2003017981-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 143
ID ADBI7073 standard; protein; 673 AA.

DE Human transmembrane PRO polypeptide (SeqID 16).
PN US2003050462-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 144
ID ADA37563 standard; protein; 673 AA.
DE Human secreted/transmembrane protein PRO1282.
PN US2003008297-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 145
ID ADA21249 standard; protein; 673 AA.
DE Human secreted/transmembrane polypeptide PRO1282.
PN US2003054404-A1.
PD 20-MAR-2003.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 146
ID ABO44246 standard; protein; 673 AA.
DE Human secreted/transmembrane polypeptide PRO 1282.
PN US2003018172-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 147
ID ADA10036 standard; protein; 673 AA.
DE Human secreted/transmembrane protein, PRO1282.
PN US2003059831-A1.
PD 27-MAR-2003.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 148
ID ADA19878 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003069394-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 149
ID ADB17261 standard; protein; 673 AA.
DE Human transmembrane PRO polypeptide (SeqID 16).
PN US2003050465-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 150
ID ADA17580 standard; protein; 673 AA.
DE Human PRO1282 polypeptide.
PN US2003054987-A1.
PD 20-MAR-2003.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 151
ID ADA27688 standard; protein; 673 AA.
DE Human secreted/transmembrane protein PRO1282.
PN US2003054359-A1.
PD 20-MAR-2003.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 152
ID ADA20050 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003055222-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 153
ID ABO34174 standard; protein; 673 AA.
DE Human secreted/transmembrane polypeptide PRO 1282.
PN US2003060601-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 154
ID ADA94268 standard; protein; 673 AA.
DE Human secreted/transmembrane protein PRO1282.
PN US2003059832-A1.
PD 27-MAR-2003.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 155
ID ADA38493 standard; protein; 673 AA.
DE Human secreted/transmembrane protein PRO1282.
PN US2003059780-A1.
PD 27-MAR-2003.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 156
ID ADA92614 standard; protein; 673 AA.
DE Human secreted/transmembrane protein PRO1282.
PN US2003060407-A1.
PD 27-MAR-2003.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 157
ID ADA00347 standard; protein; 673 AA.
DE Human secreted/transmembrane polypeptide PRO 1282.
PN US2003027992-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 158
ID ABO53118 standard; protein; 673 AA.
DE Human secreted/transmembrane protein PRO1282.
PN US2003044806-A1.
PD 06-MAR-2003.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 159
ID ADA22175 standard; protein; 673 AA.
DE Human secreted/transmembrane polypeptide PRO1282.
PN US2003040473-A1.
PD 27-FEB-2003.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 160
ID ABO22488 standard; protein; 673 AA.
DE Human secreted/transmembrane protein PRO1282.
PN US2003017982-A1.
PD 23-JAN-2003.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 161
ID ADA06341 standard; protein; 673 AA.
DE Human secreted/transmembrane PRO polypeptide #13.
PN US2003049638-A1.
PD 13-MAR-2003.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 162
ID ADA39034 standard; protein; 673 AA.
DE Human secreted/transmembrane protein PRO1282.
PN US2003059782-A1.
PD 27-MAR-2003.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;

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RESULT 163
ID ADB65589 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003049735-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 164
ID ADB96060 standard; protein; 673 AA.
DE Human PRO polypeptide #13.
PN US2003054403-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 165
ID ADB68268 standard; protein; 673 AA.
DE Human PRO1282 protein.
PN US2003065161-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 166
ID ADB68075 standard; protein; 673 AA.
DE Human PRO1282 protein.
PN US2003060600-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 167
ID ADB90892 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003083473-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 168
ID ADC57532 standard; protein; 673 AA.
DE Human PRO polypeptide #13.
PN US2003027754-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 169
ID ADC54896 standard; protein; 673 AA.
DE Human PRO polypeptide #13.
PN US2003045463-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 170
ID ADC11763 standard; protein; 673 AA.
DE Human secreted/transmembrane protein PRO1282.
PN US2003049681-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 171
ID ADC06972 standard; protein; 673 AA.
DE Human PRO1282 protein.
PN US2003060602-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 172
ID ADC56185 standard; protein; 673 AA.
DE Human PRO polypeptide #13.
PN US2003064375-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 173
ID ADC17151 standard; protein; 673 AA.
DE Mammalian PRO polypeptide (SeqID 16).
PN US2003065143-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 174
ID ADC07240 standard; protein; 673 AA.
DE Human secreted/transmembrane protein PRO1282.
PN US2003068647-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 175
ID ADC11230 standard; protein; 673 AA.
DE Human secreted/transmembrane protein PRO1282.
PN US2003069403-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 176
ID ADC14849 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003073208-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 177
ID ADC52344 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003138882-A1.
PD 24-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 178
ID ADC14352 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003082546-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 179
ID ADD07884 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003086623-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 180
ID ADC81709 standard; protein; 673 AA.
DE Human PRO polypeptide #13.
PN US2003083461-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 181
ID ADD07351 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2002193299-A1.
PD 19-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 182
ID ADC82242 standard; protein; 673 AA.
DE Human PRO polypeptide #13.
PN US2003059833-A1.
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PD 27-MAR-2003.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 183
ID ADD08422 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003073090-A1.
PD 17-APR-2003.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 184
ID ADD06671 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2002193300-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 185
ID ADC82918 standard; protein; 673 AA.
DE Human PRO polypeptide #13.
PN US2003059783-A1.
PD 27-MAR-2003.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 186
ID ADD55025 standard; protein; 673 AA.
DE Human PRO polypeptide #13.
PN US2003077593-A1.
PD 24-APR-2003.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 187
ID ADD36020 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003105298-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 188
ID ADD55983 standard; protein; 673 AA.
DE Human PRO polypeptide #13.
PN US2003077594-A1.
PD 24-APR-2003.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 189
ID ADD54421 standard; protein; 673 AA.
DE Human PRO polypeptide #13.
PN US2002132253-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 190
ID ADE26575 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003087304-A1.
PD 08-MAY-2003.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 191
ID ADE26042 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003087305-A1.
PD 08-MAY-2003.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 192
ID ADF66979 standard; protein; 673 AA.
DE Human PRO1282 amino acid sequence SEQ ID NO:52.
PN US2002198148-A1.

PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 193
ID ADG01021 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003078387-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 194
ID ADG08574 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180793-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 195
ID ADF95195 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180795-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 196
ID ADH24048 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180918-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 197
ID ADH34074 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180859-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 198
ID ADH29907 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180859-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 199
ID ADH23878 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180919-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 200
ID ADG85282 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180904-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 201
ID ADH24558 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180907-A1.
PD 25-SEP-2003.

Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 220
ID ADI2534 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181669-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 221
ID ADH9708 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181672-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 222
ID ADH9708 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181672-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 223
ID ADI35233 standard; protein; 673 AA.
DE Human PRO polypeptide #13.
PN US2003050457-A1.
PD 13-MAR-2003.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 224
ID ADI0356 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181656-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 225
ID ADH89987 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181697-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 226
ID ADH9725 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003049682-A1.
PD 13-MAR-2003.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 227
ID ADH98388 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181707-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 228
ID ADI11063 standard; protein; 673 AA.
DE Human PRO polypeptide #8.
PN US2003181682-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 229
ID ADI11573 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181684-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 230
ID ADH98218 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181709-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 231
ID ADH98558 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181708-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 232
ID ADH98048 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181673-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 233
ID ADI05036 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180848-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 234
ID ADI03386 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181654-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 235
ID ADI04781 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181657-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 236
ID ADH78235 standard; protein; 673 AA.
DE Human PRO polypeptide #8.
PN US2003181668-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 237
ID ADI19579 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181676-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 238
ID ADH90327 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.

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PN US2003181699-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 239
ID ADI03046 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181653-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 240
ID ADH77895 standard; protein; 673 AA.
DE Human PRO polypeptide #8.
PN US2003181666-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 241
ID ADH97878 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181674-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 242
ID ADI01263 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003190669-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 243
ID ADI01958 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181652-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 244
ID ADI03216 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181655-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 245
ID ADI11403 standard; protein; 673 AA.
DE Human PRO polypeptide #8.
PN US2003181681-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 246
ID ADI02305 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181650-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 247
ID ADI11743 standard; protein; 673 AA.
DE Human PRO polypeptide #8.
PN US2003181685-A1.
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PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 248
ID ADI05380 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003190716-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 249
ID ADH79452 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003191290-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 250
ID ADI19409 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181675-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 251
ID ADI05210 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181677-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 252
ID ADH79622 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003191288-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 253
ID ADI01448 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181678-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 254
ID ADI01618 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181679-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 255
ID ADI01788 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181680-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 256
ID ADH79792 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003191289-A1.
PD 09-OCT-2003.
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PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 257
ID ADI04610 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003171550-A1.
PD 11-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 258
ID ADI02746 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181651-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 259
ID ADH78065 standard; protein; 673 AA.
DE Human PRO polypeptide #8.
PN US2003181667-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 260
ID ADI25704 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181670-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 261
ID ADI25874 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181671-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 262
ID ADK65386 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003073821-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 263
ID ADH98728 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003191284-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 264
ID ADH79969 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003191287-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 265
ID ADL93700 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003040013-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.

Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 266
ID ADC52154 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003130483-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 267
ID ADF35178 standard; protein; 673 AA.
DE Human PRO1282 polypeptide.
PN US2003194760-A1.
PD 16-OCT-2003.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 268
ID ADG11428 standard; protein; 673 AA.
DE Human PRO1282 polypeptide.
PN US2003228655-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 269
ID ADH06586 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180852-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 270
ID ADH06416 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180853-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 271
ID ADG68837 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180855-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 272
ID ADH27727 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180912-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 273
ID ADH25068 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180913-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 274
ID ADH33700 standard; protein; 673 AA.
DE Human PRO polypeptide #8.
PN US2003181645-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 275
ID ADL93700 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003040013-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;

RESULT 275
ID ADH02343 standard; protein; 673 AA.
DE Human PRO polypeptide #8.
PN US2003180839-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 276
ID ADH07950 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180845-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 277
ID ADG69347 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180846-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 278
ID ADH39168 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180917-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 279
ID ADG83908 standard; protein; 673 AA.
DE Human PRO polypeptide #8.
PN US2003180842-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 280
ID ADH19298 standard; protein; 673 AA.
DE Human secreted/transmembrane protein PRO1282.
PN US2003228656-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 281
ID ADG85452 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003166848-A1.
PD 04-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 282
ID ADH06246 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180854-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 283
ID ADH30076 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180856-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 284
ID ADH20791 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180843-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 285
ID ADG69517 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180844-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 286
ID ADH07780 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180851-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 287
ID ADG85792 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180861-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 288
ID ADH39338 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180916-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 289
ID ADH33530 standard; protein; 673 AA.
DE Human PRO polypeptide #8.
PN US2003181637-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 290
ID ADH33870 standard; protein; 673 AA.
DE Human PRO polypeptide #8.
PN US2003181644-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 291
ID ADH01080 standard; protein; 673 AA.
DE Human PRO polypeptide #8.
PN US2003180838-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 292
ID ADG69687 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180843-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 293
ID ADH20791 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180843-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;

DE Human secreted/transmembrane protein PRO1282.
PN US20032243358-A1.
PD 04-DEC-2003.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 294
ID ADH02173 standard; protein; 673 AA.
DE Human PRO polypeptide #8.
PN US2003180841-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 295
ID ADG69177 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180847-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 296
ID ADG85962 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180862-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 297
ID ADH24898 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180909-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 298
ID ADH39515 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180915-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 299
ID ADH19831 standard; protein; 673 AA.
DE Human secreted/transmembrane protein PRO1282.
PN US2003219856-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 300
ID ADH02513 standard; protein; 673 AA.
DE Human PRO polypeptide #8.
PN US2003180840-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 301
ID ADG69007 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180849-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 302
ID ADH07610 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180850-A1.

PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 303
ID ADG86132 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180863-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 304
ID ADH24728 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180908-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 305
ID ADH25776 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180911-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 306
ID ADH38342 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180922-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 307
ID ADH57181 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181642-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 308
ID ADH52169 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180921-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 309
ID ADH49535 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180857-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 310
ID ADH90497 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181700-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 311
ID ADI11233 standard; protein; 673 AA.
DE Human PRO polypeptide #8.
PN US2003181683-A1.
PD 25-SEP-2003.

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PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 312
ID ADH9898 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003190698-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 313
ID ADI02128 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003190699-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 314
ID ADH98667 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181701-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 315
ID ADJ98542 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181797-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 316
ID ADJ98712 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003187228-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 317
ID ADH78871 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181703-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 318
ID ADJ99105 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003186408-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 319
ID ADJ99275 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003187196-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 320
ID ADJ98893 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003187242-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 10; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 321
ID ADH79041 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181702-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 322
ID ADK00901 standard; protein; 673 AA.
DE Human PRO polypeptide #8.
PN US2003186407-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 323
ID ADK14422 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003187229-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 324
ID ADM80871 standard; protein; 673 AA.
DE Human PRO polypeptide #8.
PN US2004058411-A1.
PD 25-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 325
ID ADR45587 standard; protein; 673 AA.
DE Human leucine-rich surface glycoprotein, LRSG-1, protein #1.
PN US2004176296-A1.
PD 03-SEP-2004.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 326
ID ADY77711 standard; protein; 673 AA.
DE Neoplastic disease detection protein PRO1282.
PN US2005059102-A1.
PD 17-MAR-2005.
PA (EATO/) EATON D L.
PA (FILV/) FILVAROFF E.
PA (GERE/) GERITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI J C.
PA (GURN/) GURNEY A L.
PA (WATA/) WATANABE C K.
PA (WOOD/) WOOD W I.
Query Match 98.4%; Score 3083.5; DB 9; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 327
ID AEA38367 standard; protein; 673 AA.
DE Human secreted/transmembrane protein, #81.
PN US2005112725-A1.
PD 26-MAY-2005.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 9; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 328
ID AEF12542 standard; protein; 673 AA.
DE Human PRO1282 protein SEQ ID NO:16.
PN US2006008901-A1.
PD 12-JAN-2006.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 10; Length 673;
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Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 329
ID AEF74231 standard; protein; 673 AA.
DE Human PRO1282 protein SEQ ID NO:16.
PN US2005260647-A1.
PD 24-NOV-2005.
PA (EATO/) EATON D L.
PA (FILV/) FILVAROFF E.
PA (GERK/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODG/) GODOWSKI P J.
PA (GRIM/) GRIMALDI J C.
PA (GURN/) GURNEY A L.
PA (WATA/) WATANABE C K.
PA (WOOD/) WOOD W L.
Query Match 98.4%; Score 3083.5; DB 10; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 330
ID AAB84689 standard; protein; 673 AA.
DE Amino acid sequence of human slit polypeptide Zslit3.
PN WO200148418-A1.
PD 28-JUN-2001.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 98.2%; Score 3078.5; DB 4; Length 673;
Best Local Similarity 88.6%; Pred. No. 1.8e-186;
RESULT 331
ID ADF69108 standard; protein; 673 AA.
DE Human MP53 protein sequence SEQ ID NO:78.
PN WO2003083047-A2.
PD 09-OCT-2003.
PA (EXEL-) EXELIXIS INC.
Query Match 98.2%; Score 3078.5; DB 7; Length 673;
Best Local Similarity 88.6%; Pred. No. 1.8e-186;
RESULT 332
ID ABO59449 standard; protein; 676 AA.
DE Human genome derived single exon protein #5683.
PN US2003194704-A1.
PD 16-OCT-2003.
PA (PENN/) PENN S G.
PA (RANK/) RANK D R.
PA (HANZ/) HANZEL D K.
Query Match 98.2%; Score 3078.5; DB 8; Length 676;
Best Local Similarity 88.6%; Pred. No. 1.8e-186;
RESULT 333
ID ADA57213 standard; protein; 672 AA.
DE Human secreted protein #496.
PN WO2002102994-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 93.6%; Score 2935; DB 6; Length 672;
Best Local Similarity 85.2%; Pred. No. 2.2e-177;
RESULT 334
ID ADA41092 standard; protein; 672 AA.
DE Human secreted protein.
PN WO2002102993-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 93.6%; Score 2935; DB 6; Length 672;
Best Local Similarity 85.2%; Pred. No. 2.2e-177;
RESULT 335
ID ABR47923 standard; protein; 672 AA.
DE Human secreted protein, SEQ ID 814.
PN WO200295010-A2.
PD 28-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 93.6%; Score 2935; DB 6; Length 672;
Best Local Similarity 85.2%; Pred. No. 2.2e-177;
RESULT 336
ID AAB38323 standard; protein; 673 AA.
DE Human secreted protein encoded by gene 3 clone HSYAV50.
PN WO200061623-A1.
PD 19-OCT-2000.
PA (HUMA-) HUMAN GENOME SCI INC.

Query Match 93.6%; Score 2935; DB 3; Length 673;
Best Local Similarity 85.2%; Pred. No. 2.2e-177;
RESULT 337
ID AAB38400 standard; peptide; 723 AA.
DE Fragment of human secreted protein encoded by gene 3 clone HSYAV50.
PN WO200061623-A1.
PD 19-OCT-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 93.6%; Score 2935; DB 3; Length 723;
Best Local Similarity 85.2%; Pred. No. 2.4e-177;
RESULT 338
ID AAU75267 standard; protein; 630 AA.
DE Human slit-like protein #2.
PN WO200212346-A2.
PD 14-FEB-2002.
PA (PHAA) PHARMACIA CORP.
Query Match 90.8%; Score 2845.5; DB 5; Length 630;
Best Local Similarity 85.2%; Pred. No. 9.4e-172;
RESULT 339
ID AAY66643 standard; protein; 611 AA.
DE Membrane-bound protein PRO1282.
PN WO9963088-A2.
PD 09-DEC-1999.
PA (GETH) GENENTECH INC.
Query Match 86.5%; Score 2712.5; DB 3; Length 611;
Best Local Similarity 79.5%; Pred. No. 2.4e-163;
RESULT 340
ID ABG78046 standard; protein; 673 AA.
DE Mouse leucine-rich surface glycoprotein (LRSG-1).
PN US2002072089-A1.
PD 13-JUN-2002.
PA (HOLT/) HOLTZMAN D A.
PA (MCCA/) MCCARTHY S A.
PA (MACB/) MACBETH K J.
PA (BUSF/) BUSFIELD S J.
PA (PANY/) PAN Y.
PA (WHIT/) WHITE D.
PA (KHOD/) KHODADOUST M M.
PA (GUWW/) GU W.
Query Match 79.4%; Score 2490; DB 5; Length 673;
Best Local Similarity 73.5%; Pred. No. 3.4e-149;
RESULT 341
ID ADR45596 standard; protein; 673 AA.
DE Human leucine-rich surface glycoprotein, LRSG-1, protein #2.
PN US2004176296-A1.
PD 09-SEP-2004.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 79.4%; Score 2490; DB 8; Length 673;
Best Local Similarity 73.5%; Pred. No. 3.4e-149;
RESULT 342
ID ADA00753 standard; protein; 673 AA.
DE Murine stromal cell derived haematopoietin factor-5 SEQ ID NO:10.
PN WO2003018805-A1.
PD 06-MAR-2003.
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
PA (NINA-) JAPAN NAT CANCER CENT.
Query Match 79.2%; Score 2484; DB 6; Length 673;
Best Local Similarity 73.4%; Pred. No. 8.1e-149;
RESULT 343
ID AAB07431 standard; protein; 493 AA.
DE A leucine-rich surface glycoprotein (LRSG).
PN WO200042170-A1.
PD 20-JUL-2000.
PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
Query Match 53.3%; Score 1672; DB 3; Length 493;
Best Local Similarity 53.3%; Pred. No. 1.6e-97;
RESULT 344
ID ABB72324 standard; protein; 281 AA.
DE Rat protein isolated from skin cells SEQ ID NO: 648.
PN WO200190357-A1.
PD 29-NOV-2001.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match 37.6%; Score 1178.5; DB 5; Length 281;

Best Local Similarity 80.7%; Pred. No. 1.5e-66;
RESULT 345
ID AAO30403 standard; protein; 311 AA.
DE Human secreted protein (SECP)-6.
PN WO2003046196-A1.
PD 05-JUN-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 31.8%; Score 997.5; DB 7; Length 311;
Best Local Similarity 68.7%; Pred. No. 4.9e-55;
RESULT 346
ID ABR58506 standard; protein; 307 AA.
DE Human secreted protein Incyte ID No: 7500228CD1 SEQ ID NO: 18.
PN WO2003029437-A2.
PD 10-APR-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 31.3%; Score 980.5; DB 6; Length 307;
Best Local Similarity 67.9%; Pred. No. 5.8e-54;
RESULT 347
ID AAO30821 standard; protein; 117 AA.
DE Human cell adhesion and extracellular matrix protein (CADECM)-11.
PN WO2003047526-A2.
PD 12-JUN-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 15.0%; Score 471; DB 7; Length 117;
Best Local Similarity 98.9%; Pred. No. 3.5e-22;
RESULT 348
ID AAE23980 standard; protein; 635 AA.
DE Human LP220 secreted protein.
PN WO200226801-A2.
PD 04-APR-2002.
PA (ELIL) LILLY & CO ELI.
Query Match 11.5%; Score 360.5; DB 5; Length 635;
Best Local Similarity 27.1%; Pred. No. 2.6e-14;
RESULT 349
ID ABP70142 standard; protein; 647 AA.
DE Human NOV44a.
PN WO200272771-A2.
PD 19-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 11.5%; Score 360.5; DB 5; Length 647;
Best Local Similarity 27.1%; Pred. No. 2.6e-14;
RESULT 350
ID AAO26256 standard; protein; 635 AA.
DE MDDT related human protein SEQ ID No 34.
PN WO200296951-A1.
PD 05-DEC-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 11.5%; Score 359.5; DB 6; Length 635;
Best Local Similarity 27.6%; Pred. No. 3e-14;
RESULT 351
ID AD209859 standard; protein; 635 AA.
DE Human breast cancer marker MGC3103 protein.
PN EP1522594-A2.
PD 13-APR-2005.
PA (FARB) BAYER HEALTHCARE AG.
Query Match 11.5%; Score 359.5; DB 9; Length 635;
Best Local Similarity 27.6%; Pred. No. 3e-14;
RESULT 352
ID ABP70144 standard; protein; 778 AA.
DE Human NOV44c.
PN WO200272771-A2.
PD 19-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 11.4%; Score 357.5; DB 5; Length 778;
Best Local Similarity 26.7%; Pred. No. 5e-14;
RESULT 353
ID ADM90979 standard; protein; 545 AA.
DE Human pharmaceutically useful protein SeqID 372.
PN WO2004020595-A2.
PD 11-MAR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
PA (RIKE-) RIKEN INST PHYSICAL & CHEM RES.
PA (DNAP-) DNAPFORM KK.

Query Match 11.2%; Score 350.5; DB 8; Length 545;
Best Local Similarity 27.9%; Pred. No. 9.2e-14;
RESULT 354
ID ABP70143 standard; protein; 566 AA.
DE Human NOV44b.
PN WO200272771-A2.
PD 19-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 10.8%; Score 339; DB 5; Length 566;
Best Local Similarity 26.9%; Pred. No. 5.1e-13;
RESULT 355
ID AAE17484 standard; protein; 551 AA.
DE Human leucine-rich repeat-8 (ZLRR8) protein #2.
PN WO200202604-A2.
PD 10-JAN-2003.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 10.8%; Score 338; DB 5; Length 551;
Best Local Similarity 27.4%; Pred. No. 5.8e-13;
RESULT 356
ID ADI21104 standard; protein; 618 AA.
DE Novel human protein #79.
PN WO2003025148-A2.
PD 27-MAR-2003.
PA (HYSE-) HYSEQ INC.
Query Match 10.7%; Score 337; DB 7; Length 618;
Best Local Similarity 27.2%; Pred. No. 7.6e-13;
RESULT 357
ID ADA23287 standard; protein; 653 AA.
DE Human SECX polypeptide, SEC5 #1.
PN US2003054514-A1.
PD 20-MAR-2003.
PA (SHIM/) SHIMKETS R A.
PA (LARO/) LAROCHELLE W J.
Query Match 10.7%; Score 337; DB 6; Length 653;
Best Local Similarity 23.6%; Pred. No. 8.1e-13;
RESULT 358
ID AAB23033 standard; protein; 694 AA.
DE Human SLIT protein-like splice variant, SECX 3352358-1.
PN WO200053742-A2.
PD 14-SEP-2000.
PA (CURA-) CURAGEN CORP.
Query Match 10.7%; Score 337; DB 3; Length 694;
Best Local Similarity 23.6%; Pred. No. 8.7e-13;
RESULT 359
ID AAB23034 standard; protein; 590 AA.
DE Human SLIT protein-like splice variant, SECX 3352358-2.
PN WO200053742-A2.
PD 14-SEP-2000.
PA (CURA-) CURAGEN CORP.
Query Match 10.6%; Score 333; DB 3; Length 590;
Best Local Similarity 25.8%; Pred. No. 1.3e-12;
RESULT 360
ID ADA23289 standard; protein; 590 AA.
DE Human SECX polypeptide, SEC6.
PN US2003054514-A1.
PD 20-MAR-2003.
PA (SHIM/) SHIMKETS R A.
PA (LARO/) LAROCHELLE W J.
Query Match 10.6%; Score 333; DB 6; Length 590;
Best Local Similarity 25.8%; Pred. No. 1.3e-12;
RESULT 361
ID AAG04827 standard; protein; 526 AA.
DE Novel human diagnostic protein #4818.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 10.6%; Score 332; DB 4; Length 526;
Best Local Similarity 26.9%; Pred. No. 1.3e-12;
RESULT 362
ID AAY28806 standard; protein; 653 AA.
DE CC359.4 secreted protein.
PN WO9950405-A1.
PD 07-OCT-1999.

PA (GEMY) GENETICS INST INC.
 Query Match 10.5%; Score 330; DB 2; Length 653;
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;
 RESULT 363
 ID AAY66694 standard; protein; 653 AA.
 DE Membrane-bound protein PRO1111.
 PN WO963088-A2.
 PD 09-DEC-1999.
 PA (GETH) GENENTECH INC.
 Query Match 10.5%; Score 330; DB 3; Length 653;
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;
 RESULT 364
 ID AAB24073 standard; protein; 653 AA.
 DE Human PRO1111 protein sequence SEQ ID NO:46.
 PN WO200053755-A2.
 PD 14-SEP-2000.
 PA (GETH) GENENTECH INC.
 Query Match 10.5%; Score 330; DB 3; Length 653;
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;
 RESULT 365
 ID AAU12390 standard; protein; 653 AA.
 DE Human PRO1111 polypeptide sequence.
 PN WO200140466-A2.
 PD 07-JUN-2001.
 PA (GETH) GENENTECH INC.
 Query Match 10.5%; Score 330; DB 4; Length 653;
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;
 RESULT 366
 ID AAEO9438 standard; protein; 653 AA.
 DE Human sbgPRO331a protein.
 PN WO200160850-A1.
 PD 23-AUG-2001.
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 Query Match 10.5%; Score 330; DB 4; Length 653;
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;
 RESULT 367
 ID AAB5217 standard; protein; 653 AA.
 DE Human PRO1111 (UNQ554) protein sequence SEQ ID NO:229.
 PN WO200073454-A1.
 PD 07-DEC-2000.
 PA (GETH) GENENTECH INC.
 Query Match 10.5%; Score 330; DB 4; Length 653;
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;
 RESULT 368
 ID ABUS8032 standard; protein; 653 AA.
 DE Human PRO polypeptide #64.
 PN US2003027163-A1.
 PD 06-FEB-2003.
 Query Match 10.5%; Score 330; DB 6; Length 653;
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;
 RESULT 369
 ID ABUS9110 standard; protein; 653 AA.
 DE Novel human secreted or transmembrane protein PRO1111.
 PN US2002132252-A1.
 PD 19-SEP-2002.
 PA (GETH) GENENTECH INC.
 Query Match 10.5%; Score 330; DB 6; Length 653;
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;
 RESULT 370
 ID ABUS9257 standard; protein; 653 AA.
 DE Human secreted/transmembrane protein PRO1111.
 PN US2003032023-A1.
 PD 13-FEB-2003.
 Query Match 10.5%; Score 330; DB 6; Length 653;
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;
 RESULT 371
 ID ABO17834 standard; protein; 653 AA.
 DE Novel human secreted and transmembrane protein PRO1111.
 PN US2003032156-A1.
 PD 13-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 10.5%; Score 330; DB 6; Length 653;
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;
 RESULT 372
 ID ABUS9257 standard; protein; 653 AA.
 DE Human secreted/transmembrane protein, #93.
 PN US2002160384-A1.
 PD 31-OCT-2002.
 PA (GETH) GENENTECH INC.
 Query Match 10.5%; Score 330; DB 6; Length 653;
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;
 RESULT 373
 ID ABUI3923 standard; protein; 653 AA.
 DE Human PRO1111 polypeptide.
 PN US2002103125-A1.
 PD 01-AUG-2002.
 PA (GETH) GENENTECH LTD.
 Query Match 10.5%; Score 330; DB 6; Length 653;
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;
 RESULT 374
 ID ABUI1088 standard; protein; 653 AA.
 DE Human PRO polypeptide #219.
 PN US2003004311-A1.
 PD 02-JAN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 10.5%; Score 330; DB 6; Length 653;
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;
 RESULT 375
 ID ABU72508 standard; protein; 653 AA.
 DE Novel human secreted and transmembrane protein PRO1111.
 PN US2003003531-A1.
 PD 02-JAN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 10.5%; Score 330; DB 6; Length 653;
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;
 RESULT 376
 ID ABUS6788 standard; protein; 653 AA.
 DE Human PRO polypeptide #219.
 PN US2003036180-A1.
 PD 20-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 10.5%; Score 330; DB 6; Length 653;
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;
 RESULT 377
 ID AAO23105 standard; protein; 653 AA.
 DE NAG14 'human modifier of p53 pathway' protein.
 PN WO2003035833-A2.
 PD 01-MAY-2003.
 PA (EXEL-) EXELIXIS INC.
 Query Match 10.5%; Score 330; DB 6; Length 653;
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;
 RESULT 378
 ID ABUS9869 standard; protein; 653 AA.
 DE Novel secreted and transmembrane protein PRO1111.
 PN US2003017563-A1.
 PD 23-JAN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 10.5%; Score 330; DB 6; Length 653;
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;
 RESULT 379
 ID ABUS9257 standard; protein; 653 AA.
 DE Human secreted/transmembrane protein, #93.
 PN US2003027162-A1.
 PD 06-FEB-2003.
 Query Match 10.5%; Score 330; DB 6; Length 653;
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;
 RESULT 380
 ID ABO25954 standard; protein; 653 AA.
 DE Human PRO1111 polypeptide.
 PN US2002127576-A1.
 PD 12-SEP-2002.
 PA (GETH) GENENTECH INC.
 Query Match 10.5%; Score 330; DB 6; Length 653;
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;
 RESULT 381
 ID ABO25954 standard; protein; 653 AA.
 DE Human secreted and transmembrane protein PRO1111.
 PN US2003032156-A1.
 PD 13-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 10.5%; Score 330; DB 6; Length 653;
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;

ID ABO25059 standard; protein; 653 AA.
DE Human secreted/transmembrane protein (PRO) #219.
PN US2003036179-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 382
ID ABUS8963 standard; protein; 653 AA.
DE Human secreted/transmembrane protein, #93.
PN US2002142961-A1.
PD 03-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 383
ID ABUS9406 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003022187-A1.
PD 30-JAN-2003.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 384
ID ABUS9406 standard; protein; 653 AA.
DE Human secreted or transmembrane protein PRO1344.
PN US2003027985-A1.
PD 06-FEB-2003.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 385
ID ABUS9406 standard; protein; 653 AA.
DE Human secreted/transmembrane, PRO, protein SEQ ID 438.
PN US2003032155-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 386
ID ABUS9406 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003017476-A1.
PD 23-JAN-2003.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 387
ID ABUS9406 standard; protein; 653 AA.
DE Human PRO polypeptide #64.
PN US2002123463-A1.
PD 05-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 388
ID ABUS9406 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2002171164-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 389
ID ABUS9406 standard; protein; 653 AA.
DE Human secreted and transmembrane polypeptide PRO1111.
PN US2002197615-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 390
ID ABO34083 standard; protein; 653 AA.
DE Human PRO1111 polypeptide.
PN US2003017981-A1.
PD 23-JAN-2003.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 391
ID ADA45957 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003022328-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 392
ID ADA76388 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003073212-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 393
ID ADA19038 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003054517-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 394
ID ADA61661 standard; protein; 653 AA.
DE Homo sapiens.
PN US2003049816-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 395
ID ADB19446 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003088796-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 396
ID ADB27987 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003082704-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 397
ID ADA86466 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003082711-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 398
ID ADB16030 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003087350-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 399
ID ADA37740 standard; protein; 653 AA.
DE Human secreted/transmembrane protein PRO1111.
PN US2003008297-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;

Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 400
ID ADA47816 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003073215-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 401
ID ADA21426 standard; protein; 653 AA.
DE Human secreted/transmembrane polypeptide PRO1111.
PN US2003054404-A1.
PD 20-MAR-2003.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 402
ID ADA10213 standard; protein; 653 AA.
DE Human secreted/transmembrane protein, PRO1111.
PN US2003059831-A1.
PD 27-MAR-2003.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 403
ID ADA67611 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003068795-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 404
ID ADB30618 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003068794-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 405
ID ADA85914 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003082693-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 406
ID ADA17757 standard; protein; 653 AA.
DE Human PRO1111 polypeptide.
PN US2003054987-A1.
PD 20-MAR-2003.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 407
ID ADA97126 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003082705-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 408
ID ADA79430 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003082763-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 409
ID ADA87569 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003044945-A1.
PD 06-MAR-2003.

PN US2003087345-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 410
ID ADB16771 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003087349-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 411
ID ADA27865 standard; protein; 653 AA.
DE Human secreted/transmembrane protein PRO1111.
PN US2003054359-A1.
PD 20-MAR-2003.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 412
ID ADA31863 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003082694-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 413
ID ADB14926 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003087351-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 414
ID ADB18887 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003073211-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 415
ID ADA94102 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003077722-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 416
ID ADB19998 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003082691-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 417
ID ADB13310 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003082710-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 418
ID ABO43367 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003044945-A1.
PD 06-MAR-2003.

PA (GETH) GENENTECH INC.
 Query Match 10.5%; Score 330; DB 6; Length 653;
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;
 RESULT 419
 ID ADA94445 standard; protein; 653 AA.
 DE Human secreted/transmembrane protein PRO1111.
 PN US2003059832-A1.
 PD 27-MAR-2003.
 Query Match 10.5%; Score 330; DB 6; Length 653;
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;
 RESULT 420
 ID ADA74564 standard; protein; 653 AA.
 DE Human PRO polypeptide #219.
 PN US2003068798-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 10.5%; Score 330; DB 6; Length 653;
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;
 RESULT 421
 ID ADB24797 standard; protein; 653 AA.
 DE Human PRO polypeptide SEQ ID NO 438.
 PN US200307713-A1.
 PD 24-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 10.5%; Score 330; DB 6; Length 653;
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;
 RESULT 422
 ID ADA82321 standard; protein; 653 AA.
 DE Human PRO polypeptide #219.
 PN US2003082701-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 10.5%; Score 330; DB 6; Length 653;
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;
 RESULT 423
 ID ADA75284 standard; protein; 653 AA.
 DE Human PRO polypeptide #219.
 PN US2003073216-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 10.5%; Score 330; DB 6; Length 653;
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;
 RESULT 424
 ID ADA8362 standard; protein; 653 AA.
 DE Novel human secreted and transmembrane protein PRO1111.
 PN US2003082695-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 10.5%; Score 330; DB 6; Length 653;
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;
 RESULT 425
 ID ADA84810 standard; protein; 653 AA.
 DE Novel human secreted and transmembrane protein PRO1111.
 PN US2003082708-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 10.5%; Score 330; DB 6; Length 653;
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;
 RESULT 426
 ID ADB30066 standard; protein; 653 AA.
 DE Human PRO polypeptide #219.
 PN US2003073214-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 10.5%; Score 330; DB 6; Length 653;
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;
 RESULT 427
 ID ADA80594 standard; protein; 653 AA.
 DE Human PRO polypeptide #219.
 PN US2003082761-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 10.5%; Score 330; DB 6; Length 653;
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;
 RESULT 428
 ID ADA75836 standard; protein; 653 AA.
 DE Human PRO polypeptide #219.
 PN US2003082703-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 10.5%; Score 330; DB 6; Length 653;
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;
 RESULT 429
 ID ADA38670 standard; protein; 653 AA.
 DE Human secreted/transmembrane protein PRO1111.
 PN US2003059780-A1.
 PD 27-MAR-2003.
 Query Match 10.5%; Score 330; DB 6; Length 653;
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;
 RESULT 430
 ID ADA47061 standard; protein; 653 AA.
 DE Human PRO polypeptide #219.
 PN US2003073210-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 10.5%; Score 330; DB 6; Length 653;
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;
 RESULT 431
 ID ADB25357 standard; protein; 653 AA.
 DE Human PRO polypeptide SEQ ID NO 438.
 PN US200307715-A1.
 PD 24-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 10.5%; Score 330; DB 6; Length 653;
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;
 RESULT 432
 ID ADA93533 standard; protein; 653 AA.
 DE Human PRO polypeptide #219.
 PN US200307721-A1.
 PD 24-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 10.5%; Score 330; DB 6; Length 653;
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;
 RESULT 433
 ID ADB26883 standard; protein; 653 AA.
 DE Human PRO polypeptide #219.
 PN US2003092147-A1.
 PD 15-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 10.5%; Score 330; DB 6; Length 653;
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;
 RESULT 434
 ID ADB31170 standard; protein; 653 AA.
 DE Human PRO polypeptide #219.
 PN US2003096386-A1.
 PD 22-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 10.5%; Score 330; DB 6; Length 653;
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;
 RESULT 435
 ID ADA92791 standard; protein; 653 AA.
 DE Human secreted/transmembrane protein PRO1111.
 PN US2003060407-A1.
 PD 27-MAR-2003.
 Query Match 10.5%; Score 330; DB 6; Length 653;
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;
 RESULT 436
 ID ADA61098 standard; protein; 653 AA.
 DE Homo sapiens.
 PN US2003049817-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 10.5%; Score 330; DB 6; Length 653;
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;
 RESULT 437
 ID ADB24245 standard; protein; 653 AA.

DE Human PRO polypeptide SEQ ID NO 438.
 PN US2003077714-A1.
 PD 24-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 10.5%; Score 330; DB 6; Length 653;
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;
 RESULT 438
 ID ADA96574 standard; protein; 653 AA.
 DE Human PRO polypeptide #219.
 PN US2003082690-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 10.5%; Score 330; DB 6; Length 653;
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;
 RESULT 439
 ID ADA81146 standard; protein; 653 AA.
 DE Human PRO polypeptide #219.
 PN US2003082702-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 10.5%; Score 330; DB 6; Length 653;
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;
 RESULT 440
 ID ADA96022 standard; protein; 653 AA.
 DE Human PRO polypeptide #219.
 PN US2003082759-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 10.5%; Score 330; DB 6; Length 653;
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;
 RESULT 441
 ID ADB26331 standard; protein; 653 AA.
 DE Human PRO polypeptide #219.
 PN US2003082760-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 10.5%; Score 330; DB 6; Length 653;
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;
 RESULT 442
 ID ADB21816 standard; protein; 653 AA.
 DE Novel human secreted and transmembrane protein PRO1111.
 PN US2003082765-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 10.5%; Score 330; DB 6; Length 653;
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;
 RESULT 443
 ID ADA77595 standard; protein; 653 AA.
 DE Human PRO polypeptide #219.
 PN US2003068797-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 10.5%; Score 330; DB 7; Length 653;
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;
 RESULT 444
 ID ADB18335 standard; protein; 653 AA.
 DE Human PRO polypeptide #219.
 PN US2003077710-A1.
 PD 24-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 10.5%; Score 330; DB 7; Length 653;
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;
 RESULT 445
 ID ADA87018 standard; protein; 653 AA.
 DE Novel human secreted and transmembrane protein PRO1111.
 PN US2003082709-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 10.5%; Score 330; DB 7; Length 653;
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;
 RESULT 446
 ID ADA88121 standard; protein; 653 AA.
 DE Novel human secreted and transmembrane protein PRO1111.

PN US2003082700-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 10.5%; Score 330; DB 7; Length 653;
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;
 RESULT 447
 ID ADA46509 standard; protein; 653 AA.
 DE Novel human secreted and transmembrane protein PRO1111.
 PN US2003054516-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 10.5%; Score 330; DB 7; Length 653;
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;
 RESULT 448
 ID ADB28539 standard; protein; 653 AA.
 DE Human PRO polypeptide #219.
 PN US2003082699-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 10.5%; Score 330; DB 7; Length 653;
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;
 RESULT 449
 ID ADB29091 standard; protein; 653 AA.
 DE Human PRO polypeptide #219.
 PN US2003082706-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 10.5%; Score 330; DB 7; Length 653;
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;
 RESULT 450
 ID ABO53169 standard; protein; 653 AA.
 DE Human secreted/transmembrane protein PRO1111.
 PN US2003044806-A1.
 PD 06-MAR-2003.
 Query Match 10.5%; Score 330; DB 7; Length 653;
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;
 RESULT 451
 ID ADA77043 standard; protein; 653 AA.
 DE Human PRO polypeptide #219.
 PN US2003059909-A1.
 PD 27-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 10.5%; Score 330; DB 7; Length 653;
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;
 RESULT 452
 ID ADA22352 standard; protein; 653 AA.
 DE Human secreted/transmembrane polypeptide PRO1111.
 PN US2003040473-A1.
 PD 27-FEB-2003.
 Query Match 10.5%; Score 330; DB 7; Length 653;
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;
 RESULT 453
 ID ADA88673 standard; protein; 653 AA.
 DE Novel human secreted and transmembrane protein PRO1111.
 PN US2003073213-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 10.5%; Score 330; DB 7; Length 653;
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;
 RESULT 454
 ID ADA97678 standard; protein; 653 AA.
 DE Human PRO polypeptide #219.
 PN US2003082686-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 10.5%; Score 330; DB 7; Length 653;
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;
 RESULT 455
 ID ADB27435 standard; protein; 653 AA.
 DE Human PRO polypeptide #219.
 PN US2003022399-A1.
 PD 30-JAN-2003.
 Query Match 10.5%; Score 330; DB 7; Length 653;

Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 456
ID ADB22368 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003087344-A1.
PD 08-MAY-2003.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 457
ID ABO22539 standard; protein; 653 AA.
DE Human secreted/transmembrane protein PRO1111.
PN US2003017982-A1.
PD 23-JAN-2003.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 458
ID ADA06518 standard; protein; 653 AA.
DE Human secreted/transmembrane PRO polypeptide #64.
PN US2003049638-A1.
PD 13-MAR-2003.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 459
ID ADA39211 standard; protein; 653 AA.
DE Human secreted/transmembrane protein PRO1111.
PN US2003059782-A1.
PD 27-MAR-2003.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 460
ID ADA67059 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003068793-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 461
ID ADB22920 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US200307711-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 462
ID ADB23693 standard; protein; 653 AA.
DE Human PRO polypeptide SEQ ID NO 438.
PN US2003077712-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 463
ID ADA92415 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003082712-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 464
ID ADB15478 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003087352-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 465
ID ADB38730 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003082766-A1.

PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 466
ID ADB96237 standard; protein; 653 AA.
DE Human PRO polypeptide #64.
PN US2003054403-A1.
PD 20-MAR-2003.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 467
ID ADB38178 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003087347-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 468
ID ADB66650 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003082689-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 469
ID ADB89730 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003082698-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 470
ID ADB90462 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003082762-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 471
ID ADB35563 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003082764-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 472
ID ADB47186 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003082687-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 473
ID ADB86793 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003082697-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 474
ID ADB77398 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003082696-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.

Query Match
Best Local Similarity 10.5%; Score 330; DB 7; Length 653;
RESULT 475
ID ADB34555 standard; protein; 653 AA.
DE Human PRO polypeptide SEQ ID NO 438.
PN US200307717-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 10.5%; Score 330; DB 7; Length 653;
RESULT 476
ID ADB35659 standard; protein; 653 AA.
DE Human PRO polypeptide SEQ ID NO 438.
PN US200307719-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 10.5%; Score 330; DB 7; Length 653;
RESULT 477
ID ADB34003 standard; protein; 653 AA.
DE Human PRO polypeptide SEQ ID NO 438.
PN US200307716-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 10.5%; Score 330; DB 7; Length 653;
RESULT 478
ID ADB35107 standard; protein; 653 AA.
DE Human PRO polypeptide SEQ ID NO 438.
PN US200307718-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 10.5%; Score 330; DB 7; Length 653;
RESULT 479
ID ADB36211 standard; protein; 653 AA.
DE Human PRO polypeptide SEQ ID NO 438.
PN US200307720-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 10.5%; Score 330; DB 7; Length 653;
RESULT 480
ID ADB46606 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003082692-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 10.5%; Score 330; DB 7; Length 653;
RESULT 481
ID ADC57709 standard; protein; 653 AA.
DE Human PRO polypeptide #64.
PN US2003027754-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 10.5%; Score 330; DB 7; Length 653;
RESULT 482
ID ADC55073 standard; protein; 653 AA.
DE Human PRO polypeptide #64.
PN US2003045463-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 10.5%; Score 330; DB 7; Length 653;
RESULT 483
ID ADC11940 standard; protein; 653 AA.
DE Human secreted/transmembrane protein PRO1111.
PN US2003049681-A1.
PD 13-MAR-2003.
Query Match
Best Local Similarity 10.5%; Score 330; DB 7; Length 653;
RESULT 484
ID ADC56362 standard; protein; 653 AA.

DE Human PRO polypeptide #64.
PN US2003064375-A1.
PD 03-APR-2003.
Query Match
Best Local Similarity 10.5%; Score 330; DB 7; Length 653;
RESULT 485
ID ADC07417 standard; protein; 653 AA.
DE Human secreted/transmembrane protein PRO1111.
PN US2003088647-A1.
PD 10-APR-2003.
Query Match
Best Local Similarity 10.5%; Score 330; DB 7; Length 653;
RESULT 486
ID ADC11407 standard; protein; 653 AA.
DE Human secreted/transmembrane protein PRO1111.
PN US2003069403-A1.
PD 10-APR-2003.
Query Match
Best Local Similarity 10.5%; Score 330; DB 7; Length 653;
RESULT 487
ID ADC50479 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003092106-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 10.5%; Score 330; DB 7; Length 653;
RESULT 488
ID ADC72026 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003092107-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 10.5%; Score 330; DB 7; Length 653;
RESULT 489
ID ADC60005 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003092105-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 10.5%; Score 330; DB 7; Length 653;
RESULT 490
ID ADC33012 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein Seq ID438.
PN US2003087365-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 10.5%; Score 330; DB 7; Length 653;
RESULT 491
ID ADC57366 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein Seq ID438.
PN US2003087366-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 10.5%; Score 330; DB 7; Length 653;
RESULT 492
ID ADC60557 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003087367-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 10.5%; Score 330; DB 7; Length 653;
RESULT 493
ID ADC51032 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003087361-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.

Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 494
ID ADC65559 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003087348-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 495
ID ADC54657 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein Seq ID438.
PN US2003087362-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 496
ID ADC53618 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein Seq ID438.
PN US2003087364-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 497
ID ADC59141 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein Seq ID438.
PN US2003087359-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 498
ID ADC56019 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein Seq ID438.
PN US2003087360-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 499
ID ADC58589 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein Seq ID438.
PN US2003087346-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 500
ID ADC14529 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003082546-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 501
ID ADD08061 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003068623-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 502
ID ADD03263 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003092104-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 503
ID ADC90255 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003087348-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 504
ID ADC81886 standard; protein; 653 AA.
DE Human PRO polypeptide #64.
PN US2003083461-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 505
ID ADC69674 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003194770-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 506
ID ADC48563 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003194773-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 507
ID ADD10092 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003194776-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 508
ID ADD07528 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2002193299-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 509
ID ADD04667 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003087354-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 510
ID ADC82419 standard; protein; 653 AA.
DE Human PRO polypeptide #64.
PN US2003059833-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 511
ID ADC80623 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003092103-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 512
ID ADD11130 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003194774-A1.

Best Local Similarity 24.3%; Pred. No. 2.3e-12; Length 653;
ID ADD53684 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003203437-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 522
ID ADD55202 standard; protein; 653 AA.
DE Human PRO polypeptide #64.
PN US2003077593-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 523
ID ADD56160 standard; protein; 653 AA.
DE Human PRO polypeptide #64.
PN US2003077594-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 524
ID ADD51840 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003194779-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 525
ID ADD02639 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US20031203431-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 526
ID ADD02073 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003203430-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 527
ID ADD54255 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003203432-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 528
ID ADD54598 standard; protein; 653 AA.
DE Human PRO polypeptide #64.
PN US2002132253-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 529
ID ADD92572 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003199030-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 530
ID ADD91468 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003194792-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.

Best Local Similarity 24.3%; Pred. No. 2.3e-12; Length 653;
ID ADD53684 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003203437-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 513
ID ADC48011 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003194771-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 514
ID ADD08599 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003073090-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 515
ID ADC80071 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003087358-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 516
ID ADD06848 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2002193300-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 517
ID ADD09540 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003194775-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 518
ID ADC83095 standard; protein; 653 AA.
DE Human PRO polypeptide #64.
PN US2003059783-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 519
ID ADD41253 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003203438-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 520
ID ADD52392 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003194769-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 521
ID ADD53132 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003194792-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;

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DE Human PRO polypeptide #219.
PN US2003199055-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.5%; Score 330; DB 7; Length 653;
  Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 532
ID ADE04082 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003199057-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.5%; Score 330; DB 7; Length 653;
  Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 533
ID ADE26752 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003087304-A1.
PD 08-MAY-2003.
  Query Match 10.5%; Score 330; DB 7; Length 653;
  Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 534
ID ADE32379 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003194765-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.5%; Score 330; DB 7; Length 653;
  Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 535
ID ADE22311 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003199056-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.5%; Score 330; DB 7; Length 653;
  Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 536
ID ADD79535 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003203428-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.5%; Score 330; DB 7; Length 653;
  Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 537
ID ADE42071 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003194772-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.5%; Score 330; DB 7; Length 653;
  Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 538
ID ADE17888 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003199023-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.5%; Score 330; DB 7; Length 653;
  Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 539
ID ADD92020 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003199053-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.5%; Score 330; DB 7; Length 653;
  Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 540
ID ADE33483 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003194767-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.5%; Score 330; DB 7; Length 653;
  Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 541
ID ADE34035 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003194791-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.5%; Score 330; DB 7; Length 653;
  Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 542
ID ADD80087 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003207417-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.5%; Score 330; DB 7; Length 653;
  Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 543
ID ADD93124 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003194768-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.5%; Score 330; DB 7; Length 653;
  Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 544
ID ADE19544 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003199025-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.5%; Score 330; DB 7; Length 653;
  Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 545
ID ADE18992 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003199026-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.5%; Score 330; DB 7; Length 653;
  Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 546
ID ADE43188 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003199033-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.5%; Score 330; DB 7; Length 653;
  Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 547
ID ADD95977 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003199059-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.5%; Score 330; DB 7; Length 653;
  Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 548
ID ADE22863 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003199064-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.5%; Score 330; DB 7; Length 653;
  Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 549
ID ADD78981 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003203429-A1.
PD 30-OCT-2003.
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PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 550
ID ADE26219 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003087305-A1.
PD 08-MAY-2003.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 551
ID ADE32931 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003194766-A1.
PD 16-OCT-2003.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 552
ID ADE42623 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003199032-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 553
ID ADD80639 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003207418-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 554
ID ADD89667 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003199028-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 555
ID ADE40951 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003199031-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 556
ID ADE04750 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003199034-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 557
ID ADE92879 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003194777-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 558
ID ADF67156 standard; protein; 653 AA.
DE Human PRO1111 amino acid sequence SEQ ID NO:229.
PN US2002198148-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;

Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 559
ID ADG21588 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207355-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 560
ID ADG23229 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207384-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 561
ID ADF97564 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003207370-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 562
ID ADG80628 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003207373-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 563
ID ADG80076 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003207372-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 564
ID ADH55368 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207381-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 565
ID ADH55920 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207379-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 566
ID ADI35410 standard; protein; 653 AA.
DE Human PRO polypeptide #64.
PN US2003050457-A1.
PD 13-MAR-2003.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 567
ID ADI64139 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207385-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 568

ID ADI5088 standard; protein; 653 AA.
 DE Novel human secreted and transmembrane protein PRO1111.
 PN US2003207386-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 10.5%; Score 330; DB 7; Length 653;
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;
 RESULT 569
 ID ADI63587 standard; protein; 653 AA.
 DE Novel human secreted and transmembrane protein PRO1111.
 PN US2003207387-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 10.5%; Score 330; DB 7; Length 653;
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;
 RESULT 570
 ID ADH82001 standard; protein; 653 AA.
 DE Novel human secreted and transmembrane protein PRO1111.
 PN US2003207388-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 10.5%; Score 330; DB 7; Length 653;
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;
 RESULT 571
 ID ADH99902 standard; protein; 653 AA.
 DE Novel human secreted and transmembrane protein PRO1111.
 PN US2003049682-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 10.5%; Score 330; DB 7; Length 653;
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;
 RESULT 572
 ID ADH81449 standard; protein; 653 AA.
 DE Novel human secreted and transmembrane protein PRO1111.
 PN US2003207377-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 10.5%; Score 330; DB 7; Length 653;
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;
 RESULT 573
 ID ADM82618 standard; protein; 653 AA.
 DE Novel human secreted and transmembrane protein PRO1111.
 PN US2003087355-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 10.5%; Score 330; DB 7; Length 653;
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;
 RESULT 574
 ID ADN16017 standard; protein; 653 AA.
 DE Novel human secreted and transmembrane protein PRO1111.
 PN US2003087353-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 10.5%; Score 330; DB 7; Length 653;
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;
 RESULT 575
 ID ADN16646 standard; protein; 653 AA.
 DE Novel human secreted and transmembrane protein PRO1111.
 PN US2003087385-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 10.5%; Score 330; DB 7; Length 653;
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;
 RESULT 576
 ID ADN15465 standard; protein; 653 AA.
 DE Novel human secreted and transmembrane protein PRO1111.
 PN US2003087356-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 10.5%; Score 330; DB 7; Length 653;
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;
 RESULT 577
 ID ADN14913 standard; protein; 653 AA.
 DE Novel human secreted and transmembrane protein PRO1111.

PN US2003087357-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 10.5%; Score 330; DB 7; Length 653;
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;
 RESULT 578
 ID ADC81175 standard; protein; 653 AA.
 DE Novel human secreted and transmembrane protein PRO1111.
 PN US2003092115-A1.
 PD 15-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 10.5%; Score 330; DB 8; Length 653;
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;
 RESULT 579
 ID ADD76623 standard; protein; 653 AA.
 DE Human PRO polypeptide #219.
 PN US2003100087-A1.
 PD 29-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 10.5%; Score 330; DB 8; Length 653;
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;
 RESULT 580
 ID ADD87987 standard; protein; 653 AA.
 DE Human PRO polypeptide #219.
 PN US2003092113-A1.
 PD 15-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 10.5%; Score 330; DB 8; Length 653;
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;
 RESULT 581
 ID ADD86391 standard; protein; 653 AA.
 DE Human PRO polypeptide #219.
 PN US2003203440-A1.
 PD 30-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 10.5%; Score 330; DB 8; Length 653;
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;
 RESULT 582
 ID ADE75839 standard; protein; 653 AA.
 DE Human PRO polypeptide #219.
 PN US2003211571-A1.
 PD 13-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 10.5%; Score 330; DB 8; Length 653;
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;
 RESULT 583
 ID ADE23415 standard; protein; 653 AA.
 DE Human PRO polypeptide #219.
 PN US2003092108-A1.
 PD 15-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 10.5%; Score 330; DB 8; Length 653;
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;
 RESULT 584
 ID ADE23967 standard; protein; 653 AA.
 DE Human PRO polypeptide #219.
 PN US2003092110-A1.
 PD 15-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 10.5%; Score 330; DB 8; Length 653;
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;
 RESULT 585
 ID ADE24610 standard; protein; 653 AA.
 DE Human PRO polypeptide #219.
 PN US2003092111-A1.
 PD 15-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 10.5%; Score 330; DB 8; Length 653;
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;
 RESULT 586
 ID ADD87435 standard; protein; 653 AA.
 DE Human PRO polypeptide #219.
 PN US2003203439-A1.

PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 587
ID ADE89301 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003199062-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 588
ID ADE18440 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003194794-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 589
ID ADE88749 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003199054-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 590
ID ADE94769 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003199027-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 591
ID ADE91180 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003199061-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 592
ID ADF35355 standard; protein; 653 AA.
DE Human PRO1111 polypeptide.
PN US2003194760-A1.
PD 16-OCT-2003.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 593
ID ADE95321 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003199052-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 594
ID ADE93431 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003199060-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 595
ID ADF35012 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003199029-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.

Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 596
ID ADE92327 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003199051-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 597
ID ADE90628 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003199063-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 598
ID ADE91775 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003199058-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 599
ID ADG11605 standard; protein; 653 AA.
DE Human PRO1111 polypeptide.
PN US2003228655-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 600
ID ADG02354 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003207352-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 601
ID ADG22140 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207360-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 602
ID ADG20210 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003207376-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 603
ID ADF98116 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003207422-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 604
ID ADG24333 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207426-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;

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Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 605
ID ADF98687 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003208055-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 606
ID ADG03518 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003207351-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 607
ID ADF99239 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003207353-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 608
ID ADG16824 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003207359-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 609
ID ADG05283 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003207375-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 610
ID ADG19550 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003207425-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 611
ID ADG13387 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003207357-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 612
ID ADG08444 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207424-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 613
ID ADG15614 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003219885-A1.
PD 27-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;

Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 614
ID ADF97012 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003207371-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 615
ID ADG06197 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003207374-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 616
ID ADG23781 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207389-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 617
ID ADG04070 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003207423-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 618
ID ADG24971 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207427-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 619
ID ADG07268 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207350-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 620
ID ADG07820 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207356-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 621
ID ADG55315 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003194778-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 622
ID ADG60979 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207390-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 623
ID ADG60979 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207390-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;

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ID ADG62083 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207428-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 624
ID ADG82284 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003207358-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 625
ID ADG57523 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207362-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 626
ID ADG56971 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207364-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 627
ID ADG5867 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207365-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 628
ID ADG58627 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207368-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 629
ID ADG70993 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207420-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 630
ID ADG58075 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207363-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 631
ID ADG53659 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207415-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 632
ID ADG71545 standard; protein; 653 AA.

DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207421-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 633
ID ADG81732 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003207805-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 634
ID ADH19475 standard; protein; 653 AA.
DE Human secreted/transmembrane protein PRO1111.
PN US2003228656-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 635
ID ADH30694 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003077723-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 636
ID ADH12061 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207419-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 637
ID ADG52483 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207414-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 638
ID ADG54211 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207416-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 639
ID ADG81180 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003194793-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 640
ID ADG56419 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207366-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 641
ID ADH12685 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207378-A1.

[illegible]

Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 660
ID ADI95870 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003077659-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 661
ID ADI96422 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207354-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 662
ID ADS32374 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2004203125-A1.
PD 14-OCT-2004.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 663
ID ADT03358 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2004214269-A1.
PD 28-OCT-2004.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 664
ID ADZ03409 standard; protein; 653 AA.
DE Human secreted/transmembrane PRO1111 protein.
PN US2005074837-A1.
PD 07-APR-2005.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 9; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 665
ID AEA38492 standard; protein; 653 AA.
DE Human secreted/transmembrane protein, #132.
PN US2005112725-A1.
PD 26-MAY-2005.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 9; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 666
ID AEA23332 standard; protein; 653 AA.
DE Tumor antigen of hematopoietic origin TAO15.
PN WO2005049075-A2.
PD 02-JUN-2005.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 9; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 667
ID AEB14155 standard; protein; 653 AA.
DE Cancer cell diagnosis method-related human protein - SEQ ID 438.
PN US2005153396-A1.
PD 14-JUL-2005.
PA (BAKE/) BAKER K P.
PA (BERE/) BERESINI M.
PA (DEFO/) DEFORGE L.
PA (DESN/) DESNOYERS L.
PA (FILV/) FILVAROFF E.
PA (GAOW/) GAO W.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (SHER/) SHERWOOD S.

PA (SMIT/) SMITH V.
PA (STEW/) STEWART T A.
PA (TUNA/) TUNAS D.
PA (WATA/) WATANABE C K.
PA (WOOD/) WOOD W I.
PA (ZHAN/) ZHANG Z.
Query Match 10.5%; Score 330; DB 9; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 668
ID AED86353 standard; protein; 653 AA.
DE Human PRO amino acid sequence, seq id 438.
PN US2005245730-A1.
PD 03-NOV-2005.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 9; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 669
ID AEF79019 standard; protein; 653 AA.
DE Human NAG14 polypeptide SEQ ID NO: 2.
PN US2006035826-A1.
PD 16-FEB-2006.
PA (LINJ/) LIN J C.
PA (ROSE/) ROSENTHAL A.
Query Match 10.5%; Score 330; DB 10; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 670
ID ABUI2069 standard; protein; 775 AA.
DE Human NOV15a CG92531-01 protein SEQ ID 58.
PN WO200281625-A2.
PD 17-OCT-2002.
PA (CURA-) CURAGEN CORP.
Query Match 10.5%; Score 329.5; DB 6; Length 775;
Best Local Similarity 26.0%; Pred. No. 3e-12;
RESULT 671
ID ABG98014 standard; protein; 649 AA.
DE Human leucine rich repeat domain protein associated protein #1.
PN WO200274959-A2.
PD 26-SEP-2002.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 10.5%; Score 329; DB 5; Length 649;
Best Local Similarity 24.6%; Pred. No. 2.6e-12;
RESULT 672
ID ADS98753 standard; protein; 824 AA.
DE Protein factor discovery related human contig polypeptide, SEQ ID 1017.
PN WO2004087874-A2.
PD 14-OCT-2004.
PA (NUVE-) NUVELO INC.
PA (DRMA/) DRMANAC R T.
Query Match 10.5%; Score 329; DB 8; Length 824;
Best Local Similarity 25.5%; Pred. No. 3.4e-12;
RESULT 673
ID ABG34079 standard; protein; 627 AA.
DE Human PRO peptide #51.
PN WO200224888-A2.
PD 28-MAR-2002.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 5; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.7e-12;
RESULT 674
ID ADA01368 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003068779-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 6; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.7e-12;
RESULT 675
ID ADA43797 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003064474-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 6; Length 627;

Best Local Similarity 24.2%; Pred. No. 2.7e-12;
RESULT 676
ID ADA43565 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003073196-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 6; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.7e-12;
RESULT 677
ID ADA01240 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003068782-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.7e-12;
RESULT 678
ID ADA01124 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003068780-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 6; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.7e-12;
RESULT 679
ID ADA43681 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003073190-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.7e-12;
RESULT 680
ID ADA06943 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003068781-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.7e-12;
RESULT 681
ID ADA08431 standard; protein; 627 AA.
DE Novel human secreted and transmembrane protein PRO34192.
PN US2003068783-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.7e-12;
RESULT 682
ID ADB99724 standard; protein; 627 AA.
DE Human PRO polypeptide SEQ ID 100.
PN US2003082728-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.7e-12;
RESULT 683
ID ADB87007 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003082726-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.7e-12;
RESULT 684
ID ADB66162 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003082729-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.7e-12;
RESULT 685
ID ADB99840 standard; protein; 627 AA.
DE Human PRO polypeptide SEQ ID 100.
PN US2003073192-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.7e-12;
RESULT 686
ID ADB99495 standard; protein; 627 AA.
DE Novel human secreted and transmembrane protein PRO34192.
PN US2003082731-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.7e-12;
RESULT 687
ID ADB66046 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003082732-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.7e-12;
RESULT 688
ID ADC23444 standard; protein; 627 AA.
DE Human transmembrane PRO polypeptide (SeqID 100).
PN US2003073193-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.7e-12;
RESULT 689
ID ADC26137 standard; protein; 627 AA.
DE Human PRO34192 protein.
PN US2003073194-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.7e-12;
RESULT 690
ID ADE04964 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003068778-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.7e-12;
RESULT 691
ID ADE11270 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003073191-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.7e-12;
RESULT 692
ID ADD88201 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003082733-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.7e-12;
RESULT 693
ID ADD95496 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003064473-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.7e-12;
RESULT 694

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ID ADE06426 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003073195-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.7e-12;
RESULT 695
ID ADE38201 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003119120-A1.
PD 26-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.7e-12;
RESULT 696
ID ADE88317 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003073189-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.7e-12;
RESULT 697
ID ADD90898 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003073188-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.7e-12;
RESULT 698
ID ADF99453 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003078401-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.7e-12;
RESULT 699
ID ADG06546 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003077742-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.7e-12;
RESULT 700
ID ADG05497 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003077741-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.7e-12;
RESULT 701
ID ADG82498 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003077744-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.7e-12;
RESULT 702
ID ADE51751 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003104560-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.7e-12;
RESULT 703
ID ADE51867 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003104561-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.7e-12;
RESULT 704
ID ADE37725 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003104564-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.7e-12;
RESULT 705
ID ADE37609 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003104565-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.7e-12;
RESULT 706
ID ADD95380 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003138901-A1.
PD 24-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.7e-12;
RESULT 707
ID ADE38080 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003104566-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.7e-12;
RESULT 708
ID ADE76169 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003124665-A1.
PD 03-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.7e-12;
RESULT 709
ID ADE39492 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003119117-A1.
PD 26-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.7e-12;
RESULT 710
ID ADE04296 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003096364-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.7e-12;
RESULT 711
ID ADE39893 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003138896-A1.
PD 24-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.7e-12;
RESULT 712
ID ADE19758 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
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PN US2003138903-A1.
PD 24-JUL-2003.
PA (GETH ) GENENTECH INC. 10.5%; Score 328.5; DB 8; Length 627;
Query Match
Best Local Similarity 24.2%; Pred. No. 2.7e-12;
RESULT 713
ID ADE77336 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003124666-A1.
PD 03-JUL-2003.
PA (GETH ) GENENTECH INC. 10.5%; Score 328.5; DB 8; Length 627;
Query Match
Best Local Similarity 24.2%; Pred. No. 2.7e-12;
RESULT 714
ID ADE65444 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003119116-A1.
PD 26-JUN-2003.
PA (GETH ) GENENTECH INC. 10.5%; Score 328.5; DB 8; Length 627;
Query Match
Best Local Similarity 24.2%; Pred. No. 2.7e-12;
RESULT 715
ID ADE76053 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003124663-A1.
PD 03-JUL-2003.
PA (GETH ) GENENTECH INC. 10.5%; Score 328.5; DB 8; Length 627;
Query Match
Best Local Similarity 24.2%; Pred. No. 2.7e-12;
RESULT 716
ID ADE37964 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003119119-A1.
PD 26-JUN-2003.
PA (GETH ) GENENTECH INC. 10.5%; Score 328.5; DB 8; Length 627;
Query Match
Best Local Similarity 24.2%; Pred. No. 2.7e-12;
RESULT 717
ID ADE64574 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003119114-A1.
PD 26-JUN-2003.
PA (GETH ) GENENTECH INC. 10.5%; Score 328.5; DB 8; Length 627;
Query Match
Best Local Similarity 24.2%; Pred. No. 2.7e-12;
RESULT 718
ID ADE38909 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003096363-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC. 10.5%; Score 328.5; DB 8; Length 627;
Query Match
Best Local Similarity 24.2%; Pred. No. 2.7e-12;
RESULT 719
ID ADE51983 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003104562-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC. 10.5%; Score 328.5; DB 8; Length 627;
Query Match
Best Local Similarity 24.2%; Pred. No. 2.7e-12;
RESULT 720
ID ADD91014 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003138902-A1.
PD 24-JUL-2003.
PA (GETH ) GENENTECH INC. 10.5%; Score 328.5; DB 8; Length 627;
Query Match
Best Local Similarity 24.2%; Pred. No. 2.7e-12;
RESULT 721
ID ADE38793 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003108996-A1.
PD 03-JUL-2003.
PA (GETH ) GENENTECH INC. 10.5%; Score 328.5; DB 8; Length 627;
Query Match
Best Local Similarity 24.2%; Pred. No. 2.7e-12;
RESULT 722
ID ADE37493 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003104563-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC. 10.5%; Score 328.5; DB 8; Length 627;
Query Match
Best Local Similarity 24.2%; Pred. No. 2.7e-12;
RESULT 723
ID ADE06309 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003138898-A1.
PD 24-JUL-2003.
PA (GETH ) GENENTECH INC. 10.5%; Score 328.5; DB 8; Length 627;
Query Match
Best Local Similarity 24.2%; Pred. No. 2.7e-12;
RESULT 724
ID ADD90169 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003138904-A1.
PD 24-JUL-2003.
PA (GETH ) GENENTECH INC. 10.5%; Score 328.5; DB 8; Length 627;
Query Match
Best Local Similarity 24.2%; Pred. No. 2.7e-12;
RESULT 725
ID ADE38677 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003119086-A1.
PD 26-JUN-2003.
PA (GETH ) GENENTECH INC. 10.5%; Score 328.5; DB 8; Length 627;
Query Match
Best Local Similarity 24.2%; Pred. No. 2.7e-12;
RESULT 726
ID ADE39608 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003119118-A1.
PD 26-JUN-2003.
PA (GETH ) GENENTECH INC. 10.5%; Score 328.5; DB 8; Length 627;
Query Match
Best Local Similarity 24.2%; Pred. No. 2.7e-12;
RESULT 727
ID ADD89213 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003138897-A1.
PD 24-JUL-2003.
PA (GETH ) GENENTECH INC. 10.5%; Score 328.5; DB 8; Length 627;
Query Match
Best Local Similarity 24.2%; Pred. No. 2.7e-12;
RESULT 728
ID ADD88980 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003138899-A1.
PD 24-JUL-2003.
PA (GETH ) GENENTECH INC. 10.5%; Score 328.5; DB 8; Length 627;
Query Match
Best Local Similarity 24.2%; Pred. No. 2.7e-12;
RESULT 729
ID ADE19874 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003138900-A1.
PD 24-JUL-2003.
PA (GETH ) GENENTECH INC. 10.5%; Score 328.5; DB 8; Length 627;
Query Match
Best Local Similarity 24.2%; Pred. No. 2.7e-12;
RESULT 730
ID ADE77452 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003124667-A1.
PD 03-JUL-2003.
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Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.7e-12;
RESULT 740
ID ADH27042 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003119135-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.7e-12;
RESULT 741
ID ADH38310 standard; protein; 627 AA.
DE Novel human secreted and transmembrane protein PRO34192.
PN US2003119124-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.7e-12;
RESULT 742
ID ADH26326 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003119134-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.7e-12;
RESULT 743
ID ADH38194 standard; protein; 627 AA.
DE Novel human secreted and transmembrane protein PRO34192.
PN US2003119123-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.7e-12;
RESULT 744
ID ADH3890 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003119141-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.7e-12;
RESULT 745
ID ADH23828 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003119142-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.7e-12;
RESULT 746
ID ADH40203 standard; protein; 627 AA.
DE Human PRO34192 protein.
PN US2003119132-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.7e-12;
RESULT 747
ID ADH40088 standard; protein; 627 AA.
DE Human PRO34192 protein.
PN US2003119133-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.7e-12;
RESULT 748
ID ADH31410 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003119138-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.7e-12;

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Best Local Similarity 24.2%; Pred. No. 2.7e-12;
RESULT 749
ID ADH29288 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003119136-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.7e-12;
RESULT 750
ID ADH49503 standard; protein; 627 AA.
DE Novel human secreted and transmembrane protein PRO34192.
PN US2003119127-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.7e-12;
RESULT 751
ID ADH51967 standard; protein; 627 AA.
DE Novel human secreted and transmembrane protein PRO34192.
PN US2003119125-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.7e-12;
RESULT 752
ID ADH49822 standard; protein; 627 AA.
DE Novel human secreted and transmembrane protein PRO34192.
PN US2003119128-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.7e-12;
RESULT 753
ID ADH52423 standard; protein; 627 AA.
DE Novel human secreted and transmembrane protein PRO34192.
PN US2003119130-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.7e-12;
RESULT 754
ID ADH52539 standard; protein; 627 AA.
DE Novel human secreted and transmembrane protein PRO34192.
PN US2003119129-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.7e-12;
RESULT 755
ID ADH58536 standard; protein; 627 AA.
DE Novel human secreted and transmembrane protein PRO34192.
PN US2003119121-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.7e-12;
RESULT 756
ID ADH51851 standard; protein; 627 AA.
DE Novel human secreted and transmembrane protein PRO34192.
PN US2003119126-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.7e-12;
RESULT 757
ID ADH58412 standard; protein; 627 AA.
DE Novel human secreted and transmembrane protein PRO34192.
PN US2003119122-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.7e-12;
RESULT 758
ID ADI13609 standard; protein; 627 AA.
DE Novel human secreted and transmembrane protein PRO34192.
PN US2003119131-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.7e-12;
RESULT 759
ID ADK00865 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003186373-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.7e-12;
RESULT 760
ID ADL08606 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003186372-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.7e-12;
RESULT 761
ID AAU32870 standard; protein; 636 AA.
DE Novel human secreted protein #361.
PN WO200179449-A2.
PD 25-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 10.4%; Score 327.5; DB 4; Length 636;
Best Local Similarity 24.2%; Pred. No. 3.2e-12;
RESULT 762
ID ABO84499 standard; protein; 626 AA.
DE Mouse cancer-associated protein MP14-035.1.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 10.3%; Score 324; DB 8; Length 626;
Best Local Similarity 24.3%; Pred. No. 5.2e-12;
RESULT 763
ID RAG5805 standard; protein; 628 AA.
DE Human leucine-rich repeat (LRR) family member, 33395 polypeptide.
PN WO200172827-A2.
PD 04-OCT-2001.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 10.3%; Score 324; DB 4; Length 628;
Best Local Similarity 24.1%; Pred. No. 5.2e-12;
RESULT 764
ID ADN95165 standard; protein; 810 AA.
DE Human BEC/JEC-related protein sequence SeqID87.
PN WO2003080640-A1.
PD 02-OCT-2003.
PA (LUDM-) LUDWIG INST CANCER RES.
PA (LICN) LICENTIA LTD.
Query Match 10.3%; Score 322.5; DB 7; Length 810;
Best Local Similarity 22.0%; Pred. No. 8.7e-12;
RESULT 765
ID ABR58642 standard; protein; 811 AA.
DE Human cancer related protein SEQ ID NO:299.
PN WO2003025138-A2.
PD 27-MAR-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 10.3%; Score 322.5; DB 6; Length 811;
Best Local Similarity 22.0%; Pred. No. 8.7e-12;
RESULT 766
ID AAO23114 standard; protein; 811 AA.
DE KIAA0644 'human modifier of p53 pathway' protein.
PN WO2003035833-A2.
PD 01-MAY-2003.
PA (EXEL-) EXELIXIS INC.
Query Match 10.3%; Score 322.5; DB 6; Length 811;
Best Local Similarity 22.0%; Pred. No. 8.7e-12;

RESULT 767
ID ADN95110 standard; protein; 811 AA.
DE Human LEC protein sequence SeqID32.
PN WO2003080640-A1.
PD 02-OCT-2003.
PA (LUDW-) LUDWIG INST CANCER RES.
PA (LICN-) LICENTIA LTD.
Query Match 10.3%; Score 322.5; DB 7; Length 811;
Best Local Similarity 22.0%; Pred. No. 8.7e-12;
RESULT 768
ID ADQ21196 standard; protein; 811 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 4016.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 10.3%; Score 322.5; DB 8; Length 811;
Best Local Similarity 22.0%; Pred. No. 8.7e-12;
RESULT 769
ID ADR45590 standard; protein; 605 AA.
DE Homologue of LRSG-1, baboon ALS.
PN US2004176296-A1.
PD 09-SEP-2004.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 10.3%; Score 322; DB 8; Length 605;
Best Local Similarity 36.2%; Pred. No. 6.6e-12;
RESULT 770
ID AAG67523 standard; protein; 628 AA.
DE Amino acid sequence of a human secreted polypeptide.
PN WO200166690-A2.
PD 13-SEP-2001.
PA (SMIK-) SMITHKLINE BEECHAM CORP.
PA (SMIK-) SMITHKLINE BEECHAM PLC.
Query Match 10.2%; Score 321; DB 4; Length 628;
Best Local Similarity 23.9%; Pred. No. 8e-12;
RESULT 771
ID AAB84469 standard; protein; 628 AA.
DE Amino acid sequence of an interferon omega-1 like protein NOV2.
PN WO200142471-A2.
PD 14-JUN-2001.
PA (CURA-) CURAGEN CORP.
Query Match 10.2%; Score 321; DB 4; Length 628;
Best Local Similarity 23.9%; Pred. No. 8e-12;
RESULT 772
ID ABP69326 standard; protein; 628 AA.
DE Human polypeptide SEQ ID NO 1373.
PN WO200270539-A2.
PD 12-SEP-2002.
PA (HYSE-) HYSEQ INC.
Query Match 10.2%; Score 321; DB 5; Length 628;
Best Local Similarity 23.9%; Pred. No. 8e-12;
RESULT 773
ID ADF69107 standard; protein; 628 AA.
DE Human MP53 protein sequence SEQ ID NO:77.
PN WO2003083047-A2.
PD 09-OCT-2003.
PA (EXEL-) EXELIXIS INC.
Query Match 10.2%; Score 321; DB 7; Length 628;
Best Local Similarity 23.9%; Pred. No. 8e-12;
RESULT 774
ID ADH71652 standard; protein; 628 AA.
DE Human protein of the invention NOV22a SEQ ID NO:548.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 10.2%; Score 321; DB 8; Length 628;
Best Local Similarity 23.9%; Pred. No. 8e-12;
RESULT 775
ID ADH71654 standard; protein; 628 AA.
DE Human protein of the invention NOV22b SEQ ID NO:550.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 10.2%; Score 321; DB 8; Length 628;

Best Local Similarity 23.9%; Pred. No. 8e-12;
RESULT 776
ID ABO84502 standard; protein; 628 AA.
DE Human cancer-associated protein HP14-035.3.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 10.2%; Score 321; DB 8; Length 628;
Best Local Similarity 23.9%; Pred. No. 8e-12;
RESULT 777
ID ABO84503 standard; protein; 628 AA.
DE Human cancer-associated protein HP14-035.4.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 10.2%; Score 321; DB 8; Length 628;
Best Local Similarity 23.9%; Pred. No. 8e-12;
RESULT 778
ID ABO84501 standard; protein; 628 AA.
DE Human cancer-associated protein HP14-035.2.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 10.2%; Score 321; DB 8; Length 628;
Best Local Similarity 23.9%; Pred. No. 8e-12;
RESULT 779
ID ABP70928 standard; protein; 762 AA.
DE Human LP341 protein.
PN WO2003029778-A2.
PD 10-APR-2003.
PA (ELIL-) LILLY & CO ELI.
Query Match 10.2%; Score 321; DB 6; Length 762;
Best Local Similarity 25.5%; Pred. No. 1e-11;
RESULT 780
ID ADI36917 standard; protein; 797 AA.
DE Human LRR protein #12.
PN US200320263-A1.
PD 27-NOV-2003.
PA (FEDE-) FEDER J N.
PA (MINT-) MINTIER G.
PA (RAMA-) RAMANATHAN C S.
Query Match 10.2%; Score 321; DB 8; Length 797;
Best Local Similarity 25.5%; Pred. No. 1.1e-11;
RESULT 781
ID ADS98018 standard; protein; 803 AA.
DE Protein factor discovery related isolated human polypeptide. SEQ ID 282.
PN WO2004087874-A2.
PD 14-OCT-2004.
PA (NUVE-) NUVELO INC.
PA (DRWA-) DRWANAC R T.
Query Match 10.2%; Score 321; DB 8; Length 803;
Best Local Similarity 25.5%; Pred. No. 1.1e-11;
RESULT 782
ID AAY13349 standard; protein; 660 AA.
DE Amino acid sequence of protein PRO265.
PN WO9914328-A2.
PD 25-MAR-1999.
PA (GETH-) GENENTECH INC.
Query Match 10.2%; Score 320; DB 2; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 783
ID ADC78348 standard; protein; 660 AA.
DE Human PRO265 protein.
PN WO200015796-A2.
PD 23-MAR-2000.
PA (GETH-) GENENTECH INC.
Query Match 10.2%; Score 320; DB 3; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 784
ID AAB80217 standard; protein; 660 AA.
DE Human PRO265 protein.
PN WO200104311-A1.
PD 18-JAN-2001.

PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 4; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 785
ID AAB31208 standard; protein; 660 AA.
DE Amino acid sequence of human polypeptide PRO265.
PN WO200077037-A2.
PD 21-DEC-2000.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 4; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 786
ID AAU12346 standard; protein; 660 AA.
DE Human PRO265 polypeptide sequence.
PN WO200140466-A2.
PD 07-JUN-2001.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 4; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 787
ID ABB84839 standard; protein; 660 AA.
DE Human PRO265 protein sequence SEQ ID NO:46.
PN WO200200690-A2.
PD 03-JAN-2002.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 5; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 788
ID ABB95445 standard; protein; 660 AA.
DE Human angiogenesis related protein PRO265 SEQ ID NO: 46.
PN WO200208284-A2.
PD 31-JAN-2002.
PA (GETH) GENENTECH INC.
PA (BAKE//) BAKER K P.
PA (FERR//) FERRARA N.
PA (GERB//) GERBER H.
PA (GERR//) GERRITSEN M E.
PA (GODD//) GODDARD A.
PA (GODO//) GODOWSKI P J.
PA (GURN//) GURNEY A L.
PA (HILL//) HILLAN K J.
PA (MARS//) MARSTERS S A.
PA (PANJ//) PAN J.
PA (PAON//) PAONI N F.
PA (STEP//) STEPHAN J F.
PA (WATA//) WATANABE C K.
PA (WILL//) WILLIAMS P M.
PA (WOOD//) WOOD W I.
Query Match 10.2%; Score 320; DB 5; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 789
ID ABU71595 standard; protein; 660 AA.
DE Human PRO polypeptide #6.
PN US2002146709-A1.
PD 10-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 790
ID ABO17790 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003032156-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 791
ID ABU71450 standard; protein; 660 AA.
DE Human PRO polypeptide #6.
PN US2002192659-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 792
ID ABO25179 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003040014-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 793
ID ABU81044 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003004311-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 794
ID ABU71896 standard; protein; 660 AA.
DE Human secreted/transmembrane protein PRO265.
PN US2003003530-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 795
ID ABO01779 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2002197671-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 796
ID ABU66744 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003036180-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 797
ID ABU54352 standard; protein; 660 AA.
DE Human secreted/transmembrane protein PRO265.
PN US2002152240-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 798
ID ABU67297 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003032063-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 799
ID AAO23116 standard; protein; 660 AA.
DE WRT2 'human modifier of p53 pathway' protein.
PN WO2003035833-A2.
PD 01-MAY-2003.
PA (EXEL-) EXELIXIS INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 800
ID ABO47367 standard; protein; 660 AA.
DE Human secreted/transmembrane polypeptide PRO265.
PN US2003044839-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;

RESULT 801
ID ABUS9825 standard; protein; 660 AA.
DE Novel secreted and transmembrane protein PRO265.
PN US2003017563-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 802
ID ABO25015 standard; protein; 660 AA.
DE Human secreted/transmembrane protein (PRO) #175.
PN US2003036179-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 803
ID ABU64504 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2002160374-A1.
PD 31-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 804
ID ABU72065 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2002177165-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 805
ID ABU67350 standard; protein; 660 AA.
DE Human secreted protein PRO265.
PN US2003023054-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 806
ID ABU67166 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003032062-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 807
ID ABO14870 standard; protein; 660 AA.
DE Human secreted / transmembrane polypeptide PRO265.
PN US2003036060-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 808
ID ABU67020 standard; protein; 660 AA.
DE Human secreted/transmembrane, PRO, protein SEQ ID 350.
PN US2003032155-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 809
ID ABU69627 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003017463-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 810

ID ABU79808 standard; protein; 660 AA.
DE Human secreted/transmembrane protein PRO265.
PN US2003032057-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 811
ID ABO14809 standard; protein; 660 AA.
DE Human secreted / transmembrane polypeptide PRO265.
PN US2003027143-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 812
ID ADA45869 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003022328-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 813
ID ADA76300 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003073212-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 814
ID ADB29233 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003092002-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 815
ID ADA18950 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003054517-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 816
ID ADA61573 standard; protein; 660 AA.
DE Homo sapiens.
PN US2003049816-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 817
ID ADB19358 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003068796-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 818
ID ADB27899 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003082704-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 819
ID ADA86378 standard; protein; 660 AA.

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DE Novel human secreted and transmembrane protein PRO265.
PN US2003082711-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 820
ID ADB15942 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003087350-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 821
ID ADA47728 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003073215-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 822
ID ADA18089 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003039971-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 823
ID ABO32761 standard; protein; 660 AA.
DE Human secreted/transmembrane protein PRO265.
PN US2003045693-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 824
ID ADA67523 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003068795-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 825
ID ADB30530 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003068794-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 826
ID ADA85826 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003082693-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 827
ID ADA97038 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003082705-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 828
ID ADA79342 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003077722-A1.
PN US2003082763-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 829
ID ADA87481 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003087345-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 830
ID ADB16683 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003087349-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 831
ID ABO34821 standard; protein; 660 AA.
DE Human PRO polypeptide #6.
PN US2003044793-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 832
ID ADA16064 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003049621-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 833
ID ADA91775 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003082694-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 834
ID ADB14838 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003087351-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 835
ID ADA47287 standard; protein; 660 AA.
DE Human secreted/transmembrane polypeptide PRO265.
PN US2003044844-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 836
ID ADB18799 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003073211-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 837
ID ADA94014 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003077722-A1.
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PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 6; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 838
ID ADB19910 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003082691-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 6; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 839
ID ADB13222 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003082710-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 6; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 840
ID ABO43323 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003044945-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 6; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 841
ID ADA74476 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003086798-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 6; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 842
ID ADA42209 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003054401-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 6; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 843
ID ADB24709 standard; protein; 660 AA.
DE Human PRO polypeptide SEQ ID NO 350.
PN US200307713-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 6; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 844
ID ADA82233 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003082701-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 6; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 845
ID ADA75196 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003073216-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 6; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 846
ID ADA85274 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003082695-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 6; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 847
ID ADA84722 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003082708-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 6; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 848
ID ABO17499 standard; protein; 660 AA.
DE Human PRO polypeptide #6.
PN US2003064367-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 6; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 849
ID ADB29978 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003073214-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 6; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 850
ID ADA80506 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003082761-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 6; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 851
ID ADA75748 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003082703-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 6; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 852
ID ADA46973 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003073210-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 6; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 853
ID ADB25269 standard; protein; 660 AA.
DE Human PRO polypeptide SEQ ID NO 350.
PN US2003077715-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 6; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 854
ID ADA93445 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003077721-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 6; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 855
ID ADB26795 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003092147-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
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Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 856
ID ADB31082 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US200307710-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 857
ID ADA61010 standard; protein; 660 AA.
DE Homo sapiens.
PN US2003049817-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 858
ID ADB24157 standard; protein; 660 AA.
DE Human PRO polypeptide SEQ ID NO 350.
PN US200307714-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 859
ID ADA96486 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003082690-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 860
ID ADA81058 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003082702-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 861
ID ADA95934 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003082759-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 862
ID ADB26243 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003082760-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 863
ID ADB21728 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003082765-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 864
ID ADA77507 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003068797-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 865
ID ADB18247 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US200307710-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 866
ID ADA86930 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003082709-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 867
ID ADA16488 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003039969-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 868
ID ADA12917 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003049622-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 869
ID ADA41785 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003082540-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 870
ID ADA88033 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003082700-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 871
ID ADA46421 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003054516-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 872
ID ADA17132 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003017498-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 873
ID ADA42635 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003054351-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
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RESULT 874
ID ADB28451 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003082699-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 875
ID ADB29003 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003082706-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 876
ID ADA76955 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003059909-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 877
ID ADA8585 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003073213-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 878
ID ADA97590 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003082686-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 879
ID ADB27347 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003022239-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 880
ID ADB22280 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003087344-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 881
ID ABO17560 standard; protein; 660 AA.
DE Human PRO polypeptide #6.
PN US2003064923-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 882
ID ABO17560 standard; protein; 660 AA.
DE Human PRO polypeptide #6.
PN US2003064923-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 883
ID ADA66971 standard; protein; 660 AA.
DE Human PRO polypeptide #175.

PN US2003068793-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 884
ID ADB2832 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003077111-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 885
ID ADB23605 standard; protein; 660 AA.
DE Human PRO polypeptide SEQ ID NO 350.
PN US200307712-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 886
ID ADA92327 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003082712-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 887
ID ADB15390 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003087352-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 888
ID ADB38642 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003082766-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 889
ID ADB38090 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003087347-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 890
ID ADB66562 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003082689-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 891
ID ADB89642 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003082698-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 892
ID ADB90374 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003082762-A1.

PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 893
ID ADB77554 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003077654-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 894
ID ADB39475 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003082764-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 895
ID ADB74690 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003082542-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 896
ID ADB47098 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003082687-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 897
ID ADB86705 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003082697-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 898
ID ADB77310 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003082696-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 899
ID ADB34467 standard; protein; 660 AA.
DE Human PRO polypeptide SEQ ID NO 350.
PN US2003077717-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 900
ID ADB35571 standard; protein; 660 AA.
DE Human PRO polypeptide SEQ ID NO 350.
PN US2003077719-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 901
ID ADB33915 standard; protein; 660 AA.
DE Human PRO polypeptide SEQ ID NO 350.
PN US2003077716-A1.
PD 24-APR-2003.

PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 902
ID ADB35019 standard; protein; 660 AA.
DE Human PRO polypeptide SEQ ID NO 350.
PN US2003077718-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 903
ID ADB36123 standard; protein; 660 AA.
DE Human PRO polypeptide SEQ ID NO 350.
PN US2003077720-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 904
ID ADB46518 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003082692-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 905
ID ADC28336 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003059772-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 906
ID ADC39536 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003059828-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 907
ID ADC40050 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003059829-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 908
ID ADC18878 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003036061-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 909
ID ADC34174 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003036094-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 910
ID ADC29229 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003049676-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.


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RESULT 929
ID ADC12272 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003082541-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 930
ID ADD031175 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003092104-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 931
ID ADC90167 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003087348-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 932
ID ADC69586 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003194770-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 933
ID ADC48475 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003194773-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 934
ID ADD10004 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003194776-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 935
ID ADD04579 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003087354-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 936
ID ADC80535 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003092103-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 937
ID ADD11042 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003194774-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 938
ID ADD52304 standard; protein; 660 AA.
DE Human secreted/transmembrane PRO polypeptide #23.
PN US2003105011-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 939
ID ADC47923 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003194771-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 940
ID ADD04827 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003104469-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 941
ID ADC79983 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003087358-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 942
ID ADD11295 standard; protein; 660 AA.
DE Human secreted/transmembrane PRO polypeptide #23.
PN US2003105013-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 943
ID ADD09452 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003194775-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 944
ID ADD03833 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003104381-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 945
ID ADD03409 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003108983-A1.
PD 12-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 946
ID ADD41165 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003203438-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 947
ID ADD52304 standard; protein; 660 AA.
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DE Human PRO polypeptide #175.
PN US2003194769-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 948
ID ADDS3044 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003194792-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 949
ID ADDS3596 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003203437-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 950
ID ADD37088 standard; protein; 660 AA.
DE Human secreted/transmembrane PRO polypeptide #23.
PN US2003105012-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 951
ID ADD51752 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003194779-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 952
ID ADD02551 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003203431-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 953
ID ADD01985 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003203430-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 954
ID ADD54167 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003203432-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 955
ID ADD92484 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003199030-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 956
ID ADD91380 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003199055-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 957
ID ADE03994 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003199057-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 958
ID ADE32291 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003194765-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 959
ID ADE22223 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003199056-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 960
ID ADD79447 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003203428-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 961
ID ADE41983 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003194772-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 962
ID ADE17800 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003199023-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 963
ID ADD91932 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003199053-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 964
ID ADE33395 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003194767-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 965
ID ADE33947 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003194791-A1.
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PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 966
ID ADD79999 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003207417-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 967
ID ADD93036 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003194768-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 968
ID ADE19456 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003199025-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 969
ID ADE34661 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003077583-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 970
ID ADE18904 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003199026-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 971
ID ADE43100 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003199033-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 972
ID ADD95889 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003199059-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 973
ID ADE22775 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003199064-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 974
ID ADD78893 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003203429-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 975
ID ADE32843 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003194766-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 976
ID ADE42535 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003199032-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 977
ID ADD80551 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003207418-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 978
ID ADD89579 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003199028-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 979
ID ADE40863 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003199031-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 980
ID ADE04662 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003199034-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 981
ID ADE92791 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003194777-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 982
ID ADG21500 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207355-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 983
ID ADG23141 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207384-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.

Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 984
ID ADF97476 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003207370-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 985
ID ADG80540 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003207373-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 986
ID ADG79988 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003207372-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 987
ID ADG63796 standard; protein; 660 AA.
DE Human secreted/transmembrane polypeptide PRO265.
PN US2003170721-A1.
PD 11-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 988
ID ADH59144 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003039972-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 989
ID ADH55280 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207381-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 990
ID ADH55832 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207379-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 991
ID ADI17923 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003054352-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 992
ID ADI65000 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207386-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;

Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 993
ID ADI63499 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207387-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 994
ID ADH81913 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207388-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 995
ID ADH81361 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207377-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 996
ID ADJ26191 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003054349-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 997
ID ADM82530 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003087355-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 998
ID ADNI5929 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003087353-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 999
ID ADNI6558 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003087385-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1000
ID ADNI5377 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003087356-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1001
ID ADNI4825 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003087357-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;

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RESULT 1002
ID ADE164051 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207385-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1003
ID ADC81087 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003092115-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1004
ID ADE79106 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003135025-A1.
PD 17-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1005
ID ADD76535 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003100087-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1006
ID ADD87899 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003092113-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1007
ID ADD86303 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003203440-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1008
ID ADE79530 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003130489-A1.
PD 10-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1009
ID ADE75751 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003211571-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1010
ID ADE73206 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003129592-A1.
PD 10-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1011
ID ADE88661 standard; protein; 660 AA.
DE Human secreted/transmembrane PRO polypeptide #23.
PN US2003100497-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1012
ID ADE23327 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003092108-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1013
ID ADE23879 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003092110-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1014
ID ADE24522 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003092111-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1015
ID ADD87347 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003203439-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1016
ID ADE89213 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003199082-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1017
ID ADE41210 standard; protein; 660 AA.
DE Human secreted/transmembrane polypeptide PRO265.
PN US2003104558-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1018
ID ADE73741 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003148370-A1.
PD 07-AUG-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1019
ID ADE18352 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003194794-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1020
ID ADE88661 standard; protein; 660 AA.
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DE Human PRO polypeptide #175.
PN US2003199054-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1021
ID ADE99295 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003211576-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1022
ID ADE94681 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003199027-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1023
ID ADE91092 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003199061-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1024
ID ADE95233 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003199052-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1025
ID ADE93343 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003199060-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1026
ID ADF34924 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003199029-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1027
ID ADE98414 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003211569-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1028
ID ADE92239 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO365.
PN US2003199051-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1029
ID ADE90540 standard; protein; 660 AA.
DE Human PRO polypeptide #175.

PN US2003199063-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1030
ID ADE91687 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003199058-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1031
ID ADE98841 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003211568-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1032
ID ADG40311 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003225253-A1.
PD 04-DEC-2003.
PA (DESN) DESNOYERS L.
PA (GODD) GODDARD A.
PA (GODO) GODOWSKI P J.
PA (GUEN) GUERNEY A L.
PA (MATH) MATHER J P.
PA (WILL) WILLIAMS P M.
PA (WOOD) WOOD W I.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1033
ID ADF73705 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003180312-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1034
ID ADG2266 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003207352-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1035
ID ADG22052 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207360-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1036
ID ADG20122 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003207376-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1037
ID ADF98028 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003207422-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.

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Query Match      10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1038
ID ADG24245 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207424-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1039
ID ADF98599 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003208055-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1040
ID ADG03430 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003207351-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1041
ID ADF9151 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003207353-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1042
ID ADG16736 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003207359-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1043
ID ADG05195 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003207375-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1044
ID ADG19462 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003207425-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1045
ID ADF73281 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003166051-A1.
PD 04-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1046
ID ADG13299 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003207357-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1047
ID ADG08356 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207424-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1048
ID ADG15526 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003219885-A1.
PD 27-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1049
ID ADF96924 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003207371-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1050
ID ADG06109 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003207374-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1051
ID ADG23693 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207389-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1052
ID ADG03982 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003207423-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1053
ID ADG24883 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207427-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1054
ID ADG07180 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207350-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1055
ID ADG07732 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207356-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
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RESULT 1056
ID ADG55227 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003194778-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1057
ID ADG60891 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO365.
PN US2003207390-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1058
ID ADG61995 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207428-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1059
ID ADG92124 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003027145-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1060
ID ADG82196 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003207358-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1061
ID ADG57435 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207362-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1062
ID ADG56883 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207364-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1063
ID ADG55779 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207365-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1064
ID ADG58539 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207368-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1065
ID ADG52395 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.

ID ADG70905 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207420-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1066
ID ADG92551 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003027146-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1067
ID ADG57987 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207363-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1068
ID ADG33571 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207415-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1069
ID ADG71457 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207421-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1070
ID ADG81644 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003207805-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1071
ID ADH30606 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003077723-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1072
ID ADG63645 standard; protein; 660 AA.
DE Human secreted/transmembrane polypeptide PRO265.
PN US2003180796-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1073
ID ADH11973 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207419-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1074
ID ADG52395 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.

PN US2003207414-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 10.2%; Score 320; DB 8; Length 660;
 Best Local Similarity 22.4%; Pred. No. 9.8e-12;
 RESULT 1075
 ID ADG54123 standard; protein; 660 AA.
 DE Novel human secreted and transmembrane protein PRO265.
 PN US2003207416-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 10.2%; Score 320; DB 8; Length 660;
 Best Local Similarity 22.4%; Pred. No. 9.8e-12;
 RESULT 1076
 ID ADG81092 standard; protein; 660 AA.
 DE Human PRO polypeptide #175.
 PN US2003194793-A1.
 PD 16-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 10.2%; Score 320; DB 8; Length 660;
 Best Local Similarity 22.4%; Pred. No. 9.8e-12;
 RESULT 1077
 ID ADG56331 standard; protein; 660 AA.
 DE Novel human secreted and transmembrane protein PRO265.
 PN US2003207366-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 10.2%; Score 320; DB 8; Length 660;
 Best Local Similarity 22.4%; Pred. No. 9.8e-12;
 RESULT 1078
 ID ADH12597 standard; protein; 660 AA.
 DE Novel human secreted and transmembrane protein PRO265.
 PN US2003207378-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 10.2%; Score 320; DB 8; Length 660;
 Best Local Similarity 22.4%; Pred. No. 9.8e-12;
 RESULT 1079
 ID ADG61443 standard; protein; 660 AA.
 DE Novel human secreted and transmembrane protein PRO265.
 PN US2003207429-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 10.2%; Score 320; DB 8; Length 660;
 Best Local Similarity 22.4%; Pred. No. 9.8e-12;
 RESULT 1080
 ID ADH28530 standard; protein; 660 AA.
 DE Human PRO polypeptide #175.
 PN US2003022331-A1.
 PD 30-JAN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 10.2%; Score 320; DB 8; Length 660;
 Best Local Similarity 22.4%; Pred. No. 9.8e-12;
 RESULT 1081
 ID ADG54675 standard; protein; 660 AA.
 DE Novel human secreted and transmembrane protein PRO265.
 PN US2003207367-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 10.2%; Score 320; DB 8; Length 660;
 Best Local Similarity 22.4%; Pred. No. 9.8e-12;
 RESULT 1082
 ID ADG59715 standard; protein; 660 AA.
 DE Novel human secreted and transmembrane protein PRO265.
 PN US2003207369-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 10.2%; Score 320; DB 8; Length 660;
 Best Local Similarity 22.4%; Pred. No. 9.8e-12;
 RESULT 1083
 ID ADH20340 standard; protein; 660 AA.
 DE Human secreted/transmembrane protein, #7.
 PN US2004005553-A1.

PD 08-JAN-2004.
 PA (GETH) GENENTECH INC.
 Query Match 10.2%; Score 320; DB 8; Length 660;
 Best Local Similarity 22.4%; Pred. No. 9.8e-12;
 RESULT 1084
 ID ADH43479 standard; protein; 660 AA.
 DE Human PRO polypeptide #23.
 PN US2003224984-A1.
 PD 04-DEC-2003.
 PA (GETH) GENENTECH INC.
 Query Match 10.2%; Score 320; DB 8; Length 660;
 Best Local Similarity 22.4%; Pred. No. 9.8e-12;
 RESULT 1085
 ID ADH07195 standard; protein; 660 AA.
 DE Human secreted/transmembrane protein, #7.
 PN US2004006211-A1.
 PD 08-JAN-2004.
 PA (DESN/) DESNOYERS L.
 PA (GODD/) GODDARD A.
 PA (GODO/) GODOWSKI P J.
 PA (GURN/) GURNEY A L.
 PA (MATH/) MATHER J P.
 PA (WILL/) WILLIAMS P M.
 PA (WOOD/) WOOD W I.
 Query Match 10.2%; Score 320; DB 8; Length 660;
 Best Local Similarity 22.4%; Pred. No. 9.8e-12;
 RESULT 1086
 ID ADH59740 standard; protein; 660 AA.
 DE Human secreted/transmembrane protein, #7.
 PN US2003215904-A1.
 PD 20-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 10.2%; Score 320; DB 8; Length 660;
 Best Local Similarity 22.4%; Pred. No. 9.8e-12;
 RESULT 1087
 ID ADH06768 standard; protein; 660 AA.
 DE Human secreted/transmembrane protein, #7.
 PN US2004005665-A1.
 PD 08-JAN-2004.
 PA (DESN/) DESNOYERS L.
 PA (GODD/) GODDARD A.
 PA (GODO/) GODOWSKI P J.
 PA (GURN/) GURNEY A L.
 PA (MATH/) MATHER J P.
 PA (WILL/) WILLIAMS P M.
 PA (WOOD/) WOOD W I.
 Query Match 10.2%; Score 320; DB 8; Length 660;
 Best Local Similarity 22.4%; Pred. No. 9.8e-12;
 RESULT 1088
 ID ADI81139 standard; protein; 660 AA.
 DE Human PRO polypeptide #175.
 PN US2003207361-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 10.2%; Score 320; DB 8; Length 660;
 Best Local Similarity 22.4%; Pred. No. 9.8e-12;
 RESULT 1089
 ID ADI18510 standard; protein; 660 AA.
 DE Human secreted/transmembrane protein, #7.
 PN US2003152999-A1.
 PD 14-AUG-2003.
 PA (GETH) GENENTECH INC.
 Query Match 10.2%; Score 320; DB 8; Length 660;
 Best Local Similarity 22.4%; Pred. No. 9.8e-12;
 RESULT 1090
 ID ADI65230 standard; protein; 660 AA.
 DE Human secreted/transmembrane protein, #7.
 PN US2003148419-A1.
 PD 07-AUG-2003.
 PA (GETH) GENENTECH INC.
 Query Match 10.2%; Score 320; DB 8; Length 660;
 Best Local Similarity 22.4%; Pred. No. 9.8e-12;
 RESULT 1091
 ID ADH20340 standard; protein; 660 AA.
 DE Human secreted/transmembrane protein, #7.
 PN US2004005553-A1.

ID ADI37493 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003096340-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1092
ID ADG09882 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2004009548-A1.
PD 15-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1093
ID ADH97297 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003190610-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1094
ID ADI15353 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207382-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1095
ID ADG09230 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2004009547-A1.
PD 15-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1096
ID ADI14685 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207383-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1097
ID ADH60400 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2004023331-A1.
PD 05-FEB-2004.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOVSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS J M.
PA (WOOD/) WOOD W I.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1098
ID ADI18280 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207349-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1099
ID ADJ99457 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003187238-A1.

PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1100
ID ADL08650 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003186358-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1101
ID ADM24995 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003096233-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1102
ID ADJ63561 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US20040319164-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1103
ID ADM29741 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003190611-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1104
ID ADJ77456 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2004038336-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1105
ID ADK82824 standard; protein; 660 AA.
DE Human PRO polypeptide #23.
PN US2004043927-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1106
ID ADJ65578 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2004038335-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1107
ID ADM27714 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2004048333-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1108
ID ADM42438 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2004058424-A1.
PD 25-MAR-2004.

PA (GETH) GENENTECH INC.
 Query Match 10.2%; Score 320; DB 8; Length 660;
 Best Local Similarity 22.4%; Pred. No. 9.8e-12;
 RESULT 1109
 ID ADO06063 standard; protein; 660 AA.
 DE Human PRO polypeptide #6.
 PN US6686451-B1.
 PD 03-FEB-2004.
 PA (GETH) GENENTECH INC.
 Query Match 10.2%; Score 320; DB 8; Length 660;
 Best Local Similarity 22.4%; Pred. No. 9.8e-12;
 RESULT 1110
 ID ADM28300 standard; protein; 660 AA.
 DE Human PRO polypeptide #175.
 PN US2004077064-A1.
 PD 22-APR-2004.
 PA (GETH) GENENTECH INC.
 Query Match 10.2%; Score 320; DB 8; Length 660;
 Best Local Similarity 22.4%; Pred. No. 9.8e-12;
 RESULT 1111
 ID ADR10915 standard; protein; 660 AA.
 DE Human secreted/transmembrane protein, #7.
 PN US2004137561-A1.
 PD 15-JUL-2004.
 PA (GETH) GENENTECH INC.
 Query Match 10.2%; Score 320; DB 8; Length 660;
 Best Local Similarity 22.4%; Pred. No. 9.8e-12;
 RESULT 1112
 ID ADR17824 standard; protein; 660 AA.
 DE Human secreted/transmembrane protein, #7.
 PN US2004147017-A1.
 PD 29-JUL-2004.
 PA (ASHK/) ASHKENAZI A.
 PA (BOTS/) BOTSTEIN D.
 PA (DESN/) DESNOYERS L.
 PA (EATO/) EATON D L.
 PA (FERR/) FERRARA N.
 PA (FILV/) FILVAROFF E.
 PA (FONG/) FONG S.
 PA (GAOW/) GAO W.
 PA (GERB/) GERBER H.
 PA (GERR/) GERRITSEN M E.
 PA (GODD/) GODDARD A.
 PA (GODO/) GODOWSKI P J.
 PA (GRIM/) GRIMALDI C J.
 PA (GURN/) GURNEY A L.
 PA (HILL/) HILLAN K J.
 PA (KLJA/) KLJAVIN I J.
 PA (MATH/) MATHER J P.
 PA (PANJ/) PAN J.
 PA (PAON/) PAONI N F.
 PA (ROYM/) ROY M A.
 PA (STEW/) STEWART T A.
 PA (TUMA/) TUMAS D.
 PA (WILL/) WILLIAMS P M.
 PA (WOOD/) WOOD W I.
 Query Match 10.2%; Score 320; DB 8; Length 660;
 Best Local Similarity 22.4%; Pred. No. 9.8e-12;
 RESULT 1113
 ID ADI95782 standard; protein; 660 AA.
 DE Human PRO polypeptide #175.
 PN US2003077659-A1.
 PD 24-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 10.2%; Score 320; DB 8; Length 660;
 Best Local Similarity 22.4%; Pred. No. 9.8e-12;
 RESULT 1114
 ID ADI96334 standard; protein; 660 AA.
 DE Novel human secreted and transmembrane protein PRO265.
 PN US2003207354-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 10.2%; Score 320; DB 8; Length 660;

Best Local Similarity 22.4%; Pred. No. 9.8e-12;
 RESULT 1115
 ID ADI65657 standard; protein; 660 AA.
 DE Human secreted/transmembrane protein, #7.
 PN US2003148371-A1.
 PD 07-AUG-2003.
 PA (GETH) GENENTECH INC.
 Query Match 10.2%; Score 320; DB 8; Length 660;
 Best Local Similarity 22.4%; Pred. No. 9.8e-12;
 RESULT 1116
 ID ADS74463 standard; protein; 660 AA.
 DE Human secreted/transmembrane protein #7.
 PN US2004185531-A1.
 PD 23-SEP-2004.
 PA (ASHK/) ASHKENAZI A.
 PA (BOTS/) BOTSTEIN D.
 PA (DESN/) DESNOYERS L.
 PA (EATO/) EATON D L.
 PA (FERR/) FERRARA N.
 PA (FILV/) FILVAROFF E.
 PA (FONG/) FONG S.
 PA (GAOW/) GAO W.
 PA (GERB/) GERBER H.
 PA (GERR/) GERRITSEN M E.
 PA (GODD/) GODDARD A.
 PA (GODO/) GODOWSKI P J.
 PA (GRIM/) GRIMALDI C J.
 PA (GURN/) GURNEY A L.
 PA (HILL/) HILLAN K J.
 PA (KLJA/) KLJAVIN I J.
 PA (MATH/) MATHER J P.
 PA (PANJ/) PAN J.
 PA (PAON/) PAONI N F.
 PA (ROYM/) ROY M A.
 PA (STEW/) STEWART T A.
 PA (TUMA/) TUMAS D.
 PA (WILL/) WILLIAMS P M.
 PA (WOOD/) WOOD W I.
 Query Match 10.2%; Score 320; DB 8; Length 660;
 Best Local Similarity 22.4%; Pred. No. 9.8e-12;
 RESULT 1117
 ID ADS32286 standard; protein; 660 AA.
 DE Novel human secreted and transmembrane protein PRO265.
 PN US2004203125-A1.
 PD 14-OCT-2004.
 PA (GETH) GENENTECH INC.
 Query Match 10.2%; Score 320; DB 8; Length 660;
 Best Local Similarity 22.4%; Pred. No. 9.8e-12;
 RESULT 1118
 ID ADT03270 standard; protein; 660 AA.
 DE Human PRO polypeptide #175.
 PN US2004214269-A1.
 PD 28-OCT-2004.
 PA (GETH) GENENTECH INC.
 Query Match 10.2%; Score 320; DB 8; Length 660;
 Best Local Similarity 22.4%; Pred. No. 9.8e-12;
 RESULT 1119
 ID ADT03500 standard; protein; 660 AA.
 DE Human secreted/transmembrane protein, #7.
 PN US2003152922-A1.
 PD 14-AUG-2003.
 PA (GETH) GENENTECH INC.
 Query Match 10.2%; Score 320; DB 8; Length 660;
 Best Local Similarity 22.4%; Pred. No. 9.8e-12;
 RESULT 1120
 ID ADU06386 standard; protein; 660 AA.
 DE Novel bronchial cancer-associated human protein SeqID610.
 PN DE10316701-A1.
 PD 04-NOV-2004.
 PA (HINZ/) HINZMANN B.
 PA (HERM/) HERMANN K.
 PA (CAST/) HEIDEN CASTANOS-VELEZ E.
 Query Match 10.2%; Score 320; DB 8; Length 660;

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Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1121
ID ADZ0321 standard; protein; 660 AA.
DE Human secreted/transmembrane PRO265 protein.
PN US2005074837-A1.
PD 07-APR-2005.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 9; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1122
ID AEA37738 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2005112725-A1.
PD 26-MAY-2005.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 9; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1123
ID AEB14067 standard; protein; 660 AA.
DE Cancer cell diagnosis method-related human protein - SEQ ID 350.
PN US2005153396-A1.
PD 14-JUL-2005.
PA (BAKE/) BAKER K P.
PA (BERE/) BERESINI M.
PA (DEFO/) DEFORGE L.
PA (DESN/) DESNOYERS L.
PA (FILV/) FILVAROFF E.
PA (GAOW/) GAO W.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (SHER/) SHERWOOD S.
PA (SMIT/) SMITH V.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WATA/) WATANABE C K.
PA (WOOD/) WOOD W I.
PA (ZHAN/) ZHANG Z.
Query Match 10.2%; Score 320; DB 9; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1124
ID AED23772 standard; protein; 660 AA.
DE Human secreted protein PRO 265, SEQ ID 28.
PN US2005214904-A1.
PD 29-SEP-2005.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 9; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1125
ID AED86265 standard; protein; 660 AA.
DE Human PRO amino acid sequence, seq id 350.
PN US2005245730-A1.
PD 03-NOV-2005.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 9; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1126
ID AEB68941 standard; protein; 660 AA.
DE Fibromodulin homologous PRO265 protein, SEQ ID 28.
PN US6974689-B1.
PD 13-DEC-2005.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 10; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1127
ID ADT77808 standard; protein; 452 AA.
DE Chimeric Nogo receptor polypeptide.
PN WO2004090103-A2.
PD 21-OCT-2004.
PA (UYRP ) UNIV ROCHESTER.
Query Match 10.2%; Score 318.5; DB 8; Length 452;
Best Local Similarity 27.3%; Pred. No. 7.9e-12;
RESULT 1128
ID ADT77802 standard; protein; 452 AA.
DE Chimeric Nogo receptor polypeptide.
PN WO2004090103-A2.
PD 21-OCT-2004.
PA (UYRP ) UNIV ROCHESTER.
Query Match 10.2%; Score 318.5; DB 8; Length 452;
Best Local Similarity 27.8%; Pred. No. 7.9e-12;
RESULT 1129
ID AEF79023 standard; protein; 648 AA.
DE Mouse NAG14 polypeptide SEQ ID NO: 6.
PN US2006035826-A1.
PD 16-FEB-2006.
PA (LINJ/) LIN J C.
PA (ROSE/) ROSENTHAL A.
Query Match 10.1%; Score 317.5; DB 10; Length 648;
Best Local Similarity 24.2%; Pred. No. 1.4e-11;
RESULT 1130
ID AAE13006 standard; protein; 713 AA.
DE Human leucine-rich repeat (LRR) family member protein.
PN WO200175105-A2.
PD 11-OCT-2001.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 10.1%; Score 317.5; DB 4; Length 713;
Best Local Similarity 23.1%; Pred. No. 1.5e-11;
RESULT 1131
ID AAU91335 standard; protein; 713 AA.
DE Human novel secreted protein LP223(a).
PN WO200214358-A2.
PD 21-FEB-2002.
PA (ELIL ) LILLY & CO ELI.
Query Match 10.1%; Score 316.5; DB 5; Length 713;
Best Local Similarity 23.1%; Pred. No. 1.8e-11;
RESULT 1132
ID ABG97991 standard; protein; 713 AA.
DE Human nervous system leucine rich repeat protein (HLRRNS1) #2.
PN WO200274959-A2.
PD 26-SEP-2002.
PA (BRIM ) BRISTOL-MYERS SQUIBB CO.
Query Match 10.1%; Score 316.5; DB 5; Length 713;
Best Local Similarity 23.1%; Pred. No. 1.8e-11;
RESULT 1133
ID ABU52381 standard; protein; 713 AA.
DE Human GPCR related protein NOV31a.
PN WO200279398-A2.
PD 10-OCT-2002.
PA (CURA-) CURAGEN CORP.
Query Match 10.1%; Score 316.5; DB 6; Length 713;
Best Local Similarity 23.1%; Pred. No. 1.8e-11;
RESULT 1134
ID ADT77796 standard; protein; 474 AA.
DE Chimeric Nogo receptor polypeptide.
PN WO2004090103-A2.
PD 21-OCT-2004.
PA (UYRP ) UNIV ROCHESTER.
Query Match 10.0%; Score 314.5; DB 8; Length 474;
Best Local Similarity 27.8%; Pred. No. 1.5e-11;
RESULT 1135
ID AAU91341 standard; protein; 656 AA.
DE Human novel secreted protein LP223(b).
PN WO200214358-A2.
PD 21-FEB-2002.
PA (ELIL ) LILLY & CO ELI.
Query Match 10.0%; Score 313.5; DB 5; Length 656;
Best Local Similarity 23.6%; Pred. No. 2.5e-11;
RESULT 1136
ID ADL24097 standard; protein; 713 AA.
DE Human NOVX polypeptide #71.
PN US2004002120-A1.
PD 01-JAN-2004.
PA (KEKU/) KEKUDA R.
PA (TCHE/) TCHERNEV V T.
PA (LIUX/) LIU X.

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(SPVT/) SPYTEK K A.
PA (PATT/) PATTURAJAN M.
PA (BURG/) BURGESS C E.
PA (VERN/) VERNET C A M.
PA (LILL/) LI L.
PA (GORM/) GORMAN L.
PA (MALY/) MALYANKAR U M.
PA (BOLD/) BOLDOG F L.
PA (GUOX/) GUO X.
PA (SHEN/) SHENOY S G.
PA (PAPI/) PADIGARU M.
PA (TAUP/) TAPIER R J.
PA (MILL/) MILLER C E.
PA (CASM/) CASMAN S J.
PA (PENA/) PENNA C E A.
PA (GANG/) GANGOLLI E A.
PA (GUSE/) GUSEV V Y.
PA (SMIT/) SMITHSON G.
PA (ZERR/) ZERHUSEN B D.
PA (GERL/) GERLACH V.
PA (POCH/) POCHART P F.
PA (FERN/) FERNANDES E R.
PA (SHIM/) SHIMKETS R A.
PA (RAST/) RASTELLI L.
PA (SPAD/) SPADERNA S K.
PA (LARO/) LAROCHELLE W J.
PA (ZHON/) ZHONG M.
PA (KHRA/) KHRAMTSOV N V.
PA (VOSS/) VOSS E Z.
PA (HERR/) HERRMANN J L.
Query Match
Best Local Similarity 10.0%; Score 313.5; DB 8; Length 713;
RESULT 1137
ID AAE09437 standard; protein; 592 AA.
DE Human sbgTango79a protein.
PN WO200160850-A1.
PD 23-AUG-2001.
PA (SMIK/) SMITHKLINE BEECHAM CORP.
PA (SMIK/) SMITHKLINE BEECHAM PLC.
Query Match
Best Local Similarity 10.0%; Score 312; DB 4; Length 592;
RESULT 1138
ID AAE25351 standard; protein; 592 AA.
DE Human LP polypeptide, LP243.
PN WO200248361-A2.
PD 20-JUN-2002.
PA (ELIL/) LILLY & CO ELI.
Query Match
Best Local Similarity 10.0%; Score 312; DB 5; Length 592;
RESULT 1139
ID AAU91329 standard; protein; 592 AA.
DE Human novel secreted protein LP243 (b).
PN WO200214358-A2.
PD 21-FEB-2002.
PA (ELIL/) LILLY & CO ELI.
Query Match
Best Local Similarity 10.0%; Score 312; DB 5; Length 592;
RESULT 1140
ID ABP60996 standard; protein; 592 AA.
DE Novel human protein. SEQ ID 83.
PN WO200250105-A1.
PD 27-JUN-2002.
PA (SMIK/) SMITHKLINE BEECHAM CORP.
PA (SMIK/) SMITHKLINE BEECHAM PLC.
PA (GLAX/) GLAXO GROUP LTD.
Query Match
Best Local Similarity 10.0%; Score 312; DB 5; Length 592;
RESULT 1141
ID AAU79167 standard; protein; 592 AA.
DE Human leucine-rich repeat proteins-like protein NOV4.
PN WO200214368-A2.
PD 21-FEB-2002.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 10.0%; Score 312; DB 5; Length 592;
RESULT 1142
ID ABG74693 standard; protein; 592 AA.
DE Human CGDD protein 6803363CD1 SEQ ID 19.
PN WO2003014322-A2.
PD 20-FEB-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match
Best Local Similarity 10.0%; Score 312; DB 6; Length 592;
RESULT 1143
ID ADE03417 standard; protein; 592 AA.
DE Human immunoglobulin superfamily member BGS-2.
PN US2003195163-A1.
PD 16-OCT-2003.
PA (WUSS/) WU S.
PA (KRYL/) KRYSTEK S R.
PA (LEEL/) LEE L.
PA (FEDE/) FEDER J N.
PA (CHEN/) CHENG J D.
Query Match
Best Local Similarity 10.0%; Score 312; DB 7; Length 592;
RESULT 1144
ID ADU02709 standard; protein; 592 AA.
DE Novel human polypeptide seqid 1176.
PN WO2004093804-A2.
PD 04-NOV-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match
Best Local Similarity 10.0%; Score 312; DB 8; Length 592;
RESULT 1145
ID ABG61770 standard; protein; 608 AA.
DE Novel leucine-rich protein.
PN WO200229058-A2.
PD 11-APR-2002.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 10.0%; Score 312; DB 5; Length 608;
RESULT 1146
ID ABG97967 standard; protein; 634 AA.
DE Human nervous system leucine rich repeat protein (HLRRNS1) #1.
PN WO200274959-A2.
PD 26-SEP-2002.
PA (BRIM/) BRISTOL-MYERS SQUIBB CO.
Query Match
Best Local Similarity 9.9%; Score 311; DB 5; Length 634;
RESULT 1147
ID ABR55628 standard; protein; 420 AA.
DE Amino acid sequence of rat Nogo-66 receptor homologue NgrH1.
PN WO2003035687-A1.
PD 01-MAY-2003.
PA (NOVS/) NOVARTIS AG.
PA (NOVS/) NOVARTIS PHARMA GMBH.
Query Match
Best Local Similarity 9.9%; Score 310.5; DB 6; Length 420;
RESULT 1148
ID ADT77788 standard; protein; 420 AA.
DE Rat Nogo receptor 2 polypeptide.
PN WO2004090103-A2.
PD 21-OCT-2004.
PA (UYRP/) UNIV ROCHESTER.
Query Match
Best Local Similarity 9.9%; Score 310.5; DB 8; Length 420;
RESULT 1149
ID AAO23115 standard; protein; 674 AA.
DE FLRT1 'human modifier of p53 pathway' protein.
PN WO2003035833-A2.
PD 01-MAY-2003.
PA (EXEL-) EXELIXIS INC.
Query Match
Best Local Similarity 9.9%; Score 310.5; DB 6; Length 674;
RESULT 1150
ID ADH17606 standard; protein; 674 AA.

```
DE Human NOV19a protein - SEQ ID 296.
PN WO2003093432-A2.
PD 13-NOV-2003.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 9.9%; Score 310.5; DB 8; Length 674;
RESULT 1151
ID ADHI17628 standard; protein; 674 AA.
DE Human NOV191 protein - SEQ ID 318.
PN WO2003093432-A2.
PD 13-NOV-2003.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 9.9%; Score 310.5; DB 8; Length 674;
RESULT 1152
ID ADHI17630 standard; protein; 674 AA.
DE Human NOV19m protein - SEQ ID 320.
PN WO2003093432-A2.
PD 13-NOV-2003.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 9.9%; Score 310.5; DB 8; Length 674;
RESULT 1153
ID ADHI17634 standard; protein; 674 AA.
DE Human NOV19o protein - SEQ ID 324.
PN WO2003093432-A2.
PD 13-NOV-2003.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 9.9%; Score 310.5; DB 8; Length 674;
RESULT 1154
ID ADHI17632 standard; protein; 674 AA.
DE Human NOV19n protein - SEQ ID 322.
PN WO2003093432-A2.
PD 13-NOV-2003.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 9.9%; Score 310.5; DB 8; Length 674;
RESULT 1155
ID ABO27346 standard; protein; 585 AA.
DE Human secreted/transmembrane polypeptide PRO1865.
PN US2003009012-A1.
PD 09-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 585;
RESULT 1156
ID ABO34232 standard; protein; 585 AA.
DE Human secreted/transmembrane polypeptide PRO 1865.
PN US2003060601-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 585;
RESULT 1157
ID AAU29215 standard; protein; 649 AA.
DE Human PRO polypeptide sequence #192.
PN WO200168848-A2.
PD 20-SEP-2001.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 4; Length 649;
RESULT 1158
ID AAB70533 standard; protein; 649 AA.
DE Human PRO3 protein sequence SEQ ID NO:6.
PN WO200110902-A2.
PD 15-FEB-2001.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 9.9%; Score 309; DB 4; Length 649;
RESULT 1159
ID AAB87591 standard; protein; 649 AA.
DE Human PRO1865.
PN WO200116318-A2.
PD 08-MAR-2001.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 4; Length 649;
RESULT 1160
ID ABG95916 standard; protein; 649 AA.
DE Human secreted/transmembrane protein PRO1865.
PN US2002119130-A1.
PD 29-AUG-2002.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 5; Length 649;
RESULT 1161
ID ABB84953 standard; protein; 649 AA.
DE Human PRO1865 protein sequence SEQ ID NO:274.
PN WO200200690-A2.
PD 03-JAN-2002.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 5; Length 649;
RESULT 1162
ID ABP70109 standard; protein; 649 AA.
DE Human NOV27a.
PN WO200272771-A2.
PD 19-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 9.9%; Score 309; DB 5; Length 649;
RESULT 1163
ID ABB95559 standard; protein; 649 AA.
DE Human angiogenesis related protein PRO1865 SEQ ID NO: 274.
PN WO200208284-A2.
PD 31-JAN-2002.
PA (GETH ) GENENTECH INC.
PA (BAKE/) BAKER K P.
PA (FERR/) FERRARA N.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (MARS/) MARSTERS S A.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (STEP/) STEPHAN J F.
PA (WATA/) WATANABE C K.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match
Best Local Similarity 9.9%; Score 309; DB 5; Length 649;
RESULT 1164
ID ABUS8591 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003027272-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1165
ID ABUS8139 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
PN US2003032127-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1166
ID ABUS4454 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003032112-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
DE Human PRO1865.
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RESULT 1167
 ID ABR66328 standard; protein; 649 AA.
 DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
 PN US2003027278-A1.
 PD 06-FEB-2003.
 Query Match
 Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
 22.3%; Pred. No. 4.8e-11;
 RESULT 1168
 ID ABR65718 standard; protein; 649 AA.
 DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
 PN US2003036159-A1.
 PD 20-FEB-2003.
 Query Match
 Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
 22.3%; Pred. No. 4.8e-11;
 RESULT 1169
 ID ABR99658 standard; protein; 649 AA.
 DE Human secreted/transmembrane protein (PRO) #192.
 PN US2003040070-A1.
 PD 27-FEB-2003.
 Query Match
 Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
 22.3%; Pred. No. 4.8e-11;
 RESULT 1170
 ID ABR62897 standard; protein; 649 AA.
 DE Human PRO polypeptide #192.
 PN US2003032113-A1.
 PD 13-FEB-2003.
 Query Match
 Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
 22.3%; Pred. No. 4.8e-11;
 RESULT 1171
 ID ABR90018 standard; protein; 649 AA.
 DE Novel human secreted and transmembrane protein PRO1865.
 PN US2003036147-A1.
 PD 20-FEB-2003.
 Query Match
 Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
 22.3%; Pred. No. 4.8e-11;
 RESULT 1172
 ID ABR68267 standard; protein; 649 AA.
 DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
 PN US2003027264-A1.
 PD 06-FEB-2003.
 Query Match
 Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
 22.3%; Pred. No. 4.8e-11;
 RESULT 1173
 ID ABR96320 standard; protein; 649 AA.
 DE Novel human secreted and transmembrane protein PRO1865.
 PN US2003036144-A1.
 PD 20-FEB-2003.
 Query Match
 Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
 22.3%; Pred. No. 4.8e-11;
 RESULT 1174
 ID ABR92751 standard; protein; 649 AA.
 DE Human secreted/transmembrane protein (PRO) #192.
 PN US2003036149-A1.
 PD 20-FEB-2003.
 Query Match
 Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
 22.3%; Pred. No. 4.8e-11;
 RESULT 1175
 ID ABR08828 standard; protein; 649 AA.
 DE Human secreted/transmembrane protein (PRO) #192.
 PN US2003044923-A1.
 PD 06-MAR-2003.
 Query Match
 Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
 22.3%; Pred. No. 4.8e-11;
 RESULT 1176
 ID ABR02880 standard; protein; 649 AA.
 DE Human secreted/transmembrane protein (PRO) #192.
 PN US2003040062-A1.
 PD 27-FEB-2003.
 Query Match
 Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
 22.3%; Pred. No. 4.8e-11;
 RESULT 1177
 ID ABR75034 standard; protein; 649 AA.
 DE Human secreted polypeptide PRO1865, SEQ ID NO:384.

PN US2003040056-A1.
 PD 27-FEB-2003.
 Query Match
 Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
 22.3%; Pred. No. 4.8e-11;
 RESULT 1178
 ID ABR94796 standard; protein; 649 AA.
 DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
 PN US2003044926-A1.
 PD 06-MAR-2003.
 Query Match
 Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
 22.3%; Pred. No. 4.8e-11;
 RESULT 1179
 ID ABR65769 standard; protein; 649 AA.
 DE Human PRO polypeptide #192.
 PN US2003036140-A1.
 PD 20-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match
 Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
 22.3%; Pred. No. 4.8e-11;
 RESULT 1180
 ID ABR98929 standard; protein; 649 AA.
 DE Novel human secreted and transmembrane protein PRO1865.
 PN US2003013153-A1.
 PD 16-JAN-2003.
 Query Match
 Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
 22.3%; Pred. No. 4.8e-11;
 RESULT 1181
 ID ABR98144 standard; protein; 649 AA.
 DE Novel human secreted and transmembrane protein PRO1865.
 PN US2003017544-A1.
 PD 23-JAN-2003.
 Query Match
 Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
 22.3%; Pred. No. 4.8e-11;
 RESULT 1182
 ID ABR91850 standard; protein; 649 AA.
 DE Novel human secreted and transmembrane protein PRO1865.
 PN US2003027277-A1.
 PD 06-FEB-2003.
 Query Match
 Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
 22.3%; Pred. No. 4.8e-11;
 RESULT 1183
 ID ABR9543 standard; protein; 649 AA.
 DE Human PRO polypeptide #192.
 PN US2003036141-A1.
 PD 20-FEB-2003.
 Query Match
 Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
 22.3%; Pred. No. 4.8e-11;
 RESULT 1184
 ID ABR6384 standard; protein; 649 AA.
 DE Human secreted/transmembrane protein (PRO) #192.
 PN US2003036146-A1.
 PD 20-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match
 Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
 22.3%; Pred. No. 4.8e-11;
 RESULT 1185
 ID ABR67597 standard; protein; 649 AA.
 DE Human secreted/transmembrane protein (PRO) #192.
 PN US2003036162-A1.
 PD 20-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match
 Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
 22.3%; Pred. No. 4.8e-11;
 RESULT 1186
 ID ABR0625 standard; protein; 649 AA.
 DE Human PRO protein #192.
 PN US2003036137-A1.
 PD 20-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match
 Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
 22.3%; Pred. No. 4.8e-11;
 RESULT 1187
 ID ABR90941 standard; protein; 649 AA.

DE Novel human secreted and transmembrane protein PRO1865.
PN US2003018173-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC. 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1188
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
ID ABO34000 standard; protein; 649 AA.
DE Human secreted/transmembrane protein PRO1865.
PN US2003009013-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC. 9.9%; Score 309; DB 6; Length 649;
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1189
ID ABR99543 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003040063-A1.
PD 27-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1190
ID ABR98933 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003040084-A1.
PD 27-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1191
ID ABO16456 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003027267-A1.
PD 06-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1192
ID ABR2356 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003036160-A1.
PD 20-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1193
ID ABO18997 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003044925-A1.
PD 06-MAR-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1194
ID ABR78418 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003054474-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC. 9.9%; Score 309; DB 6; Length 649;
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1195
ID ABUT2017 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
PN US2003018183-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC. 9.9%; Score 309; DB 6; Length 649;
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1196
ID ABUS154 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
PN US2003032114-A1.
PD 13-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1197

ID ABO00293 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
PN US2003032101-A1.
PD 13-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1198
ID ABO11625 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003036124-A1.
PD 20-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1199
ID ABO02270 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003040054-A1.
PD 27-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1200
ID ABUS8844 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
PN US2003036133-A1.
PD 20-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1201
ID ABUS3539 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003036134-A1.
PD 20-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1202
ID ABO06340 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
PN US2003022294-A1.
PD 30-JAN-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1203
ID ABR59376 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003027275-A1.
PD 06-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1204
ID ABO09438 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003027324-A1.
PD 06-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1205
ID ABO19302 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
PN US2003036118-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC. 9.9%; Score 309; DB 6; Length 649;
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1206
ID ABO11320 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003036123-A1.
PD 20-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1207
ID ABR66938 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.

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PN US2003036148-A1.
PD 20-FEB-2003.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1208
ID ABO16151 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003040060-A1.
PD 27-FEB-2003.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1209
ID ABO13857 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003044916-A1.
PD 06-MAR-2003.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1210
ID ABO71571 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865.
PN US2003013855-A1.
PD 16-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1211
ID ABO65760 standard; protein; 649 AA.
DE Human secreted/transmembrane protein, SEQ ID 384.
PN US2003036156-A1.
PD 20-FEB-2003.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1212
ID ABO07608 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003032117-A1.
PD 13-FEB-2003.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1213
ID ABO03795 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003036128-A1.
PD 20-FEB-2003.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1214
ID ABR67243 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003027266-A1.
PD 06-FEB-2003.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1215
ID ABO15846 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003054483-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1216
ID ABO56127 standard; protein; 649 AA.
DE Human secreted/transmembrane protein, PRO1865.
PN US2003022298-A1.
PD 30-JAN-2003.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1217
ID ABO72352 standard; protein; 649 AA.
DE Human PRO polypeptide #66.
PN US2002182638-A1.
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PD 05-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1218
ID ABO65455 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003032102-A1.
PD 13-FEB-2003.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1219
ID ABO95400 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
PN US2003036117-A1.
PD 20-FEB-2003.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1220
ID ABO71303 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003036143-A1.
PD 20-FEB-2003.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1221
ID ABO07913 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003032130-A1.
PD 13-FEB-2003.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1222
ID ABR70154 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003032138-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1223
ID ABR69487 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003036132-A1.
PD 20-FEB-2003.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1224
ID ABO01628 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003008353-A1.
PD 09-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1225
ID ABO81430 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003017542-A1.
PD 23-JAN-2003.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1226
ID ABR60227 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003032137-A1.
PD 13-FEB-2003.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1227
ID ABO91025 standard; protein; 649 AA.
DE Human PRO polypeptide #66.
PN US2003018168-A1.
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PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1228
ID ABR67962 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003027269-A1.
PD 06-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1229
ID ABR65350 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003027268-A1.
PD 06-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1230
ID ABR68572 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003027274-A1.
PD 06-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1231
ID ABR71984 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003032135-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1232
ID ABR85464 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003022295-A1.
PD 30-JAN-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1233
ID ABR89154 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003022297-A1.
PD 30-JAN-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1234
ID ABR83234 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003032105-A1.
PD 13-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1235
ID ABR95090 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
PN US2003032123-A1.
PD 13-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1236
ID ABR90638 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
PN US2003032108-A1.
PD 13-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1237
ID ABR84149 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003032111-A1.
PD 13-FEB-2003.

Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1238
ID ABR93800 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
PN US2003032119-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1239
ID ABR65045 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003027283-A1.
PD 06-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1240
ID ABR68877 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003027271-A1.
PD 06-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1241
ID ABO06693 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003036125-A1.
PD 20-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1242
ID ABR99238 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003040068-A1.
PD 27-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1243
ID ABR57122 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003027280-A1.
PD 06-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1244
ID ABR86074 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
PN US2003022300-A1.
PD 30-JAN-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1245
ID ABR2361 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
PN US2003036136-A1.
PD 20-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1246
ID ABR87372 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003036138-A1.
PD 20-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1247
ID ABR83844 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003032109-A1.
PD 13-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1248
ID ABR83844 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003032109-A1.
PD 13-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;

RESULT 1248
ID ABO08218 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003040066-A1.
PD 27-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1249
ID ABU92541 standard; protein; 649 AA.
DE Human secreted/transmembrane protein PRO1865.
PN US2003045684-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1250
ID ABU81929 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
PN US2003032104-A1.
PD 13-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1251
ID ABU66093 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
PN US2003036157-A1.
PD 20-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1252
ID ABU81211 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865.
PN US2003027212-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1253
ID ABR59922 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003032120-A1.
PD 13-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1254
ID ABU94110 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
PN US2003036155-A1.
PD 20-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1255
ID ABU99963 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
PN US2003022296-A1.
PD 30-JAN-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1256
ID ABR66633 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003027281-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1257
ID ABR91051 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003040058-A1.
PD 27-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1258
ID ABO53325 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
PN US2003027986-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1259
ID ABU94478 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003017540-A1.
PD 23-JAN-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1260
ID ABU79360 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003032106-A1.
PD 13-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1261
ID ABU86689 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003032129-A1.
PD 13-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1262
ID ABU86994 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
PN US2003032131-A1.
PD 13-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1263
ID ABU94783 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003032103-A1.
PD 13-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1264
ID ABO04710 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003032107-A1.
PD 13-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1265
ID ABR70459 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003032139-A1.
PD 13-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1266
ID ABU98624 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003022301-A1.
PD 30-JAN-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1267
ID ABR66023 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003036165-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1268
ID ABR66023 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003036165-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;

ID ABR64740 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003027262-A1.
PD 06-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1269
ID ABU79665 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003032110-A1.
PD 13-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1270
ID ABU93056 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003036142-A1.
PD 20-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1271
ID ABU96015 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003036145-A1.
PD 20-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1272
ID ABU91235 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
PN US2003036154-A1.
PD 20-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1273
ID ABU90328 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
PN US2003036153-A1.
PD 20-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1274
ID ABO09743 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003044931-A1.
PD 06-MAR-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1275
ID ABO11015 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003036150-A1.
PD 20-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1276
ID ABR71069 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003040069-A1.
PD 27-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1277
ID ABU98328 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
PN US2002183493-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1278
ID ABU87677 standard; protein; 649 AA.
DE Human PRO polypeptide #192.

PN US2003022293-A1.
PD 30-JAN-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1279
ID ABU91545 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003032128-A1.
PD 13-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1280
ID ABU93333 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
PN US2003036634-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1281
ID ABU84759 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003032116-A1.
PD 13-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1282
ID ABR69849 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003032122-A1.
PD 13-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1283
ID ABU80226 standard; protein; 649 AA.
DE Human PRO protein #192.
PN US2003036139-A1.
PD 20-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1284
ID ABU82540 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
PN US2002183494-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1285
ID ABU93495 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003017541-A1.
PD 23-JAN-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1286
ID ABO10048 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003017543-A1.
PD 23-JAN-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1287
ID ABO09133 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003036152-A1.
PD 20-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1288
ID ABU96504 standard; protein; 649 AA.
DE Human PRO polypeptide #86.
PN US2003027993-A1.

PD 06-FEB-2003.
PA (GETH) GENENTECH INC. 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1289
ID ABRU10701 standard; protein; 649 AA.
DE Human secreted/transmembrane protein #192.
PN US2002127584-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC. 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1290
ID ABRU72174 standard; protein; 649 AA.
DE Human PRO polypeptide #66.
PN US2003023042-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC. 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1291
ID ABRU95710 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003032115-A1.
PD 13-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1292
ID ABRU96919 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
PN US2003032140-A1.
PD 13-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1293
ID ABR70764 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003040076-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC. 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1294
ID ABO05115 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
PN US2003008352-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC. 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1295
ID ABO08523 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003044922-A1.
PD 06-MAR-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1296
ID ABO05730 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003032118-A1.
PD 13-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1297
ID ABR74119 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003036135-A1.
PD 20-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1298
ID ABR95711 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.

DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003054455-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC. 9.9%; Score 309; DB 6; Length 649;
Query Match 22.3%; Pred. No. 4.8e-11;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1299
ID ABR81008 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003049741-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC. 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1300
ID ABR81313 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003049743-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC. 9.9%; Score 309; DB 6; Length 649;
Query Match 22.3%; Pred. No. 4.8e-11;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1301
ID ABRM01009 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003049769-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC. 9.9%; Score 309; DB 6; Length 649;
Query Match 22.3%; Pred. No. 4.8e-11;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1302
ID ABR88611 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003068743-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC. 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1303
ID ABRM7432 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003054479-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC. 9.9%; Score 309; DB 6; Length 649;
Query Match 22.3%; Pred. No. 4.8e-11;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1304
ID ABO28916 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003068685-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC. 9.9%; Score 309; DB 6; Length 649;
Query Match 22.3%; Pred. No. 4.8e-11;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1305
ID ABO31661 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003068725-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC. 9.9%; Score 309; DB 6; Length 649;
Query Match 22.3%; Pred. No. 4.8e-11;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1306
ID ABRM08078 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003068752-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC. 9.9%; Score 309; DB 6; Length 649;
Query Match 22.3%; Pred. No. 4.8e-11;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1307
ID ABO40558 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.

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PN US2003068682-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC. 9.9%; Score 309; DB 6; Length 649;
Query Match 22.3%; Pred. No. 4.8e-11;
Best Local Similarity
RESULT 1308
ID ABO35983 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003068701-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC. 9.9%; Score 309; DB 6; Length 649;
Query Match 22.3%; Pred. No. 4.8e-11;
Best Local Similarity
RESULT 1309
ID ABO44122 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003068755-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC. 9.9%; Score 309; DB 6; Length 649;
Query Match 22.3%; Pred. No. 4.8e-11;
Best Local Similarity
RESULT 1310
ID ADA78136 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003073180-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC. 9.9%; Score 309; DB 6; Length 649;
Query Match 22.3%; Pred. No. 4.8e-11;
Best Local Similarity
RESULT 1311
ID ABM24917 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003104539-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC. 9.9%; Score 309; DB 6; Length 649;
Query Match 22.3%; Pred. No. 4.8e-11;
Best Local Similarity
RESULT 1312
ID ABO03185 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003036131-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC. 9.9%; Score 309; DB 6; Length 649;
Query Match 22.3%; Pred. No. 4.8e-11;
Best Local Similarity
RESULT 1313
ID ABR90441 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003040075-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC. 9.9%; Score 309; DB 6; Length 649;
Query Match 22.3%; Pred. No. 4.8e-11;
Best Local Similarity
RESULT 1314
ID ABM17355 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003054459-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC. 9.9%; Score 309; DB 6; Length 649;
Query Match 22.3%; Pred. No. 4.8e-11;
Best Local Similarity
RESULT 1315
ID ABR95101 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003044930-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC. 9.9%; Score 309; DB 6; Length 649;
Query Match 22.3%; Pred. No. 4.8e-11;
Best Local Similarity
RESULT 1316
ID ABR95406 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003040071-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC. 9.9%; Score 309; DB 6; Length 649;
Query Match 22.3%; Pred. No. 4.8e-11;
Best Local Similarity
RESULT 1317
ID ABB17189 standard; protein; 649 AA.
DE Human transmembrane PRO polypeptide (SeqID 132).
PN US2003050462-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC. 9.9%; Score 309; DB 6; Length 649;
Query Match 22.3%; Pred. No. 4.8e-11;
Best Local Similarity
RESULT 1318
ID ABO21644 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003054471-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC. 9.9%; Score 309; DB 6; Length 649;
Query Match 22.3%; Pred. No. 4.8e-11;
Best Local Similarity
RESULT 1319
ID ABR97908 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003064452-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC. 9.9%; Score 309; DB 6; Length 649;
Query Match 22.3%; Pred. No. 4.8e-11;
Best Local Similarity
RESULT 1320
ID ABR87696 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003068705-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC. 9.9%; Score 309; DB 6; Length 649;
Query Match 22.3%; Pred. No. 4.8e-11;
Best Local Similarity
RESULT 1321
ID ABM77737 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003054473-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC. 9.9%; Score 309; DB 6; Length 649;
Query Match 22.3%; Pred. No. 4.8e-11;
Best Local Similarity
RESULT 1322
ID ABM27967 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003064440-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC. 9.9%; Score 309; DB 6; Length 649;
Query Match 22.3%; Pred. No. 4.8e-11;
Best Local Similarity
RESULT 1323
ID ABM06248 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003068704-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC. 9.9%; Score 309; DB 6; Length 649;
Query Match 22.3%; Pred. No. 4.8e-11;
Best Local Similarity
RESULT 1324
ID ABM03754 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003068722-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC. 9.9%; Score 309; DB 6; Length 649;
Query Match 22.3%; Pred. No. 4.8e-11;
Best Local Similarity
RESULT 1325
ID ABM35205 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003073183-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC. 9.9%; Score 309; DB 6; Length 649;
Query Match 22.3%; Pred. No. 4.8e-11;
Best Local Similarity
RESULT 1326
ID ABM26442 standard; protein; 649 AA.
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DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
 PN US2003104549-A1.
 PD 05-JUN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 9.9%; Score 309; DB 6; Length 649;
 Best Local Similarity 22.3%; Pred. No. 4.8e-11;
 RESULT 1327
 ID ABO48224 standard; protein; 649 AA.
 DE Human secreted/transmembrane protein (PRO) #192.
 PN US2003049749-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 9.9%; Score 309; DB 6; Length 649;
 Best Local Similarity 22.3%; Pred. No. 4.8e-11;
 RESULT 1328
 ID ABR92966 standard; protein; 649 AA.
 DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
 PN US2003064462-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 9.9%; Score 309; DB 6; Length 649;
 Best Local Similarity 22.3%; Pred. No. 4.8e-11;
 RESULT 1329
 ID ABO24727 standard; protein; 649 AA.
 DE Human secreted/transmembrane protein (PRO) #192.
 PN US2003065159-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 9.9%; Score 309; DB 6; Length 649;
 Best Local Similarity 22.3%; Pred. No. 4.8e-11;
 RESULT 1330
 ID ABO41738 standard; protein; 649 AA.
 DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
 PN US2003064447-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 9.9%; Score 309; DB 6; Length 649;
 Best Local Similarity 22.3%; Pred. No. 4.8e-11;
 RESULT 1331
 ID ABO2839 standard; protein; 649 AA.
 DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
 PN US2003073184-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 9.9%; Score 309; DB 6; Length 649;
 Best Local Similarity 22.3%; Pred. No. 4.8e-11;
 RESULT 1332
 ID ABO16135 standard; protein; 649 AA.
 DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
 PN US2003064463-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 9.9%; Score 309; DB 6; Length 649;
 Best Local Similarity 22.3%; Pred. No. 4.8e-11;
 RESULT 1333
 ID ABO27696 standard; protein; 649 AA.
 DE Human secreted/transmembrane protein (PRO) #192.
 PN US2003064451-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 9.9%; Score 309; DB 6; Length 649;
 Best Local Similarity 22.3%; Pred. No. 4.8e-11;
 RESULT 1334
 ID ABO29187 standard; protein; 649 AA.
 DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
 PN US2003068721-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 9.9%; Score 309; DB 6; Length 649;
 Best Local Similarity 22.3%; Pred. No. 4.8e-11;
 RESULT 1335
 ID ABO71163 standard; protein; 649 AA.
 DE Human secreted polypeptide PRO1865, SEQ ID NO:384.

PN US2003068699-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 9.9%; Score 309; DB 6; Length 649;
 Best Local Similarity 22.3%; Pred. No. 4.8e-11;
 RESULT 1336
 ID ABO21257 standard; protein; 649 AA.
 DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
 PN US2003068707-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 9.9%; Score 309; DB 6; Length 649;
 Best Local Similarity 22.3%; Pred. No. 4.8e-11;
 RESULT 1337
 ID ABO09603 standard; protein; 649 AA.
 DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
 PN US2003073175-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 9.9%; Score 309; DB 6; Length 649;
 Best Local Similarity 22.3%; Pred. No. 4.8e-11;
 RESULT 1338
 ID ABO41473 standard; protein; 649 AA.
 DE Human secreted/transmembrane protein (PRO) #192.
 PN US2003068695-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 9.9%; Score 309; DB 6; Length 649;
 Best Local Similarity 22.3%; Pred. No. 4.8e-11;
 RESULT 1339
 ID ABO36288 standard; protein; 649 AA.
 DE Human PRO polypeptide #192.
 PN US2003068703-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 9.9%; Score 309; DB 6; Length 649;
 Best Local Similarity 22.3%; Pred. No. 4.8e-11;
 RESULT 1340
 ID ABO43817 standard; protein; 649 AA.
 DE Human PRO polypeptide #192.
 PN US2003068732-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 9.9%; Score 309; DB 6; Length 649;
 Best Local Similarity 22.3%; Pred. No. 4.8e-11;
 RESULT 1341
 ID ABO76517 standard; protein; 649 AA.
 DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
 PN US2003082717-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 9.9%; Score 309; DB 6; Length 649;
 Best Local Similarity 22.3%; Pred. No. 4.8e-11;
 RESULT 1342
 ID ABO76213 standard; protein; 649 AA.
 DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
 PN US2003104548-A1.
 PD 05-JUN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 9.9%; Score 309; DB 6; Length 649;
 Best Local Similarity 22.3%; Pred. No. 4.8e-11;
 RESULT 1343
 ID ABO25832 standard; protein; 649 AA.
 DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
 PN US2003104542-A1.
 PD 05-JUN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 9.9%; Score 309; DB 6; Length 649;
 Best Local Similarity 22.3%; Pred. No. 4.8e-11;
 RESULT 1344
 ID ABO26137 standard; protein; 649 AA.
 DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
 PN US2003104543-A1.
 PD 05-JUN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 9.9%; Score 309; DB 6; Length 649;
 Best Local Similarity 22.3%; Pred. No. 4.8e-11;

Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1345
ID ABO3490 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003036127-A1.
PD 20-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1346
ID ABO2575 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003040061-A1.
PD 27-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1347
ID ABO44304 standard; protein; 649 AA.
DE Human secreted/transmembrane polypeptide PRO 1865.
PN US2003018172-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1348
ID ABR90746 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003036130-A1.
PD 20-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1349
ID ABR73814 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003054468-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1350
ID ABO17066 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003054470-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1351
ID ABR94491 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003044917-A1.
PD 06-MAR-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1352
ID ABR75998 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003044929-A1.
PD 06-MAR-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1353
ID ABR71374 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003059880-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1354
ID ABR93271 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003064465-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1355
ID ABR91576 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003054478-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1356
ID ABR88001 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003068718-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1357
ID ABO30136 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003064461-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1358
ID ABO30136 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003064461-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1359
ID ABO33345 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003068724-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1360
ID ABO5033 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003068727-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1361
ID ABO8993 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003068772-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1362
ID ABO36593 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003068714-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1363
ID ABO35678 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003068758-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.

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Query Match 9.9%; Score 309; DB 6; Length 649;
 Best Local Similarity 22.3%; Pred. No. 4.8e-11;
 RESULT 1364
 ID ABO39643 standard; protein; 649 AA.
 DE Human secreted/transmembrane protein (PRO) #192.
 PN US2003068776-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 9.9%; Score 309; DB 6; Length 649;
 Best Local Similarity 22.3%; Pred. No. 4.8e-11;
 RESULT 1365
 ID ABM10518 standard; protein; 649 AA.
 DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
 PN US2003069407-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 9.9%; Score 309; DB 6; Length 649;
 Best Local Similarity 22.3%; Pred. No. 4.8e-11;
 RESULT 1366
 ID ABM12043 standard; protein; 649 AA.
 DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
 PN US2003104555-A1.
 PD 05-JUN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 9.9%; Score 309; DB 6; Length 649;
 Best Local Similarity 22.3%; Pred. No. 4.8e-11;
 RESULT 1367
 ID ABO52189 standard; protein; 649 AA.
 DE Human PRO polypeptide #192.
 PN US2003049768-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 9.9%; Score 309; DB 6; Length 649;
 Best Local Similarity 22.3%; Pred. No. 4.8e-11;
 RESULT 1368
 ID ABO52494 standard; protein; 649 AA.
 DE Human PRO polypeptide #192.
 PN US2003049771-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 9.9%; Score 309; DB 6; Length 649;
 Best Local Similarity 22.3%; Pred. No. 4.8e-11;
 RESULT 1369
 ID ADA19994 standard; protein; 649 AA.
 DE Novel human secreted and transmembrane protein PRO1865.
 PN US2003069394-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 9.9%; Score 309; DB 6; Length 649;
 Best Local Similarity 22.3%; Pred. No. 4.8e-11;
 RESULT 1370
 ID ABO23812 standard; protein; 649 AA.
 DE Human secreted/transmembrane protein (PRO) #192.
 PN US2003032134-A1.
 PD 13-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 9.9%; Score 309; DB 6; Length 649;
 Best Local Similarity 22.3%; Pred. No. 4.8e-11;
 RESULT 1371
 ID ADB17377 standard; protein; 649 AA.
 DE Human transmembrane PRO polypeptide (SeqID 132).
 PN US2003050465-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 9.9%; Score 309; DB 6; Length 649;
 Best Local Similarity 22.3%; Pred. No. 4.8e-11;
 RESULT 1372
 ID ABR97298 standard; protein; 649 AA.
 DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
 PN US2003054481-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 9.9%; Score 309; DB 6; Length 649;
 Best Local Similarity 22.3%; Pred. No. 4.8e-11;

RESULT 1373
 ID ABR87086 standard; protein; 649 AA.
 DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
 PN US2003049778-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 9.9%; Score 309; DB 6; Length 649;
 Best Local Similarity 22.3%; Pred. No. 4.8e-11;
 RESULT 1374
 ID ABM11128 standard; protein; 649 AA.
 DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
 PN US2003049782-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 9.9%; Score 309; DB 6; Length 649;
 Best Local Similarity 22.3%; Pred. No. 4.8e-11;
 RESULT 1375
 ID ABM28272 standard; protein; 649 AA.
 DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
 PN US2003054476-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 9.9%; Score 309; DB 6; Length 649;
 Best Local Similarity 22.3%; Pred. No. 4.8e-11;
 RESULT 1376
 ID ABO32271 standard; protein; 649 AA.
 DE Human secreted/transmembrane protein (PRO) #192.
 PN US2003068733-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 9.9%; Score 309; DB 6; Length 649;
 Best Local Similarity 22.3%; Pred. No. 4.8e-11;
 RESULT 1377
 ID ABM15398 standard; protein; 649 AA.
 DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
 PN US2003068692-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 9.9%; Score 309; DB 6; Length 649;
 Best Local Similarity 22.3%; Pred. No. 4.8e-11;
 RESULT 1378
 ID ABM06553 standard; protein; 649 AA.
 DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
 PN US2003068709-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 9.9%; Score 309; DB 6; Length 649;
 Best Local Similarity 22.3%; Pred. No. 4.8e-11;
 RESULT 1379
 ID ABM04364 standard; protein; 649 AA.
 DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
 PN US2003068716-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 9.9%; Score 309; DB 6; Length 649;
 Best Local Similarity 22.3%; Pred. No. 4.8e-11;
 RESULT 1380
 ID ABM22477 standard; protein; 649 AA.
 DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
 PN US2003068740-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 9.9%; Score 309; DB 6; Length 649;
 Best Local Similarity 22.3%; Pred. No. 4.8e-11;
 RESULT 1381
 ID ABM07773 standard; protein; 649 AA.
 DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
 PN US2003068751-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 9.9%; Score 309; DB 6; Length 649;
 Best Local Similarity 22.3%; Pred. No. 4.8e-11;
 RESULT 1382

ID ABO40863 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003068684-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1393
ID ABR80703 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003049740-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1393
ID ABM01314 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003049770-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1394
ID ABR88916 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003073169-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1395
ID ABM13568 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003064457-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1396
ID ABM20952 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003068711-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1397
ID ABO42083 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003049745-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1398
ID ABO42693 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003049751-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1399
ID ABM10213 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003067478-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1400
ID ABO38728 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003068773-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1391
ID ABR97603 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003059885-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.

ID ABO40863 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003068684-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1383
ID ABM35510 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003073179-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1384
ID ABM33273 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003087374-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1385
ID ABO52799 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003049773-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1386
ID ABO50359 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003049777-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1387
ID ABU99353 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003040055-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1388
ID ABO04405 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003036164-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1389
ID ABO06035 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003040074-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1390
ID ABM18575 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003054480-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1391
ID ABR97603 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003059885-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.

RESULT 1401
ID ABM32968 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003073185-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
22.3%; Pred. No. 4.8e-11;
RESULT 1402
ID ABM22782 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003087373-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
22.3%; Pred. No. 4.8e-11;
RESULT 1403
ID ABM74993 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003096353-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
22.3%; Pred. No. 4.8e-11;
RESULT 1404
ID ADA79928 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003073173-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
22.3%; Pred. No. 4.8e-11;
RESULT 1405
ID ABR96383 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003054458-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
22.3%; Pred. No. 4.8e-11;
RESULT 1406
ID ABM02534 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003059886-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
22.3%; Pred. No. 4.8e-11;
RESULT 1407
ID ABR86476 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003049758-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
22.3%; Pred. No. 4.8e-11;
RESULT 1408
ID ABR86781 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003049772-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
22.3%; Pred. No. 4.8e-11;
RESULT 1409
ID ABM16745 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003064448-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
22.3%; Pred. No. 4.8e-11;
RESULT 1410
ID ABM29797 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003064456-A1.
PD 03-APR-2003.

PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
22.3%; Pred. No. 4.8e-11;
RESULT 1411
ID ABO29221 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003068693-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
22.3%; Pred. No. 4.8e-11;
RESULT 1412
ID ABM24002 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003068735-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
22.3%; Pred. No. 4.8e-11;
RESULT 1413
ID ABM23392 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003068753-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
22.3%; Pred. No. 4.8e-11;
RESULT 1414
ID ABM22172 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003068742-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
22.3%; Pred. No. 4.8e-11;
RESULT 1415
ID ABO37813 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003068756-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
22.3%; Pred. No. 4.8e-11;
RESULT 1416
ID ABM28577 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003082715-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
22.3%; Pred. No. 4.8e-11;
RESULT 1417
ID ABM28882 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003082716-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
22.3%; Pred. No. 4.8e-11;
RESULT 1418
ID ABM66526 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003068737-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
22.3%; Pred. No. 4.8e-11;
RESULT 1419
ID ABM75908 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003104547-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
22.3%; Pred. No. 4.8e-11;

RESULT 1420

ID ABM34188 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
FN US2003096359-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC. 9.9%; Score 309; DB 6; Length 649;
Query Match Similarity 22.3%; Pred. No. 4.8e-11;
Best Local Similarity

RESULT 1421

ID ABM34493 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
FN US2003100061-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC. 9.9%; Score 309; DB 6; Length 649;
Query Match Similarity 22.3%; Pred. No. 4.8e-11;
Best Local Similarity

RESULT 1422

ID ABO20424 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
FN US2003032125-A1.
PD 13-FEB-2003.
Query Match Similarity 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
Best Local Similarity

RESULT 1423

ID ABO21339 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
FN US2003054454-A1.
PD 20-MAR-2003.
Query Match Similarity 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
Best Local Similarity

RESULT 1424

ID ABO22254 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
FN US2003054477-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC. 9.9%; Score 309; DB 6; Length 649;
Query Match Similarity 22.3%; Pred. No. 4.8e-11;
Best Local Similarity

RESULT 1425

ID ADA20166 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
FN US2003055222-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC. 9.9%; Score 309; DB 6; Length 649;
Query Match Similarity 22.3%; Pred. No. 4.8e-11;
Best Local Similarity

RESULT 1426

ID ABR96688 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
FN US2003054460-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC. 9.9%; Score 309; DB 6; Length 649;
Query Match Similarity 22.3%; Pred. No. 4.8e-11;
Best Local Similarity

RESULT 1427

ID ABR85866 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
FN US2003049753-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC. 9.9%; Score 309; DB 6; Length 649;
Query Match Similarity 22.3%; Pred. No. 4.8e-11;
Best Local Similarity

RESULT 1428

ID ABR99848 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
FN US2003049763-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC. 9.9%; Score 309; DB 6; Length 649;
Query Match Similarity 22.3%; Pred. No. 4.8e-11;
Best Local Similarity

RESULT 1429

ID ABW00399 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
FN US2003049763-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC. 9.9%; Score 309; DB 6; Length 649;
Query Match Similarity 22.3%; Pred. No. 4.8e-11;
Best Local Similarity

PN US2003073172-A1.
PD 17-APR-2003.

Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
Result 1430 22.3%; Pred. No. 4.8e-11;

ID ABM00704 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
FN US2003073172-A1.
PD 17-APR-2003.

Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
Result 1431 22.3%; Pred. No. 4.8e-11;

ID ABO29831 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
FN US2003068700-A1.
PD 10-APR-2003.

PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
Result 1432 22.3%; Pred. No. 4.8e-11;

ID ABE23697 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
FN US2003068736-A1.
PD 10-APR-2003.

PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
Result 1433 22.3%; Pred. No. 4.8e-11;

ID ABE29492 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
FN US2003068679-A1.
PD 10-APR-2003.

PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
Result 1434 22.3%; Pred. No. 4.8e-11;

ID ABO38423 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
FN US2003068767-A1.
PD 10-APR-2003.

PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
Result 1435 22.3%; Pred. No. 4.8e-11;

ID ABO45723 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
FN US2003073182-A1.
PD 17-APR-2003.

PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
Result 1436 22.3%; Pred. No. 4.8e-11;

ID ABE20647 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
FN US2003104557-A1.
PD 05-JUN-2003.

PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
Result 1437 22.3%; Pred. No. 4.8e-11;

ID ADA81655 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
FN US2003092121-A1.
PD 15-MAY-2003.

PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
Result 1438 22.3%; Pred. No. 4.8e-11;

ID ABO16761 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
FN US2003027276-A1.
PD 06-FEB-2003.

Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
Result 1439 22.3%; Pred. No. 4.8e-11;

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Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1439
ID ABO18387 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003044920-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
22.3%; Pred. No. 4.8e-11;
RESULT 1440
ID ABO22814 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US200302785-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
22.3%; Pred. No. 4.8e-11;
RESULT 1441
ID ABO23119 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003054461-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
22.3%; Pred. No. 4.8e-11;
RESULT 1442
ID ABR92661 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003064446-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
22.3%; Pred. No. 4.8e-11;
RESULT 1443
ID ABR81618 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003049744-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
22.3%; Pred. No. 4.8e-11;
RESULT 1444
ID ABR78042 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003049783-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
22.3%; Pred. No. 4.8e-11;
RESULT 1445
ID ABR89831 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003073171-A1.
PD 17-APR-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
22.3%; Pred. No. 4.8e-11;
RESULT 1446
ID ABM26747 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003032121-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
22.3%; Pred. No. 4.8e-11;
RESULT 1447
ID ABM13873 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003064458-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
22.3%; Pred. No. 4.8e-11;
RESULT 1448
ID ABO28611 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003064460-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
22.3%; Pred. No. 4.8e-11;
RESULT 1449
ID ABO30441 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003064464-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
22.3%; Pred. No. 4.8e-11;
RESULT 1450
ID ABM07468 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003068702-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
22.3%; Pred. No. 4.8e-11;
RESULT 1451
ID ABM04059 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003068734-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
22.3%; Pred. No. 4.8e-11;
RESULT 1452
ID ABO37203 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003068719-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
22.3%; Pred. No. 4.8e-11;
RESULT 1453
ID ABO41778 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003068729-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
22.3%; Pred. No. 4.8e-11;
RESULT 1454
ID ABO35373 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003068738-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
22.3%; Pred. No. 4.8e-11;
RESULT 1455
ID ABM25222 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003104540-A1.
PD 05-JUN-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
22.3%; Pred. No. 4.8e-11;
RESULT 1456
ID ABO47614 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003049742-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
22.3%; Pred. No. 4.8e-11;
RESULT 1457
ID ABO47919 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003049747-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
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Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1458
ID ABO48529 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003049750-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1459
ID ABO51579 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003049766-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1460
ID ABO51884 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003049767-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1461
ID ABO50664 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003049779-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1462
ID ABR79788 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003040059-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1463
ID ABM17050 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003040078-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1464
ID ABO18082 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003044918-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1465
ID ABO21034 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003032132-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1466
ID ABR96993 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003054462-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
ID ABM12348 standard; protein; 649 AA.

DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003064445-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1468
ID ABM16440 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003064449-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1469
ID ABM24307 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003064441-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1470
ID ABM14788 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003068696-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1471
ID ABM04669 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003068712-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1472
ID ABM06858 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003068730-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1473
ID ABM09298 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003073174-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1474
ID ABO39338 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003068775-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1475
ID ABM75603 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003104545-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1476
ID ABM25527 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003104541-A1.
PD 05-JUN-2003.

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Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1477
ID ABO20037 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003104554-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1478
ID ABO46943 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003049762-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1479
ID ABO47248 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003049765-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1480
ID ADA83453 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003049752-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1481
ID ABR71679 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003032133-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1482
ID ABR72289 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003032136-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1483
ID ABR98628 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003036129-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1484
ID ABO06998 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003040053-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1485
ID ABR84951 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003040057-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1486
ID ABR73509 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003054467-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1487
ID ABR76603 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003044932-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1488
ID ABR73204 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003027270-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1489
ID ABM18270 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003054469-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1490
ID ABO20729 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003032126-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1491
ID ABO25472 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003054463-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1492
ID ABO25777 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003054466-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1493
ID ABR94186 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003059879-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1494
ID ABR80093 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003049738-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1495
ID ABM11433 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003064469-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1496
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ID ABO33040 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003064453-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC. 9.9%; Score 309; DB 6; Length 649;
Query Match
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1497
ID ABO30746 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003064466-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC. 9.9%; Score 309; DB 6; Length 649;
Query Match
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1498
ID ABO31051 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003064468-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC. 9.9%; Score 309; DB 6; Length 649;
Query Match
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1499
ID ABM27357 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003068760-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC. 9.9%; Score 309; DB 6; Length 649;
Query Match
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1500
ID AEF74347 standard; protein; 649 AA.
DE Human PRO1865 protein SEQ ID NO:132.
PN US2005260647-A1.
PD 24-NOV-2005.
PA (EATO/) EATON D L.
PA (FILV/) FILVAROFF E.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI J C.
PA (GURN/) GURNEY A L.
PA (WATA/) WATANABE C K.
PA (WOOD/) WOOD W L.
Query Match
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101	292.5	9.3	640	2	US-09-906-679A-292	Sequence 292, App	174	252	8.0	567	2	US-10-037-417-105	Sequence 105, App
102	292.5	9.3	640	3	US-09-988-726-501	Sequence 501, App	175	251	8.0	622	2	US-10-188-495-48	Sequence 48, Appl
103	292.5	9.3	640	3	US-09-997-514-501	Sequence 501, App	176	249.5	8.0	789	2	US-09-831-846-2	Sequence 2, Appli
104	292.5	9.3	640	3	US-09-988-728-501	Sequence 501, App	177	248	7.9	481	2	US-09-853-753-2	Sequence 2, Appli
105	292.5	9.3	640	3	US-09-907-841-232	Sequence 292, App	178	248	7.9	485	2	US-09-949-016-8704	Sequence 8704, Ap
106	292.5	9.3	640	3	US-09-997-349-501	Sequence 501, App	179	247.5	7.9	1525	2	US-09-191-647-2	Sequence 2, Appli
107	292.5	9.3	640	3	US-09-997-653-501	Sequence 501, App	180	247.5	7.9	1525	2	US-09-540-245A-2	Sequence 2, Appli
108	292.5	9.3	640	3	US-09-989-233A-501	Sequence 501, App	181	247.5	7.9	1525	2	US-09-540-153-2	Sequence 2, Appli
109	287.5	9.2	713	2	US-09-907-794A-245	Sequence 245, App	182	247.5	7.9	1525	2	US-10-289-776-2	Sequence 2, Appli
110	287.5	9.2	713	2	US-09-905-125A-245	Sequence 245, App	183	247.5	7.9	1529	2	US-10-188-495-67	Sequence 67, Appl
111	287.5	9.2	713	2	US-09-902-775A-245	Sequence 245, App	184	246.5	7.9	1529	2	US-09-312-283C-396	Sequence 396, App
112	287.5	9.2	713	2	US-09-906-700-245	Sequence 245, App	185	244	7.8	708	2	US-09-131-648C-2	Sequence 2, Appli
113	287.5	9.2	713	2	US-09-903-603A-245	Sequence 245, App	186	244	7.8	708	2	US-09-907-794A-69	Sequence 69, Appl
114	287.5	9.2	713	2	US-09-904-920A-245	Sequence 245, App	187	244	7.8	708	2	US-09-905-125A-69	Sequence 69, Appl
115	287.5	9.2	713	2	US-09-909-064-245	Sequence 245, App	188	244	7.8	708	2	US-09-902-775A-69	Sequence 69, Appl
116	287.5	9.2	713	2	US-09-906-618-245	Sequence 245, App	189	244	7.8	708	2	US-09-906-700-69	Sequence 69, Appl
117	287.5	9.2	713	2	US-09-906-646-245	Sequence 245, App	190	244	7.8	708	2	US-09-903-603A-69	Sequence 69, Appl
118	287.5	9.2	713	2	US-09-904-462-245	Sequence 245, App	191	244	7.8	708	2	US-09-904-920A-69	Sequence 69, Appl
119	287.5	9.2	713	2	US-09-906-722A-245	Sequence 245, App	192	244	7.8	708	2	US-09-909-064-69	Sequence 69, Appl
120	287.5	9.2	713	2	US-09-905-449-245	Sequence 245, App	193	244	7.8	708	2	US-09-905-381A-69	Sequence 69, Appl
121	287.5	9.2	713	2	US-09-906-618-245	Sequence 245, App	194	244	7.8	708	2	US-09-906-618-69	Sequence 69, Appl
122	287.5	9.2	713	2	US-09-903-562B-245	Sequence 245, App	195	244	7.8	708	2	US-09-906-646-69	Sequence 69, Appl
123	287.5	9.2	713	2	US-09-906-679A-245	Sequence 245, App	196	244	7.8	708	2	US-09-904-462-69	Sequence 69, Appl
124	287.5	9.2	713	3	US-09-907-841-245	Sequence 245, App	197	244	7.8	708	2	US-09-902-736A-69	Sequence 69, Appl
125	287.5	9.2	713	2	US-10-104-047-2955	Sequence 2955, Ap	198	244	7.8	708	2	US-09-906-722A-69	Sequence 69, Appl
126	284.5	9.1	745	2	US-10-104-047-2960	Sequence 2960, Ap	199	244	7.8	708	2	US-09-905-449-69	Sequence 69, Appl
127	282.5	9.0	745	2	US-08-190-802A-50	Sequence 50, Appl	200	244	7.8	708	2	US-09-903-562B-69	Sequence 69, Appl
128	281.5	9.0	603	2	US-08-477-346-50	Sequence 50, Appl	201	244	7.8	708	3	US-09-906-679A-69	Sequence 69, Appl
129	281.5	9.0	603	2	US-08-473-089-50	Sequence 50, Appl	202	244	7.8	708	2	US-09-907-841-69	Sequence 69, Appl
130	281.5	9.0	603	2	US-08-487-072A-50	Sequence 50, Appl	203	243.5	7.8	312	2	US-10-037-417-108	Sequence 108, App
131	281.5	9.0	603	2	US-08-386-485-6	Sequence 98, Appl	204	242.5	7.7	545	3	US-10-114-270-40	Sequence 40, Appl
132	271.5	8.7	353	2	US-10-037-417-98	Sequence 8448, Ap	205	242.5	7.7	545	3	US-10-114-270-40	Sequence 40, Appl
133	271.5	8.7	1504	2	US-09-949-016-8448	Sequence 400, App	206	241	7.7	380	2	US-10-012-542-161	Sequence 161, App
134	271	8.6	473	2	US-09-959-833A-400	Sequence 400, App	207	241	7.7	380	2	US-10-115-123-161	Sequence 161, App
135	271	8.6	473	2	US-10-020-445A-400	Sequence 400, App	208	240	7.7	560	2	US-08-592-500-2	Sequence 2, Appli
136	271	8.6	473	2	US-09-978-189-400	Sequence 400, App	209	240	7.7	560	2	US-08-195-006-2	Sequence 4, Appli
137	271	8.6	473	2	US-10-017-085A-400	Sequence 400, App	210	240	7.7	560	2	US-09-063-950-4	Sequence 4, Appli
138	271	8.6	473	3	US-10-145-129A-400	Sequence 400, App	211	240	7.7	560	2	US-09-775-803-14	Sequence 14, Appl
139	271	8.6	473	3	US-10-013-929A-400	Sequence 400, App	212	240	7.7	560	2	PCT-US94-07644A-2	Sequence 2, Appli
140	271	8.6	473	3	US-07-821-717B-6	Sequence 6, Appli	213	240	7.7	560	5	PCT-US91-09055-3	Sequence 3, Appli
141	271	8.6	610	1	US-08-119-262B-6	Sequence 6, Appli	214	236.5	7.5	231	2	US-08-986-485-7	Sequence 7, Appli
142	259	8.3	610	1	US-08-135-929A-11	Sequence 11, Appl	215	236.5	7.5	231	2	US-10-068-426-1	Sequence 1, Appli
143	259	8.3	610	1	US-08-135-929A-11	Sequence 11, Appl	216	230.5	7.4	544	2	US-10-068-426-1	Sequence 14, Appl
144	259	8.3	610	1	US-08-234-265A-11	Sequence 21, Appl	217	227	7.2	568	2	US-09-673-245-14	Sequence 3, Appli
145	259	8.3	610	1	US-09-182-024A-2	Sequence 21, Appl	218	226.5	7.2	557	2	US-10-037-417-95	Sequence 95, Appl
146	258	8.2	1523	2	US-10-012-231A-198	Sequence 198, App	219	226.5	7.2	557	2	US-10-094-749-2001	Sequence 2001, Ap
147	258	8.2	1523	2	US-10-015-389A-198	Sequence 198, App	220	226.5	7.2	719	2	US-10-068-426-2	Sequence 2, Appli
148	258	8.2	1523	2	US-10-006-768A-198	Sequence 198, App	221	225.5	7.2	544	2	US-09-191-647-9	Sequence 9, Appli
149	258	8.2	1523	2	US-10-015-671A-198	Sequence 198, App	222	225	7.2	735	2	US-09-540-245A-9	Sequence 9, Appli
150	258	8.2	1523	2	US-10-015-393A-198	Sequence 198, App	223	225	7.2	735	2	US-09-540-153-9	Sequence 9, Appli
151	258	8.2	1523	2	US-10-011-833A-198	Sequence 198, App	224	225	7.2	735	2	US-10-289-776-9	Sequence 9, Appli
152	258	8.2	1523	2	US-10-011-833A-198	Sequence 198, App	225	225	7.2	735	2	US-09-538-092-992	Sequence 992, App
153	258	8.2	1523	2	US-10-006-041A-198	Sequence 198, App	226	222.5	7.1	536	5	PCT-US91-09055-5	Sequence 5, Appli
154	258	8.2	1523	2	US-10-012-064A-198	Sequence 198, App	227	222	7.1	196	2	US-10-188-495-51	Sequence 51, Appl
155	258	8.2	1523	2	US-10-015-392A-198	Sequence 198, App	228	222	7.1	498	2	US-10-188-495-50	Sequence 50, Appl
156	258	8.2	1523	3	US-10-011-795B-198	Sequence 198, App	229	222	7.1	591	2	US-10-188-495-50	Sequence 94, Appl
157	258	8.2	1523	3	US-10-015-386A-198	Sequence 198, App	230	221.5	7.1	557	2	US-10-037-417-94	Sequence 657, App
158	258	8.2	1523	3	US-10-012-121A-198	Sequence 198, App	231	220.5	7.0	841	2	US-09-935-430-657	Sequence 2, Appli
159	258	8.2	1523	3	US-10-006-485A-198	Sequence 198, App	232	220.5	7.0	841	2	US-09-964-956-2	Sequence 2, Appli
160	258	8.2	1523	3	US-10-006-746A-198	Sequence 198, App	233	218.5	7.0	359	2	US-09-949-016-9732	Sequence 9732, Ap
161	258	8.2	1523	3	US-10-012-752A-198	Sequence 198, App	234	217.5	6.9	562	2	US-09-673-245-7	Sequence 7, Appli
162	258	8.2	1523	3	US-10-017-253A-198	Sequence 198, App	235	217.5	6.9	837	2	US-09-984-956-5	Sequence 5, Appli
163	258	8.2	1523	3	US-10-015-519A-198	Sequence 198, App	236	214.5	6.8	255	2	US-09-984-956-5	Sequence 232, App
164	258	8.2	1523	3	US-10-015-519A-198	Sequence 198, App	237	212	6.8	531	2	US-10-068-426-6	Sequence 6, Appli
165	258	8.2	1523	3	US-10-007-236A-198	Sequence 198, App	238	211	6.7	513	2	US-10-012-231A-385	Sequence 385, App
166	255.5	8.1	1480	2	US-09-191-647-7	Sequence 7, Appli	239	211	6.7	513	2	US-10-015-389A-385	Sequence 385, App
167	255.5	8.1	1480	2	US-09-540-245A-7	Sequence 7, Appli	240	211	6.7	513	2	US-10-006-768A-385	Sequence 385, App
168	255.5	8.1	1480	2	US-09-540-153-7	Sequence 7, Appli	241	211	6.7	513	2	US-10-006-768A-385	Sequence 385, App
169	255.5	8.1	1480	2	US-09-182-024A-5	Sequence 5, Appli	242	211	6.7	513	2	US-10-015-393A-385	Sequence 385, App
170	255.5	8.1	1480	2	US-10-289-776-7	Sequence 7, Appli	243	211	6.7	513	2	US-10-011-833A-385	Sequence 385, App
171	255.5	8.1	1480	5	PCT-US91-09055-2	Sequence 2, Appli	244	211	6.7	513	2	US-10-006-041A-385	Sequence 385, App
172	253	8.1	567	2	US-10-037-417-106	Sequence 106, App	245	211	6.7	513	2	US-10-012-064A-385	Sequence 385, App

246	211	6.7	513	2	US-10-015-392A-385	Sequence 385, App	319	197.5	6.3	616	3	US-10-015-715A-24	Sequence 24, Appl
247	211	6.7	513	3	US-10-011-795B-385	Sequence 385, App	320	197.5	6.3	616	3	US-10-007-236A-24	Sequence 24, Appl
248	211	6.7	513	3	US-10-015-386A-385	Sequence 385, App	321	196.5	6.3	716	2	US-09-312-283C-183	Sequence 183, App
249	211	6.7	513	3	US-10-012-121A-385	Sequence 385, App	322	196.5	6.3	771	2	US-09-188-930-183	Sequence 183, App
250	211	6.7	513	3	US-10-006-485A-385	Sequence 385, App	323	195.5	6.2	553	2	US-10-037-417-28	Sequence 28, Appl
251	211	6.7	513	3	US-10-006-746A-385	Sequence 385, App	324	195	6.2	620	2	US-09-907-794A-73	Sequence 73, Appl
252	211	6.7	513	3	US-10-012-752A-385	Sequence 385, App	325	195	6.2	620	2	US-09-905-125A-73	Sequence 73, Appl
253	211	6.7	513	3	US-10-017-253A-385	Sequence 385, App	326	195	6.2	620	2	US-09-902-775A-73	Sequence 73, Appl
254	211	6.7	513	3	US-10-015-519A-385	Sequence 385, App	327	195	6.2	620	2	US-09-906-700-73	Sequence 73, Appl
255	211	6.7	513	3	US-10-015-715A-385	Sequence 385, App	328	195	6.2	620	2	US-09-903-603A-73	Sequence 73, Appl
256	211	6.7	513	3	US-10-007-236A-385	Sequence 385, App	329	195	6.2	620	2	US-09-904-920A-73	Sequence 73, Appl
257	211	6.7	531	2	US-10-068-426-5	Sequence 5, Appl	330	195	6.2	620	2	US-09-909-064-73	Sequence 73, Appl
258	210.5	6.7	4302	2	US-08-658-136-5	Sequence 5, Appl	331	195	6.2	620	2	US-09-905-381A-73	Sequence 73, Appl
259	210.5	6.7	4302	2	US-09-052-463-8	Sequence 8, Appl	332	195	6.2	620	2	US-09-906-618-73	Sequence 73, Appl
260	210.5	6.7	4302	2	US-08-422-582-8	Sequence 8, Appl	333	195	6.2	620	2	US-09-906-646-73	Sequence 73, Appl
261	210.5	6.7	4302	2	US-09-052-262-8	Sequence 8, Appl	334	195	6.2	620	2	US-09-904-462-73	Sequence 73, Appl
262	210	6.7	531	2	US-10-068-426-4	Sequence 4, Appl	335	195	6.2	620	2	US-09-907-841-73	Sequence 73, Appl
263	209	6.7	353	2	US-10-012-231A-397	Sequence 397, App	336	195	6.2	742	2	US-10-104-047-2807	Sequence 2807, Ap
264	209	6.7	353	2	US-10-015-389A-397	Sequence 397, App	337	195	6.2	832	2	US-09-935-430-660	Sequence 660, App
265	209	6.7	353	2	US-10-006-768A-397	Sequence 397, App	338	195	6.2	853	2	US-09-964-956-30	Sequence 30, Appl
266	209	6.7	353	2	US-10-015-671A-397	Sequence 397, App	339	195	6.2	699	2	US-09-949-016-6073	Sequence 6073, Ap
267	209	6.7	353	2	US-10-015-393A-397	Sequence 397, App	340	195	6.2	720	2	US-09-949-016-9819	Sequence 9819, Ap
268	209	6.7	353	2	US-10-011-833A-397	Sequence 397, App	341	195	6.2	224	5	PCT-US91-09055-4	Sequence 4, Appl
269	209	6.7	353	2	US-10-006-041A-397	Sequence 397, App	342	195	6.2	542	2	US-10-037-417-97	Sequence 97, Appl
270	209	6.7	353	2	US-10-012-064A-397	Sequence 397, App	343	195	6.2	1059	2	US-09-907-794A-290	Sequence 290, App
271	209	6.7	353	2	US-10-015-392A-397	Sequence 397, App	344	194.5	6.2	1059	2	US-09-905-125A-290	Sequence 290, App
272	209	6.7	353	3	US-10-011-795B-397	Sequence 397, App	345	194.5	6.2	1059	2	US-09-902-775A-290	Sequence 290, App
273	209	6.7	353	3	US-10-015-386A-397	Sequence 397, App	346	193.5	6.2	1059	2	US-09-906-700-290	Sequence 290, App
274	209	6.7	353	3	US-10-013-121A-397	Sequence 397, App	347	193.5	6.2	1059	2	US-09-903-603A-290	Sequence 290, App
275	209	6.7	353	3	US-10-006-485A-397	Sequence 397, App	348	190	6.1	1059	2	US-09-904-920A-290	Sequence 290, App
276	209	6.7	353	3	US-10-006-746A-397	Sequence 397, App	349	190	6.1	1059	2	US-09-909-064-290	Sequence 290, App
277	209	6.7	353	3	US-10-012-752A-397	Sequence 397, App	350	190	6.1	1059	2	US-09-905-381A-290	Sequence 290, App
278	209	6.7	353	3	US-10-017-253A-397	Sequence 397, App	351	190	6.1	1059	2	US-09-906-618-290	Sequence 290, App
279	209	6.7	353	3	US-10-015-519A-397	Sequence 397, App	352	190	6.1	1059	2	US-09-906-646-290	Sequence 290, App
280	209	6.7	353	3	US-10-015-715A-397	Sequence 397, App	353	190	6.1	1059	2	US-09-904-462-290	Sequence 290, App
281	209	6.7	353	3	US-10-007-236A-397	Sequence 397, App	354	190	6.1	1059	2	US-09-907-841-290	Sequence 290, App
282	209	6.7	1091	2	US-08-986-485-5	Sequence 5, Appl	355	190	6.1	1059	2	US-09-905-125A-294	Sequence 294, App
283	208.5	6.7	424	2	US-09-949-016-6625	Sequence 7950, Ap	356	190	6.1	1119	2	US-09-905-381A-294	Sequence 294, App
284	208.5	6.6	415	2	US-09-935-430-659	Sequence 6950, App	357	190	6.1	1119	2	US-09-902-775A-294	Sequence 294, App
285	207.5	6.6	440	2	US-09-964-956-29	Sequence 29, Appl	358	190	6.1	1119	2	US-09-903-603A-294	Sequence 294, App
286	207.5	6.6	798	2	US-09-935-430-658	Sequence 658, App	359	190	6.1	1119	2	US-09-904-920A-294	Sequence 294, App
287	207.5	6.6	798	2	US-09-964-956-28	Sequence 28, Appl	360	190	6.1	1119	2	US-09-909-064-294	Sequence 294, App
288	206.5	6.6	1101	2	US-08-986-485-2	Sequence 2, Appl	361	190	6.1	1119	2	US-09-905-125A-294	Sequence 294, App
289	206	6.6	428	2	US-09-949-016-6625	Sequence 6625, Ap	362	190	6.1	1119	2	US-09-902-775A-294	Sequence 294, App
290	206	6.6	433	2	US-09-949-016-8521	Sequence 8521, Ap	363	190	6.1	1119	2	US-09-906-618-294	Sequence 294, App
291	205	6.5	4339	2	US-09-052-469-6	Sequence 6, Appl	364	190	6.1	1119	2	US-09-906-646-294	Sequence 294, App
292	205	6.5	4339	2	US-08-423-582-6	Sequence 6, Appl	365	190	6.1	1119	2	US-09-904-462-294	Sequence 294, App
293	205	6.5	4339	2	US-09-052-262-6	Sequence 6, Appl	366	190	6.1	1119	2	US-09-907-841-290	Sequence 290, App
294	203.5	6.5	4303	1	US-08-460-751-2	Sequence 2, Appl	367	190	6.1	1119	2	US-09-905-381A-294	Sequence 294, App
295	203.5	6.5	4303	2	US-09-479-467A-2	Sequence 2, Appl	368	190	6.1	1119	2	US-09-905-125A-294	Sequence 294, App
296	203.5	6.5	4303	2	US-09-655-160-2	Sequence 2, Appl	369	190	6.1	1119	2	US-09-902-775A-294	Sequence 294, App
297	201.5	6.4	606	2	US-10-094-749-2313	Sequence 2513, Ap	370	190	6.1	1119	2	US-09-903-603A-294	Sequence 294, App
298	200.5	6.4	302	2	US-09-482-273-105	Sequence 105, App	371	190	6.1	1119	2	US-09-904-920A-294	Sequence 294, App
299	200.5	6.4	724	2	US-10-104-047-2224	Sequence 2224, Ap	372	190	6.1	1119	2	US-09-909-064-294	Sequence 294, App
300	199	6.3	321	2	US-10-104-047-2504	Sequence 2504, Ap	373	190	6.1	1119	2	US-09-905-125A-294	Sequence 294, App
301	198.5	6.3	1338	3	US-09-631-603-2	Sequence 2, Appl	374	190	6.1	1119	2	US-09-905-381A-294	Sequence 294, App
302	197.5	6.3	616	2	US-10-012-231A-24	Sequence 24, Appl	375	190	6.1	1119	2	US-09-906-618-294	Sequence 294, App
303	197.5	6.3	616	2	US-10-015-389A-24	Sequence 24, Appl	376	190	6.1	1119	2	US-09-906-646-294	Sequence 294, App
304	197.5	6.3	616	2	US-10-006-768A-24	Sequence 24, Appl	377	190	6.1	1119	2	US-09-904-462-294	Sequence 294, App
305	197.5	6.3	616	2	US-10-015-671A-24	Sequence 24, Appl	378	190	6.1	1119	2	US-09-907-841-290	Sequence 290, App
306	197.5	6.3	616	2	US-10-015-393A-24	Sequence 24, Appl	379	190	6.1	1119	2	US-09-905-125A-294	Sequence 294, App
307	197.5	6.3	616	2	US-10-011-833A-24	Sequence 24, Appl	380	190	6.1	1119	2	US-09-902-775A-294	Sequence 294, App
308	197.5	6.3	616	2	US-10-006-041A-24	Sequence 24, Appl	381	190	6.1	1119	3	US-09-907-841-294	Sequence 294, App
309	197.5	6.3	616	2	US-10-013-064A-24	Sequence 24, Appl	382	189.5	6.0	301	2	US-10-068-426-9	Sequence 9, Appl
310	197.5	6.3	616	2	US-10-015-392A-24	Sequence 24, Appl	383	186.5	5.9	196	5	PCT-US91-09055-6	Sequence 6, Appl
311	197.5	6.3	616	3	US-10-011-795B-24	Sequence 24, Appl	384	186.5	5.9	799	3	US-09-396-985B-4	Sequence 4, Appl
312	197.5	6.3	616	3	US-10-015-386A-24	Sequence 24, Appl	385	186.5	5.9	839	3	US-09-396-985B-2	Sequence 2, Appl
313	197.5	6.3	616	3	US-10-012-121A-24	Sequence 24, Appl	386	186.5	5.9	839	3	US-09-396-985B-38	Sequence 98, Appl
314	197.5	6.3	616	3	US-10-006-485A-24	Sequence 24, Appl	387	186.5	5.9	844	2	US-09-949-016-9438	Sequence 9438, Ap
315	197.5	6.3	616	3	US-10-006-746A-24	Sequence 24, Appl	388	186	5.9	440	2	US-09-538-092-999	Sequence 999, App
316	197.5	6.3	616	3	US-10-012-752A-24	Sequence 24, Appl	389	186	5.9	451	2	US-09-949-016-9282	Sequence 9282, Ap
317	197.5	6.3	616	3	US-10-017-253A-24	Sequence 24, Appl	390	184	5.9	302	2	US-10-068-426-7	Sequence 7, Appl
318	197.5	6.3	616	3	US-10-015-519A-24	Sequence 24, Appl	391	184	5.9	320	1	US-07-613-083B-1	Sequence 1, Appl

392	184	5.9	368	2	US-09-949-016-6115	Sequence 6115, Ap	465	166	5.3	835	3	US-09-396-985B-6	Sequence 6, Appli
393	184	5.9	382	2	US-09-715-836A-9115	Sequence 9, Appli	466	166	5.3	1112	2	US-09-353-885-2	Sequence 2, Appli
394	184	5.9	382	2	US-09-949-016-10542	Sequence 10542, A	467	164.5	5.2	501	2	US-09-907-794A-185	Sequence 185, App
395	183	5.8	662	2	US-09-538-092-1325	Sequence 1325, Ap	468	164.5	5.2	501	2	US-09-905-125A-185	Sequence 185, App
396	183	5.8	662	2	US-09-949-016-6619	Sequence 6619, Ap	469	164.5	5.2	501	2	US-09-902-775A-185	Sequence 185, App
397	183	5.8	665	2	US-09-949-016-10710	Sequence 10710, A	470	164.5	5.2	501	2	US-09-906-700-185	Sequence 185, App
398	182.5	5.8	379	2	US-09-866-028-2	Sequence 2, Appli	471	164.5	5.2	501	2	US-09-903-603A-185	Sequence 185, App
399	182.5	5.8	379	2	US-09-944-457-2	Sequence 2, Appli	472	164.5	5.2	501	2	US-09-904-920A-185	Sequence 185, App
400	182.5	5.8	379	2	US-09-945-584-2	Sequence 2, Appli	473	164.5	5.2	501	2	US-09-909-064-185	Sequence 185, App
401	182.5	5.8	379	2	US-09-944-584-2	Sequence 2, Appli	474	164.5	5.2	501	2	US-09-905-381A-185	Sequence 185, App
402	182.5	5.8	379	2	US-09-945-587-2	Sequence 2, Appli	475	164.5	5.2	501	2	US-09-906-618-185	Sequence 185, App
403	182.5	5.8	379	2	US-09-944-884-2	Sequence 2, Appli	476	164.5	5.2	501	2	US-09-906-646-185	Sequence 185, App
404	182.5	5.8	958	2	US-09-706-594-5	Sequence 5, Appli	477	164.5	5.2	501	2	US-09-904-462-185	Sequence 185, App
405	182.5	5.8	966	2	US-09-964-956-32	Sequence 32, Appl	478	164.5	5.2	501	2	US-09-902-736A-185	Sequence 185, App
406	182	5.8	378	2	US-09-689-486-62	Sequence 62, Appl	479	164.5	5.2	501	2	US-09-906-722A-185	Sequence 185, App
407	182	5.8	378	2	US-09-973-424A-62	Sequence 62, Appl	480	164.5	5.2	501	2	US-09-905-449-185	Sequence 185, App
408	180	5.7	493	2	US-10-037-417-30	Sequence 30, Appl	481	164.5	5.2	501	2	US-09-903-562B-185	Sequence 185, App
409	180	5.7	989	2	US-09-954-987B-171	Sequence 171, App	482	164.5	5.2	501	2	US-09-906-679A-185	Sequence 185, App
410	179.5	5.7	515	3	US-10-162-335-92	Sequence 92, Appl	483	164.5	5.2	501	3	US-09-907-841-185	Sequence 185, App
411	179	5.7	290	2	US-10-068-426-10	Sequence 10, Appl	484	164.5	5.2	582	2	US-09-081-149-8	Sequence 8, Appli
412	179	5.7	290	2	US-10-068-426-11	Sequence 11, Appl	485	164.5	5.2	582	2	US-09-949-016-10752	Sequence 10752, A
413	179	5.7	290	2	US-10-068-426-12	Sequence 12, Appl	486	164.5	5.2	858	2	US-10-104-047-2918	Sequence 2918, Ap
414	179	5.7	302	2	US-10-068-426-8	Sequence 8, Appli	487	164	5.2	696	2	US-09-907-794A-91	Sequence 91, Appl
415	178	5.7	368	1	US-08-303-238-3	Sequence 3, Appli	488	164	5.2	696	2	US-09-905-125A-91	Sequence 91, Appl
416	178	5.7	368	2	US-08-458-834-3	Sequence 3, Appli	489	164	5.2	696	2	US-09-902-775A-91	Sequence 91, Appl
417	178	5.7	522	2	US-09-991-181-278	Sequence 278, App	490	164	5.2	696	2	US-09-906-700-91	Sequence 91, Appl
418	178	5.7	522	2	US-09-990-444-278	Sequence 278, App	491	164	5.2	696	2	US-09-903-603A-91	Sequence 91, Appl
419	178	5.7	522	2	US-09-997-333-278	Sequence 278, App	492	164	5.2	696	2	US-09-904-920A-91	Sequence 91, Appl
420	178	5.7	522	2	US-09-992-598-278	Sequence 278, App	493	164	5.2	696	2	US-09-909-064-91	Sequence 91, Appl
421	178	5.7	522	2	US-09-989-735-278	Sequence 278, App	494	164	5.2	696	2	US-09-905-381A-91	Sequence 91, Appl
422	178	5.7	522	2	US-10-094-749-2689	Sequence 2689, Ap	495	164	5.2	696	2	US-09-906-618-91	Sequence 91, Appl
423	178	5.7	522	3	US-09-989-726-278	Sequence 278, App	496	164	5.2	696	2	US-09-906-646-91	Sequence 91, Appl
424	178	5.7	522	3	US-09-997-514-278	Sequence 278, App	497	164	5.2	696	2	US-09-904-462-91	Sequence 91, Appl
425	178	5.7	522	3	US-09-989-728-278	Sequence 278, App	498	164	5.2	696	2	US-09-902-736A-91	Sequence 91, Appl
426	178	5.7	522	3	US-09-997-349-278	Sequence 278, App	499	164	5.2	696	2	US-09-905-449-91	Sequence 91, Appl
427	178	5.7	522	3	US-09-997-653-278	Sequence 278, App	500	164	5.2	696	2	US-09-903-562B-91	Sequence 91, Appl
428	178	5.7	522	3	US-09-989-293A-278	Sequence 278, App	501	164	5.2	696	2	US-09-906-679A-91	Sequence 91, Appl
429	178	5.7	1049	2	US-09-999-833A-496	Sequence 496, App	502	164	5.2	696	3	US-09-907-841-91	Sequence 91, Appl
430	178	5.7	1049	2	US-09-954-987B-170	Sequence 170, App	503	164	5.2	696	2	US-09-906-618-91	Sequence 91, Appl
431	178	5.7	1049	2	US-10-020-445A-496	Sequence 496, App	504	164	5.2	904	2	US-09-949-002-352	Sequence 352, App
432	178	5.7	1049	2	US-09-978-189-496	Sequence 496, App	505	164	5.2	910	2	US-09-949-003-483	Sequence 483, App
433	178	5.7	1049	3	US-10-017-085A-496	Sequence 496, App	506	163	5.2	582	2	US-09-081-149-7	Sequence 7, Appli
434	178	5.7	1049	3	US-10-145-129A-496	Sequence 496, App	507	163	5.2	753	2	US-09-056-383-13	Sequence 13, Appl
435	178	5.7	1049	3	US-10-013-929A-496	Sequence 496, App	508	161	5.1	559	2	US-09-081-149-2	Sequence 2, Appli
436	178	5.7	1052	2	US-10-013-917A-496	Sequence 496, App	509	160	5.1	942	2	US-10-101-464A-911	Sequence 911, App
437	178	5.7	1052	2	US-09-949-016-11508	Sequence 11508, A	510	158.5	5.1	1032	2	US-09-954-987B-192	Sequence 192, App
438	177.5	5.7	1050	2	US-09-954-987B-175	Sequence 175, App	511	158	5.0	257	2	US-09-270-767-41554	Sequence 41554, A
439	176.5	5.6	368	7	5340934-2	Sequence 2664, Ap	512	158	5.0	352	2	US-09-949-016-6781	Sequence 6781, Ap
440	175	5.6	368	7	5340934-2	Patent No. 5340934	513	157.5	5.0	374	2	US-09-949-016-7689	Sequence 7689, Ap
441	173.5	5.5	998	2	US-10-101-464A-914	Sequence 914, App	514	157.5	5.0	236	1	US-08-442-063A-42	Sequence 42, Appl
442	172.5	5.5	282	1	US-08-442-063A-45	Sequence 45, Appl	515	157.5	5.0	672	2	US-09-949-002-522	Sequence 522, App
443	172.5	5.5	307	1	US-08-442-063A-48	Sequence 48, Appl	516	157.5	5.0	796	2	US-10-104-047-2293	Sequence 2293, Ap
444	172.5	5.5	333	1	US-08-442-063A-27	Sequence 27, Appl	517	156.5	5.0	376	2	US-09-538-092-1276	Sequence 1276, Ap
445	172.5	5.5	338	2	US-09-689-486-63	Sequence 63, Appl	518	156	5.0	975	2	US-09-949-016-7595	Sequence 7595, Ap
446	172.5	5.5	338	2	US-09-973-424A-63	Sequence 2, Appli	519	155	4.9	1041	2	US-09-999-833A-498	Sequence 498, App
447	172.5	5.5	342	1	US-08-272-919-2	Sequence 2, Appli	520	155	4.9	1041	2	US-09-954-987B-184	Sequence 184, App
448	172.5	5.5	342	1	US-08-619-916-2	Sequence 2, Appli	521	155	4.9	1041	2	US-09-954-987B-186	Sequence 186, App
449	172.5	5.5	342	1	PCT-US95-08542-2	Sequence 2, Appli	522	155	4.9	1041	2	US-10-020-445A-498	Sequence 498, App
450	172.5	5.5	359	1	US-08-303-238-4	Sequence 4, Appli	523	155	4.9	1041	2	US-09-978-189-498	Sequence 498, App
451	172.5	5.5	359	2	US-08-458-834-4	Sequence 4, Appli	524	155	4.9	1041	3	US-10-017-085A-498	Sequence 498, App
452	172.5	5.5	359	2	US-09-538-092-868	Sequence 868, App	525	155	4.9	1041	3	US-10-145-129A-498	Sequence 498, App
453	172.5	5.5	359	2	US-09-949-016-6143	Sequence 6143, Ap	526	155	4.9	1041	3	US-10-013-929A-498	Sequence 498, App
454	172.5	5.5	360	2	US-09-949-016-7925	Sequence 7925, Ap	527	155	4.9	1059	2	US-10-013-917A-498	Sequence 498, App
455	172.5	5.5	1388	2	US-10-153-469A-10	Sequence 10, Appl	528	155	4.9	377	2	US-09-954-987B-187	Sequence 187, App
456	172.5	5.5	1388	2	US-10-104-889-10	Sequence 10, Appl	529	154.5	4.9	1495	2	US-09-949-016-7949	Sequence 7949, Ap
457	170.5	5.4	373	2	US-09-724-864-43	Sequence 43, Appl	530	154.5	4.9	1495	2	US-08-522-726B-1	Sequence 1, Appli
458	170	5.4	907	2	US-09-170-496D-264	Sequence 264, App	531	154.5	4.9	894	1	US-09-337-384-1	Sequence 2, Appli
459	170	5.4	907	2	US-09-170-496D-278	Sequence 278, App	532	153.5	4.9	894	1	US-08-372-892-2	Sequence 34, Appl
460	169.5	5.4	353	7	5340934-4	Patent No. 5340934	533	153.5	4.9	894	1	US-08-445-640-34	Sequence 34, Appl
461	168	5.4	1049	2	US-09-954-987B-172	Sequence 172, App	534	153.5	4.9	894	2	US-08-170-558-34	Sequence 34, Appl
462	167	5.3	746	5	PCT-US95-10509-2	Sequence 2, Appli	535	153.5	4.9	894	2	US-08-447-314-34	Sequence 34, Appl
463	167	5.3	1112	2	US-09-353-585-3	Sequence 3, Appli	536	153.5	4.9	894	2	US-08-445-461-34	Sequence 34, Appl
464	166.5	5.3	224	2	US-09-482-273-174	Sequence 174, App	537	153.5	4.9	894	2	US-09-223-490-34	Sequence 34, Appl

538	153.5	4.9	894	3	US-10-646-760-34	Sequence 34, Appl	611	143	4.6	935	2	US-09-477-962-107	Sequence 107, App
539	153.5	4.9	1032	2	US-09-954-987B-6	Sequence 6, Appl	612	142.5	4.5	141	2	US-09-270-767-31706	Sequence 31706, A
540	153	4.9	679	2	US-09-252-991A-18857	Sequence 18857, A	613	142.5	4.5	141	2	US-09-270-767-46923	Sequence 46923, A
541	153	4.9	699	2	US-10-237-551-143	Sequence 143, App	614	142.5	4.5	805	2	US-09-103-429A-4	Sequence 4, Appl
542	153	4.9	699	2	US-10-237-551-254	Sequence 254, App	615	142.5	4.5	807	2	US-09-294-663-4	Sequence 4, Appl
543	153	4.9	1248	2	US-10-042-810-4	Sequence 2, Appl	616	142	4.5	326	2	US-09-689-486-64	Sequence 64, Appl
544	153	4.9	1278	2	US-10-042-810-4	Sequence 4, Appl	617	142	4.5	326	2	US-09-973-424A-64	Sequence 64, Appl
545	152.5	4.9	564	2	US-10-104-047-2127	Sequence 2127, Ap	618	142	4.5	363	2	US-10-188-495-6	Sequence 6, Appl
546	152	4.8	786	2	US-09-949-002-351	Sequence 351, App	619	142	4.5	363	2	US-10-188-495-6	Sequence 6, Appl
547	152	4.8	796	2	US-09-949-002-386	Sequence 386, App	620	142	4.5	365	2	US-10-101-464A-901	Sequence 901, App
548	152	4.8	802	2	US-09-949-002-386	Sequence 386, App	621	142	4.5	365	2	US-10-101-464A-901	Sequence 901, App
549	151.5	4.8	455	2	US-10-188-495-3	Sequence 3, Appl	622	140.5	4.5	661	2	US-10-037-417-107	Sequence 107, App
550	151.5	4.8	1964	2	US-09-467-997-1	Sequence 1, Appl	623	140.5	4.5	376	1	US-08-303-238-1	Sequence 802, App
551	151	4.8	632	2	US-09-270-767-46234	Sequence 46234, A	624	140.5	4.5	376	2	US-08-458-834-1	Sequence 1, Appl
552	151	4.8	835	3	US-09-396-988B-99	Sequence 99, Appl	625	140	4.5	283	2	US-09-949-016-7910	Sequence 7910, Ap
553	151	4.8	835	3	US-09-396-988B-104	Sequence 104, App	626	140	4.5	547	2	US-10-101-464A-928	Sequence 928, App
554	150.5	4.8	695	1	US-08-487-886-2	Sequence 2, Appl	627	139	4.4	5179	2	US-09-538-092-1258	Sequence 1258, Ap
555	150.5	4.8	695	2	US-08-482-855-2	Sequence 2, Appl	628	138.5	4.4	710	2	US-10-104-047-3402	Sequence 3402, Ap
556	150.5	4.8	695	2	US-08-474-986-2	GENERAL INFORMA	629	138.5	4.4	811	2	US-09-991-181-57	Sequence 57, Appl
557	150	4.8	259	2	US-09-907-794A-71	Sequence 71, Appl	630	138.5	4.4	811	2	US-09-990-444-57	Sequence 57, Appl
558	150	4.8	259	2	US-09-905-125A-71	Sequence 71, Appl	631	138.5	4.4	811	2	US-09-997-333-57	Sequence 57, Appl
559	150	4.8	259	2	US-09-902-775A-71	Sequence 71, Appl	632	138.5	4.4	811	2	US-09-992-598-57	Sequence 57, Appl
560	150	4.8	259	2	US-09-906-700-71	Sequence 71, Appl	633	138.5	4.4	811	3	US-09-989-735-57	Sequence 57, Appl
561	150	4.8	259	2	US-09-903-603A-71	Sequence 71, Appl	634	138.5	4.4	811	3	US-09-989-726-57	Sequence 57, Appl
562	150	4.8	259	2	US-09-904-920A-71	Sequence 71, Appl	635	138.5	4.4	811	3	US-09-997-514-57	Sequence 57, Appl
563	150	4.8	259	2	US-09-909-064-71	Sequence 71, Appl	636	138.5	4.4	811	3	US-09-989-728-57	Sequence 57, Appl
564	150	4.8	259	2	US-09-905-381A-71	Sequence 71, Appl	637	138.5	4.4	811	3	US-09-997-349-57	Sequence 57, Appl
565	150	4.8	259	2	US-09-906-618-71	Sequence 71, Appl	638	138.5	4.4	811	3	US-09-997-653-57	Sequence 57, Appl
566	150	4.8	259	2	US-09-906-646-71	Sequence 71, Appl	639	138.5	4.4	811	3	US-09-989-293A-57	Sequence 57, Appl
567	150	4.8	259	2	US-09-904-462-71	Sequence 71, Appl	640	138	4.4	323	2	US-09-949-016-7924	Sequence 7924, Ap
568	150	4.8	259	2	US-09-902-736A-71	Sequence 71, Appl	641	138	4.4	1003	2	US-10-094-749-2528	Sequence 2528, Ap
569	150	4.8	259	2	US-09-906-722A-71	Sequence 71, Appl	642	137.5	4.4	141	2	US-10-094-749-2528	Sequence 45511, A
570	150	4.8	259	2	US-09-905-449-71	Sequence 71, Appl	643	137.5	4.4	884	7	5208144-8	Patent No. 5208144
571	150	4.8	259	2	US-09-903-562B-71	Sequence 71, Appl	644	137	4.4	4544	1	US-08-469-486-52	Sequence 52, Appl
572	150	4.8	259	2	US-09-906-679A-71	Sequence 71, Appl	645	137	4.4	4544	1	US-08-469-658-52	Sequence 52, Appl
573	150	4.8	259	3	US-09-907-841-71	Sequence 71, Appl	646	136.5	4.4	2972	2	US-10-101-464A-919	Sequence 919, App
574	150	4.8	513	2	US-09-068-804-14	Sequence 14, Appl	647	136.5	4.4	2972	2	US-09-579-181-2	Sequence 2, Appl
575	149	4.8	503	2	US-10-037-417-104	Sequence 104, App	648	136.5	4.4	3118	2	US-10-104-047-3292	Sequence 1, Appl
576	149	4.8	1012	1	US-08-475-891A-4	Sequence 4, Appl	649	136	4.3	287	2	US-10-104-047-3292	Sequence 3292, Ap
577	149	4.8	1025	1	US-08-567-375-4	Sequence 4, Appl	650	136	4.3	692	2	US-07-757-342D-6	Sequence 6, Appl
578	149	4.8	1025	1	US-08-567-680A-4	Sequence 4, Appl	651	136	4.3	692	2	US-09-461-657B-6	Sequence 6, Appl
579	149	4.8	1026	2	US-09-623-551-18	Sequence 18, Appl	652	135.5	4.3	536	2	US-09-252-991A-31124	Sequence 31124, A
580	149	4.8	1504	2	US-09-364-206-2	Sequence 2, Appl	653	135.5	4.3	743	2	US-09-771-161A-164	Sequence 164, App
581	149	4.8	1874	2	US-09-331-403-2	Sequence 2, Appl	654	135.5	4.3	743	2	US-09-771-161A-254	Sequence 254, App
582	148.5	4.7	375	1	US-08-458-834-2	Sequence 2, Appl	655	135	4.3	446	2	US-10-101-464A-733	Sequence 733, App
583	148.5	4.7	375	1	US-08-565-501A-104	Sequence 104, App	656	135	4.3	538	2	US-09-616-289-43	Sequence 43, Appl
584	147.5	4.7	570	2	US-09-639-206A-104	Sequence 104, App	657	135	4.3	538	2	US-09-976-740-43	Sequence 43, Appl
585	147.5	4.7	570	2	US-09-874-923-104	Sequence 104, App	658	135	4.3	696	2	US-10-094-749-2425	Sequence 2425, Ap
586	147.5	4.7	570	2	US-09-949-002-532	Sequence 532, App	659	135	4.3	723	2	US-09-434-408-2	Sequence 2, Appl
587	147.5	4.7	1728	2	US-09-270-767-32705	Sequence 32705, A	660	135	4.3	723	2	US-10-104-047-2572	Sequence 2, Appl
588	147	4.7	177	2	US-09-270-767-47922	Sequence 47922, A	661	135	4.3	907	2	US-08-783-774-2	Sequence 2, Appl
589	147	4.7	265	2	US-09-270-767-47922	Sequence 47922, A	662	135	4.3	907	2	US-09-328-599A-1	Sequence 1, Appl
590	147	4.7	265	2	US-09-270-767-47922	Sequence 47922, A	663	135	4.3	907	5	PCT-US95-04611A-19	Sequence 19, Appl
591	147	4.7	2414	1	US-08-227-536-2	Sequence 2, Appl	664	134.5	4.3	802	2	US-09-823-240A-2	Sequence 2, Appl
592	147	4.7	2414	1	US-09-538-092-1289	Sequence 1289, Ap	665	134	4.3	536	2	US-09-292-225-21	Sequence 21, Appl
593	147	4.7	2414	5	PCT-US95-04682-2	Sequence 2, Appl	666	134	4.3	550	2	US-09-616-289-47	Sequence 47, Appl
594	146.5	4.7	325	2	US-10-104-047-3320	Sequence 3320, Ap	667	134	4.3	550	2	US-09-976-740-47	Sequence 47, Appl
595	146.5	4.7	344	2	US-10-104-047-3358	Sequence 3358, Ap	668	134	4.3	555	2	US-09-292-225-15	Sequence 15, Appl
596	146.5	4.7	1404	1	US-08-400-159-2	Sequence 2, Appl	669	134	4.3	555	2	US-09-292-225-18	Sequence 18, Appl
597	146.5	4.7	1404	2	US-08-611-729A-2	Sequence 2, Appl	670	133.5	4.3	1166	2	US-10-101-464A-900	Sequence 900, App
598	146.5	4.7	1404	2	US-09-195-524-2	Sequence 2, Appl	671	133	4.2	652	2	US-10-104-047-3364	Sequence 3364, Ap
599	146	4.7	788	2	US-09-103-429A-3	Sequence 3, Appl	672	133	4.2	4391	2	US-10-006-011A-2	Sequence 2, Appl
600	146	4.7	788	2	US-09-294-663-3	Sequence 3, Appl	673	132.5	4.2	390	2	US-08-460-576-2	Sequence 2, Appl
601	146	4.7	885	1	US-08-372-892-4	Sequence 4, Appl	674	132.5	4.2	463	1	US-08-162-402B-9	Sequence 9, Appl
602	146	4.7	885	1	US-09-919-497-52	Sequence 52, Appl	675	132.5	4.2	579	2	US-09-325-932A-185	Sequence 185, App
603	145.5	4.6	2142	2	US-09-538-092-1142	Sequence 1142, Ap	676	132.5	4.2	583	2	US-09-641-612-2	Sequence 2, Appl
604	145.5	4.6	2142	2	US-09-949-002-371	Sequence 371, App	677	132.5	4.2	2035	1	US-08-046-585-5	Sequence 5, Appl
605	145	4.6	353	2	US-09-949-016-7923	Sequence 7923, Ap	678	132.5	4.2	2035	1	US-08-393-703-5	Sequence 5, Appl
606	145	4.6	1032	2	US-09-954-987B-3	Sequence 3, Appl	679	132.5	4.2	2035	5	PCT-US93-11721-5	Sequence 5, Appl
607	144	4.6	661	1	US-08-514-014-4	Sequence 4, Appl	680	132.5	4.2	2045	2	US-09-949-016-10491	Sequence 10491, A
608	144	4.6	661	1	US-08-833-823-4	Sequence 4, Appl	681	132.5	4.2	3122	2	US-10-237-551-201	Sequence 201, App
609	143.5	4.6	1274	1	US-09-095-443-2	Sequence 2, Appl	682	132.5	4.2	3122	2	US-10-237-551-250	Sequence 250, App
610	143.5	4.6	1636	3	US-10-433-794-1	Sequence 1, Appl	683	132	4.2	287	2	US-09-893-737-110	Sequence 110, App

684	132	4.2	465	1	US-08-162-402B-8	Sequence 8, Appli	757	126.5	4.0	685	2	US-09-641-612-7	Sequence 7, Appli
685	132	4.2	705	2	US-10-101-464A-894	Sequence 894, App	758	126.5	4.0	685	3	US-10-241-476-25	Sequence 25, Appl
686	132	4.2	979	2	US-08-514-213A-2	Sequence 2, Appli	759	126.5	4.0	919	2	US-10-101-464A-642	Sequence 642, App
687	132	4.2	979	2	US-09-015-399-5	Sequence 5, Appli	760	126.5	4.0	999	1	US-08-473-553A-5	Sequence 5, Appli
688	132	4.2	1003	2	US-09-949-016-11260	Sequence 11260, A	761	126	4.0	143	2	US-09-893-737-190	Sequence 190, App
689	131.5	4.2	461	2	US-10-037-417-96	Sequence 96, Appl	762	126	4.0	152	2	US-09-270-767-33594	Sequence 33594, A
690	131.5	4.2	571	2	US-09-252-991A-30533	Sequence 30533, A	763	126	4.0	775	2	US-09-949-016-8799	Sequence 8799, Ap
691	131	4.2	180	2	US-08-986-485-8	Sequence 8, Appli	764	126	4.0	1485	2	US-09-762-569-4	Sequence 4, Appli
692	131	4.2	227	2	US-10-101-464A-666	Sequence 666, App	765	126	4.0	1821	2	US-09-949-016-5938	Sequence 5938, Ap
693	131	4.2	279	2	US-09-270-767-41558	Sequence 41558, A	766	125.5	4.0	258	2	US-10-012-231A-153	Sequence 153, App
694	131	4.2	407	2	US-09-270-767-46649	Sequence 46649, A	767	125.5	4.0	258	2	US-10-015-389A-153	Sequence 153, App
695	131	4.2	799	2	US-09-180-439-6	Sequence 6, Appli	768	125.5	4.0	258	2	US-10-006-768A-153	Sequence 153, App
696	131	4.2	947	2	US-09-228-986-73	Sequence 73, Appl	769	125.5	4.0	258	2	US-10-015-671A-153	Sequence 153, App
697	131	4.2	947	2	US-10-101-464A-73	Sequence 73, Appl	770	125.5	4.0	258	2	US-10-015-393A-153	Sequence 153, App
698	131	4.2	1062	2	US-09-902-540-16313	Sequence 16313, A	771	125.5	4.0	258	2	US-10-011-833A-153	Sequence 153, App
699	131	4.2	1196	2	US-08-881-706-2	Sequence 2, Appli	772	125.5	4.0	258	2	US-10-006-041A-153	Sequence 153, App
700	131	4.2	1196	2	US-09-823-394-2	Sequence 2, Appli	773	125.5	4.0	258	2	US-10-012-064A-153	Sequence 153, App
701	131	4.2	1938	2	US-09-949-016-6609	Sequence 6609, Ap	774	125.5	4.0	258	3	US-10-011-795B-153	Sequence 153, App
702	130.5	4.2	843	2	US-10-101-464A-893	Sequence 893, App	775	125.5	4.0	258	3	US-10-015-386A-153	Sequence 153, App
703	130.5	4.2	878	2	US-09-556-706B-2	Sequence 2, Appli	776	125.5	4.0	258	3	US-10-012-752A-153	Sequence 153, App
704	130.5	4.2	878	2	US-09-724-418A-2	Sequence 2, Appli	777	125.5	4.0	258	3	US-10-006-485A-153	Sequence 153, App
705	130.5	4.2	3729	1	US-08-804-227C-4	Sequence 4, Appli	778	125.5	4.0	258	3	US-10-006-746A-153	Sequence 153, App
706	130	4.1	619	2	US-10-037-417-34	Sequence 34, Appl	779	125.5	4.0	258	3	US-10-012-752A-153	Sequence 153, App
707	130	4.1	645	2	US-10-101-464A-920	Sequence 920, App	780	125.5	4.0	258	3	US-10-017-253A-153	Sequence 153, App
708	129.5	4.1	550	2	US-09-252-991A-21295	Sequence 21295, A	781	125.5	4.0	258	3	US-10-015-519A-153	Sequence 153, App
709	129.5	4.1	912	5	PCN-US95-03747-2	Sequence 2, Appli	782	125.5	4.0	258	3	US-10-007-236A-153	Sequence 153, App
710	129.5	4.1	1251	3	US-10-114-270-80	Sequence 80, Appl	783	125.5	4.0	258	3	US-08-985-335-3	Sequence 3, Appli
711	129	4.1	363	2	US-09-270-767-44030	Sequence 44030, A	784	125.5	4.0	440	2	US-09-410-372-3	Sequence 54, Appl
712	129	4.1	823	2	US-09-252-991A-23655	Sequence 23655, A	785	125.5	4.0	440	2	US-07-741-453A-54	Sequence 60, Appl
713	129	4.1	885	2	US-09-252-991A-26129	Sequence 26129, A	786	125.5	4.0	764	2	US-07-741-453A-60	Sequence 2, Appli
714	129	4.1	1133	2	US-10-101-464A-809	Sequence 809, App	787	125.5	4.0	1129	2	US-09-023-905A-2	Sequence 237, App
715	129	4.1	1940	1	US-08-644-271-30	Sequence 30, Appl	788	125.5	4.0	419	2	US-10-002-344A-237	Sequence 25918, A
716	129	4.1	1940	2	US-09-077-955-34	Sequence 34, Appl	789	125.5	4.0	957	2	US-09-252-991A-17231	Sequence 2, Appli
717	129	4.1	1940	2	US-10-016-283-34	Sequence 34, Appl	790	125	4.0	1139	2	US-09-513-505-2	Sequence 86, Appl
718	129	4.1	2321	2	US-09-230-652-2	Sequence 2, Appli	791	125	4.0	2023	2	US-09-491-356C-8	Sequence 1377, Ap
719	129	4.1	2321	2	US-09-612-226B-2	Sequence 2, Appli	792	125	4.0	2026	2	US-09-487-598B-86	Sequence 17231, A
720	128.5	4.1	188	1	US-08-836-854-15	Sequence 15, Appl	793	125	4.0	2124	2	US-09-538-092-1377	Sequence 61021, A
721	128.5	4.1	508	2	US-10-104-047-3233	Sequence 3233, Ap	794	125	4.0	2294	2	US-09-252-991A-17231	Sequence 4, Appli
722	128.5	4.1	653	2	US-10-101-464A-953	Sequence 953, App	795	125	4.0	283	2	US-10-211-689-4	Sequence 17, Appl
723	128.5	4.1	864	2	US-10-101-464A-896	Sequence 896, App	796	124.5	4.0	298	2	US-09-232-160-17	Sequence 87, Appl
724	128.5	4.1	865	2	US-09-902-540-10416	Sequence 10416, A	797	124.5	4.0	298	2	US-09-800-729-87	Sequence 121, App
725	128.5	4.1	1023	1	US-08-475-891A-2	Sequence 2, Appli	798	124.5	4.0	298	2	US-09-800-729-121	Sequence 22, Appl
726	128.5	4.1	1023	1	US-08-567-375-2	Sequence 2, Appli	799	124.5	4.0	298	2	US-10-000-489-22	Sequence 50, Appl
727	128.5	4.1	1023	1	US-08-587-680A-2	Sequence 2, Appli	800	124.5	4.0	298	2	US-09-832-129-50	Sequence 2, Appli
728	128.5	4.1	475	2	US-09-252-991A-30242	Sequence 30242, A	801	124.5	4.0	298	2	US-10-211-689-2	Sequence 22, Appl
729	128	4.1	538	1	US-08-541-759B-2	Sequence 2, Appli	802	124.5	4.0	298	2	US-09-992-095B-22	Sequence 22, Appl
730	128	4.1	717	2	US-10-101-464A-810	Sequence 810, App	803	124.5	4.0	307	2	US-09-949-016-9817	Sequence 9817, Ap
731	128	4.1	1006	3	US-10-415-147-12	Sequence 12, Appl	804	124.5	4.0	307	2	US-09-907-794A-250	Sequence 250, App
732	127.5	4.1	1006	3	US-10-114-270-84	Sequence 84, Appl	805	124.5	4.0	307	2	US-09-905-125A-250	Sequence 250, App
733	127.5	4.1	1522	2	US-10-144-198-31	Sequence 31, Appl	806	124.5	4.0	307	2	US-09-902-775A-250	Sequence 250, App
734	127.5	4.1	1581	2	US-09-949-002-414	Sequence 414, App	807	124.5	4.0	307	2	US-10-000-986A-22	Sequence 22, Appl
735	127.5	4.1	3969	2	US-08-061-376-5	Sequence 5, Appli	808	124.5	4.0	307	2	US-09-907-794A-250	Sequence 9818, Ap
736	127.5	4.1	3969	2	US-09-538-092-1262	Sequence 1262, Ap	809	124.5	4.0	307	2	US-09-905-125A-250	Sequence 250, App
737	127.5	4.1	3969	2	US-09-270-767-32658	Sequence 32658, A	810	124.5	4.0	307	2	US-09-902-775A-250	Sequence 250, App
738	127	4.1	260	2	US-09-252-991A-26695	Sequence 26695, A	811	124.5	4.0	307	2	US-09-906-700A-250	Sequence 250, App
739	127	4.1	615	2	US-09-270-767-32244	Sequence 32244, A	812	124.5	4.0	307	2	US-09-903-603A-250	Sequence 250, App
740	126.5	4.0	141	2	US-09-270-767-47461	Sequence 47461, A	813	124.5	4.0	307	2	US-09-904-920A-250	Sequence 250, App
741	126.5	4.0	438	2	US-09-991-181-129	Sequence 129, App	814	124.5	4.0	307	2	US-09-904-920A-250	Sequence 250, App
742	126.5	4.0	438	2	US-09-990-444-129	Sequence 129, App	815	124.5	4.0	307	2	US-09-905-125A-250	Sequence 250, App
743	126.5	4.0	438	2	US-09-997-333-129	Sequence 129, App	816	124.5	4.0	307	2	US-09-906-618-250	Sequence 250, App
744	126.5	4.0	438	2	US-09-992-598-129	Sequence 129, App	817	124.5	4.0	307	2	US-09-906-618-250	Sequence 250, App
745	126.5	4.0	438	2	US-09-989-735-129	Sequence 129, App	818	124.5	4.0	307	2	US-09-906-618-250	Sequence 250, App
746	126.5	4.0	438	2	US-09-989-726-129	Sequence 129, App	819	124.5	4.0	307	2	US-09-906-618-250	Sequence 250, App
747	126.5	4.0	438	2	US-09-997-514-129	Sequence 129, App	820	124.5	4.0	307	2	US-09-906-618-250	Sequence 250, App
748	126.5	4.0	438	2	US-09-989-728-129	Sequence 129, App	821	124.5	4.0	307	2	US-09-906-618-250	Sequence 250, App
749	126.5	4.0	438	2	US-09-997-349-129	Sequence 129, App	822	124.5	4.0	307	2	US-09-906-618-250	Sequence 250, App
750	126.5	4.0	438	2	US-09-997-653-129	Sequence 129, App	823	124.5	4.0	307	2	US-09-906-618-250	Sequence 250, App
751	126.5	4.0	438	2	US-09-989-293A-129	Sequence 3, Appli	824	124.5	4.0	307	2	US-09-906-618-250	Sequence 250, App
752	126.5	4.0	659	2	US-09-423-753-3	Sequence 3, Appli	825	124.5	4.0	307	2	US-09-906-618-250	Sequence 250, App
753	126.5	4.0	659	2	US-10-241-476-3	Sequence 2, Appli	826	124.5	4.0	307	2	US-09-906-618-250	Sequence 250, App
754	126.5	4.0	685	3	US-08-872-855-2	Sequence 2, Appli	827	124.5	4.0	307	2	US-09-906-618-250	Sequence 250, App
755	126.5	4.0	685	3	US-09-423-753-25	Sequence 25, Appli	828	124.5	4.0	307	2	US-09-906-618-250	Sequence 250, App
756	126.5	4.0	685	2			829	124.5	4.0	307	2	US-09-906-618-250	Sequence 250, App

830	124.5	4.0	1709	2	US-09-949-016-10503	Sequence 10503, A	903	120.5	3.8	141	1	US-08-442-063A-36	Sequence 36, Appl
831	124	4.0	277	2	US-07-741-453A-58	Sequence 58, Appl	904	120.5	3.8	426	2	US-09-252-991A-24450	Sequence 24450, A
832	124	4.0	707	2	US-09-228-986-80	Sequence 80, Appl	905	120.5	3.8	464	2	US-09-716-964B-4	Sequence 4, Appl1
833	124	4.0	707	2	US-10-101-464A-80	Sequence 80, Appl	906	120.5	3.8	562	2	US-09-903-540-13269	Sequence 13269, A
834	124	4.0	1457	2	US-08-665-259-27	Sequence 27, Appl	907	120.5	3.8	787	2	US-09-721-383-2	Sequence 2, Appl1
835	124	4.0	1457	2	US-08-762-500-27	Sequence 27, Appl	908	120.5	3.8	787	2	US-09-721-137-2	Sequence 2, Appl1
836	124	4.0	1472	2	US-09-032-438C-119	Sequence 119, App	909	120.5	3.8	787	2	US-09-721-251-2	Sequence 2, Appl1
837	123.5	3.9	1312	2	US-09-041-886-19	Sequence 19, App	910	120.5	3.8	787	2	US-10-114-764-2	Sequence 2, Appl1
838	123.5	3.9	1312	2	US-09-648-281-2	Sequence 2, Appl1	911	120.5	3.8	998	2	US-10-101-464A-931	Sequence 931, App
839	123.5	3.9	1312	2	US-09-707-919A-19	Sequence 19, Appl	912	120.5	3.8	1104	2	US-09-981-953A-4	Sequence 4, Appl1
840	123.5	3.9	1312	2	US-08-083-268-3	Sequence 3, Appl1	913	120.5	3.8	1587	2	US-09-949-002-354	Sequence 354, App
841	123.5	3.9	1312	2	US-08-981-998A-3	Sequence 3, Appl1	914	120.5	3.8	1610	2	US-09-548-473B-4	Sequence 4, Appl1
842	123	3.9	526	2	US-10-101-464A-998	Sequence 998, App	915	120.5	3.8	1665	2	US-09-858-664A-2	Sequence 2, Appl1
843	123	3.9	526	2	US-09-252-991A-23688	Sequence 23688, A	916	120.5	3.8	1665	2	US-10-274-978-2	Sequence 2, Appl1
844	123	3.9	557	2	US-09-248-796A-26892	Sequence 26892, A	917	120.5	3.8	1665	2	US-10-697-263-2	Sequence 2, Appl1
845	123	3.9	888	1	US-08-445-640-35	Sequence 35, Appl	918	120.5	3.8	2596	2	US-09-548-473B-6	Sequence 6, Appl1
846	123	3.9	888	1	US-08-170-558-35	Sequence 35, Appl	919	120.5	3.8	2630	3	US-10-077-130-2	Sequence 2, Appl1
847	123	3.9	888	2	US-08-447-314-35	Sequence 35, Appl	920	120.5	3.8	7968	3	US-10-077-130-5	Sequence 5, Appl1
848	123	3.9	888	2	US-08-445-461-35	Sequence 35, Appl	921	120.5	3.8	130	2	US-09-270-767-33086	Sequence 33086, A
849	123	3.9	888	2	US-09-223-490-35	Sequence 35, Appl	922	120	3.8	130	2	US-09-270-767-48303	Sequence 48303, A
850	123	3.9	888	3	US-10-646-760-35	Sequence 35, Appl	923	120	3.8	467	2	US-09-046-736-2	Sequence 2, Appl1
851	123	3.9	924	1	US-08-481-130-28	Sequence 28, Appl	924	120	3.8	523	1	US-08-473-553A-3	Sequence 3, Appl1
852	123	3.9	924	1	US-08-656-984A-28	Sequence 28, Appl	925	120	3.8	569	2	US-09-514-245-22	Sequence 22, Appl
853	123	3.9	924	1	US-08-485-604-28	Sequence 28, Appl	926	120	3.8	603	2	US-09-906-779-4	Sequence 4, Appl1
854	123	3.9	924	1	US-08-487-595-28	Sequence 28, Appl	927	120	3.8	696	2	US-09-758-759-125	Sequence 125, App
855	122.5	3.9	335	3	US-10-114-270-34	Sequence 34, Appl	928	120	3.8	710	2	US-10-094-749-2315	Sequence 2315, App
856	122.5	3.9	335	3	US-10-114-270-36	Sequence 36, Appl	929	120	3.8	2556	2	US-08-185-432-17	Sequence 17, Appl
857	122.5	3.9	494	2	US-09-248-796A-16546	Sequence 16546, A	930	120	3.8	2556	2	US-08-899-232-2	Sequence 2, Appl1
858	122.5	3.9	585	2	US-09-641-612-5	Sequence 5, Appl1	931	120	3.8	2556	2	US-09-121-457-2	Sequence 2, Appl1
859	122.5	3.9	596	2	US-09-253-991A-18875	Sequence 18875, A	932	119.5	3.8	520	2	US-09-107-433-3721	Sequence 3721, App
860	122.5	3.9	968	2	US-09-180-439-3	Sequence 3, Appl1	933	119.5	3.8	608	2	US-09-949-016-11148	Sequence 11148, A
861	122.5	3.9	968	2	US-09-180-439-4	Sequence 4, Appl1	934	119.5	3.8	608	2	US-09-949-016-11149	Sequence 11149, A
862	122.5	3.9	1016	2	US-09-180-439-8	Sequence 8, Appl1	935	119.5	3.8	608	2	US-09-949-016-11150	Sequence 11150, A
863	122.5	3.9	1036	2	US-09-771-161A-255	Sequence 255, App	936	119.5	3.8	608	2	US-09-949-016-11151	Sequence 11151, A
864	122.5	3.9	1036	2	US-09-771-161A-256	Sequence 256, App	937	119.5	3.8	1034	2	US-09-252-991A-28921	Sequence 28921, A
865	122	3.9	191	2	US-09-461-325-186	Sequence 186, App	938	119.5	3.8	1048	2	US-09-171-699-10	Sequence 10, Appl
866	122	3.9	191	2	US-10-012-542-186	Sequence 186, App	939	119.5	3.8	1149	2	US-08-560-005-5	Sequence 5, Appl1
867	122	3.9	191	2	US-10-012-542-186	Sequence 186, App	940	119.5	3.8	1149	2	US-09-418-540-5	Sequence 5, Appl1
868	122	3.9	206	2	US-09-461-325-186	Sequence 186, App	941	119.5	3.8	1149	2	US-09-969-528-5	Sequence 5, Appl1
869	122	3.9	206	2	US-09-461-325-186	Sequence 186, App	942	119.5	3.8	1345	3	US-10-433-794-17	Sequence 17, Appl
870	122	3.9	206	2	US-10-012-542-412	Sequence 412, App	943	119.5	3.8	1596	2	US-09-538-092-887	Sequence 887, App
871	122	3.9	312	2	US-10-115-123-412	Sequence 412, App	944	119	3.8	304	2	US-10-101-464A-717	Sequence 717, App
872	122	3.9	328	1	US-08-270-767-31750	Sequence 31750, A	945	119	3.8	319	2	US-08-630-172-12	Sequence 12, Appl
873	122	3.9	328	1	US-08-414-926A-9	Sequence 9, Appl1	946	119	3.8	319	2	US-09-375-419-12	Sequence 12, Appl
874	122	3.9	328	1	US-08-928-922-9	Sequence 9, Appl1	947	119	3.8	528	2	US-08-928-213B-8	Sequence 8, Appl1
875	122	3.9	328	2	US-09-253-682-9	Sequence 9, Appl1	948	119	3.8	593	2	US-09-252-991A-20441	Sequence 20441, A
876	122	3.9	328	2	US-09-527-657-9	Sequence 9, Appl1	949	119	3.8	784	2	US-09-982-308B-23	Sequence 23, Appl
877	122	3.9	481	2	US-09-892-100-9	Sequence 9, Appl1	950	119	3.8	1081	2	US-09-369-364A-17	Sequence 17, Appl
878	122	3.9	495	2	US-09-949-016-9748	Sequence 9748, App	951	118.5	3.8	171	2	US-09-270-767-43049	Sequence 43049, A
879	122	3.9	515	2	US-09-252-991A-31949	Sequence 31949, A	952	118.5	3.8	422	2	US-09-949-016-8251	Sequence 8251, App
880	122	3.9	527	2	US-09-370-838-216	Sequence 216, App	953	118.5	3.8	430	2	US-09-949-016-8782	Sequence 8782, App
881	122	3.9	527	2	US-09-854-133-216	Sequence 216, App	954	118.5	3.8	486	1	US-08-450-360-2	Sequence 2, Appl1
882	122	3.9	529	2	US-09-716-964B-2	Sequence 2, Appl1	955	118.5	3.8	883	2	US-10-188-495-72	Sequence 72, Appl
883	121.5	3.9	320	2	US-09-325-932A-190	Sequence 190, App	956	118.5	3.8	1166	2	US-10-104-047-2949	Sequence 2949, App
884	121.5	3.9	344	2	US-10-094-749-2951	Sequence 2951, App	957	118.5	3.8	1321	1	US-08-317-310A-64	Sequence 64, Appl
885	121.5	3.9	477	2	US-09-252-991A-19831	Sequence 19831, A	958	118	3.8	149	2	US-09-270-767-32618	Sequence 32618, A
886	121.5	3.9	615	2	US-09-248-796A-18020	Sequence 18020, A	959	118	3.8	149	2	US-09-270-767-47835	Sequence 47835, A
887	121.5	3.9	698	2	US-10-104-047-2546	Sequence 2546, App	960	118	3.8	462	2	US-09-252-991A-20814	Sequence 20814, A
888	121.5	3.9	1225	2	US-09-501-171-4	Sequence 4, Appl1	961	118	3.8	947	2	US-09-252-991A-21335	Sequence 21335, A
889	121.5	3.9	1225	2	US-09-949-016-6063	Sequence 6063, App	962	118	3.8	1044	2	US-09-252-991A-18853	Sequence 18853, A
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891	121.5	3.9	1252	1	US-08-199-780-3	Sequence 3, Appl1	964	118	3.8	1084	2	US-09-227-725A-3	Sequence 3, Appl1
892	121.5	3.9	1252	1	US-08-316-650-3	Sequence 3, Appl1	965	118	3.8	1084	2	US-10-071-900-3	Sequence 3, Appl1
893	121.5	3.9	1253	2	US-08-479-722B-4	Sequence 4, Appl1	966	118	3.8	1864	1	US-08-804-227C-3	Sequence 3, Appl1
894	121.5	3.9	1253	2	US-09-592-685-4	Sequence 4, Appl1	967	118	3.8	2471	1	US-08-185-432-16	Sequence 16, Appl
895	121	3.9	499	2	US-09-043-672A-1	Sequence 1, Appl1	968	118	3.8	2471	1	US-08-083-590A-19	Sequence 19, Appl
896	121	3.9	739	2	US-09-902-540-10606	Sequence 10606, A	969	118	3.8	2471	2	US-08-532-384-19	Sequence 19, Appl
897	121	3.9	910	2	US-09-228-986-72	Sequence 72, Appl	970	118	3.8	2471	2	US-08-899-232-1	Sequence 1, Appl1
898	121	3.9	910	2	US-10-101-464A-72	Sequence 72, Appl	971	118	3.8	2471	2	US-09-121-457-1	Sequence 1, Appl1
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900	121	3.9	1139	2	US-09-513-505-4	Sequence 4, Appl1	973	117.5	3.7	189	2	US-10-101-464A-517	Sequence 517, App
901	121	3.9	1742	3	US-09-958-359-23	Sequence 23, Appl	974	117.5	3.7	190	1	US-08-441-629-4	Sequence 4, Appl1
902	120.5	3.8	54	2	US-09-973-424A-71	Sequence 71, Appl	975	117.5	3.7	190	2	US-08-776-207-4	Sequence 4, Appl1

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977	117.5	3.7	190	2	US-10-036-447-4	Sequence 4, Appli	1050	115	3.7	305	2	US-09-325-932A-188	Sequence 188, App
978	117.5	3.7	190	5	PCT-US95-09172-4	Sequence 4, Appli	1051	115	3.7	447	1	US-08-450-360-4	Sequence 4, Appli
979	117.5	3.7	247	2	US-10-101-464A-730	Sequence 730, App	1052	115	3.7	717	2	US-10-094-749-2120	Sequence 2120, Ap
980	117.5	3.7	563	2	US-09-252-991A-17549	Sequence 17549, A	1053	115	3.7	764	2	US-07-741-453A-59	Sequence 59, Appl
981	117.5	3.7	635	1	US-08-484-101B-36	Sequence 36, Appl	1054	115	3.7	764	2	US-07-741-453A-61	Sequence 61, Appl
982	117.5	3.7	635	1	US-08-484-101B-50	Sequence 50, Appl	1055	115	3.7	984	2	US-09-287-354-2	Sequence 2, Appli
983	117.5	3.7	635	2	US-08-714-524D-36	Sequence 36, Appl	1056	115	3.7	984	2	US-09-287-354-2	Sequence 2, Appli
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985	117.5	3.7	996	2	US-10-101-464A-889	Sequence 889, App	1058	115	3.7	1093	2	US-09-513-505-6	Sequence 21827, A
986	117.5	3.7	996	2	US-10-101-464A-933	Sequence 933, App	1059	115	3.7	1189	2	US-09-252-991A-21827	Sequence 4, Appli
987	117.5	3.7	1118	2	US-09-252-991A-24340	Sequence 24340, A	1060	115	3.7	1189	2	US-09-949-016-6931	Sequence 6931, Ap
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1004	117	3.7	1055	2	US-09-214-278-2	Sequence 2, Appli	1077	114.5	3.7	1017	2	US-09-566-047-7	Sequence 7, Appli
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1018	117	3.7	2038	3	US-09-310-685-6	Sequence 6, Appli	1091	114.5	3.7	1218	2	US-09-068-740A-11	Sequence 11, Appl
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1021	116.5	3.7	296	2	US-09-270-767-37980	Sequence 37980, A	1094	114.5	3.7	1218	2	US-09-917-254-85	Sequence 85, Appl
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1030	116.5	3.7	4655	2	US-08-652-877-86	Sequence 86, Appl	1103	114	3.6	224	2	US-09-347-613C-16	Sequence 16, Appl
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1036	116	3.7	1053	2	US-10-094-749-2006	Sequence 2006, App	1109	114	3.6	644	2	US-08-866-757-2	Sequence 2, Appli
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					Sequence 55, Appl							US-10-101-464A-918	Sequence 918, App

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1127	113	3.6	369	2	US-09-252-991A-25394	Sequence 25394, A	1200	111.5	3.6	1398	2	US-08-843-659-2	Sequence 2, Appli
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1131	113	3.6	723	2	US-10-104-047-2246	Sequence 2246, Ap	1204	111	3.5	267	2	US-08-818-111-137	Sequence 137, App
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1133	113	3.6	979	2	US-09-538-092-990	Sequence 990, App	1206	111	3.5	267	2	US-09-072-596-137	Sequence 137, App
1134	113	3.6	1247	2	US-09-501-171-6	Sequence 6, Appli	1207	111	3.5	267	2	US-09-072-967-142	Sequence 142, App
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1141	112.5	3.6	694	2	US-09-949-016-8774	Sequence 8774, Ap	1214	111	3.5	492	1	US-08-644-271-32	Sequence 32, Appl
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1151	112	3.6	241	2	US-08-470-339-195	Sequence 195, App	1224	111	3.5	1318	2	US-10-237-551-197	Sequence 197, App
1152	112	3.6	241	2	US-08-467-602-389	Sequence 389, App	1225	111	3.5	1358	1	US-08-404-665-4	Sequence 4, Appli
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1154	112	3.6	241	2	US-08-411-295F-94	Sequence 94, Appl	1227	111	3.5	1358	1	US-08-404-781-4	Sequence 4, Appli
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1159	112	3.6	388	2	US-09-142-027A-12	Sequence 12, Appl	1232	111	3.5	1719	1	US-08-399-411-4	Sequence 4, Appli
1160	112	3.6	388	2	US-09-644-858-11	Sequence 11, Appl	1233	111	3.5	1719	1	US-08-399-411-4	Sequence 4, Appli
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1163	112	3.6	417	2	US-09-644-858-8	Sequence 8, Appli	1236	111	3.5	1719	2	US-09-528-706-4	Sequence 4, Appli
1164	112	3.6	422	2	US-09-644-858-13	Sequence 13, Appl	1237	111	3.5	1719	2	US-10-024-450-4	Sequence 4, Appli
1165	112	3.6	479	2	US-09-252-991A-23144	Sequence 23144, A	1238	111	3.5	1719	2	US-10-142-650-1	Sequence 1, Appli
1166	112	3.6	513	1	US-08-480-229C-14	Sequence 14, Appl	1239	111	3.5	2254	2	US-09-949-016-9270	Sequence 9270, Ap
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1171	112	3.6	764	2	US-09-461-657B-5	Sequence 5, Appli	1244	111	3.5	2523	2	US-09-121-457-3	Sequence 3, Appli
1172	112	3.6	764	2	US-09-826-509-395	Sequence 395, App	1245	110.5	3.5	273	2	US-09-252-991A-30433	Sequence 30433, A
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1174	112	3.6	764	2	US-09-826-509-403	Sequence 403, App	1247	110.5	3.5	565	2	US-08-937-067-8	Sequence 8, Appli
1175	112	3.6	764	2	US-09-826-509-407	Sequence 407, App	1248	110.5	3.5	645	2	US-09-964-899-17	Sequence 17, Appl
1176	112	3.6	764	2	US-09-826-509-411	Sequence 411, App	1249	110.5	3.5	675	2	US-09-332-063-2	Sequence 2, Appli
1177	112	3.6	764	2	US-09-826-509-415	Sequence 415, App	1250	110.5	3.5	675	2	US-09-332-063-3	Sequence 3, Appli
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1179	112	3.6	764	2	US-09-826-509-423	Sequence 423, App	1252	110.5	3.5	728	2	US-09-252-991A-31891	Sequence 31891, A
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1183	112	3.6	1833	2	US-08-479-722B-2	Sequence 2, Appli	1256	110.5	3.5	1346	2	US-09-320-878-4	Sequence 4, Appli
1184	112	3.6	1833	2	US-09-592-685-2	Sequence 2, Appli	1257	110.5	3.5	1346	2	US-09-105-537-37	Sequence 37, Appl
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1186	111.5	3.6	228	2	US-09-902-540-15349	Sequence 15349, A	1259	110.5	3.5	1346	2	US-09-657-440-4	Sequence 4, Appli
1187	111.5	3.6	281	2	US-09-252-991A-23962	Sequence 23962, A	1260	110.5	3.5	1346	2	US-09-793-708-4	Sequence 4, Appli
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1193	111.5	3.6	445	2	US-09-252-991A-22368	Sequence 22368, A	1266	110.5	3.5	11877	2	US-09-105-537-6	Sequence 6, Appli
1194	111.5	3.6	766	2	US-09-902-540-10602	Sequence 10602, A	1267	110	3.5	195	2	US-09-858-664A-11	Sequence 11, Appl

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1272	110	3.5	626	2	US-09-862-027-43	Sequence 43, Appl	1345	109	3.5	850	1	US-08-286-105A-7	Sequence 7, Appli
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1274	110	3.5	739	2	US-09-035-648-24	Sequence 24, Appl	1347	109	3.5	850	1	US-08-440-816A-7	Sequence 7, Appli
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1283	109.5	3.5	381	2	US-10-101-464A-660	Sequence 660, App	1356	109	3.5	1336	2	US-08-940-035A-58	Sequence 58, Appl
1284	109.5	3.5	400	2	US-10-101-464A-939	Sequence 939, App	1357	109	3.5	1336	2	US-08-935-105A-58	Sequence 58, Appl
1285	109.5	3.5	401	7	5252556-1	Patent No. 5252556	1358	109	3.5	1336	2	US-09-648-797-58	Sequence 58, Appl
1286	109.5	3.5	456	2	US-08-470-335-246	Sequence 246, App	1359	109	3.5	1336	2	US-09-386-123-58	Sequence 58, Appl
1287	109.5	3.5	456	2	US-08-467-602-303	Sequence 303, App	1360	109	3.5	1336	2	US-10-038-937-58	Sequence 58, Appl
1288	109.5	3.5	456	2	US-08-411-295F-229	Sequence 229, App	1361	109	3.5	1336	2	US-10-007-747-58	Sequence 58, Appl
1289	109.5	3.5	490	2	US-08-467-602-345	Sequence 345, App	1362	109	3.5	1336	2	US-09-945-901-58	Sequence 58, Appl
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1299	109.5	3.5	690	2	US-10-101-464A-69	Sequence 69, Appl	1372	108.5	3.5	542	2	US-09-252-991A-21862	Sequence 21862, A
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1303	109.5	3.5	788	2	US-09-150-460B-8	Sequence 8, Appli	1376	108.5	3.5	702	2	US-09-068-740A-9	Sequence 9, Appli
1304	109.5	3.5	839	1	US-08-359-705B-6	Sequence 6, Appli	1377	108.5	3.5	723	2	US-09-068-740A-9	Sequence 27, Appl
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1308	109.5	3.5	839	2	US-08-942-562-6	Sequence 6, Appli	1381	108.5	3.5	904	2	US-09-248-796A-17307	Sequence 17307, A
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1312	109.5	3.5	1235	2	US-09-949-016-8456	Sequence 8456, Ap	1385	108.5	3.5	1125	2	US-09-430-656-152	Sequence 152, App
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1316	109	3.5	259	2	US-10-094-749-2303	Sequence 2303, Ap	1389	108.5	3.5	1527	2	US-09-695-795A-4	Sequence 4, Appli
1317	109	3.5	416	2	US-08-978-289-12	Sequence 12, Appl	1390	108.5	3.5	1610	2	US-09-513-783A-22	Sequence 22, Appl
1318	109	3.5	416	2	US-09-601-478-1	Sequence 1, Appli	1391	108.5	3.5	1610	2	US-09-430-656-22	Sequence 22, Appl
1319	109	3.5	416	2	US-09-601-478-4	Sequence 4, Appli	1392	108.5	3.5	1610	2	US-10-100-957A-22	Sequence 22, Appl
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1322	109	3.5	437	1	US-08-481-814A-7	Sequence 7, Appli	1395	108	3.4	152	2	US-09-214-909-22	Sequence 22, Appl
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1335	109	3.5	762	1	US-08-397-633A-26	Sequence 26, Appl	1408	108	3.4	1189	2	US-09-287-354-3	Sequence 3, Appli
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1337	109	3.5	828	2	US-10-101-464A-934	Sequence 934, App	1410	108	3.4	1320	2	US-10-164-595-58	Sequence 78, Appl
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1418	108	3.4	4551	1	US-09-657-440-1	Sequence 1, Appli
1419	108	3.4	4551	2	US-09-793-708-1	Sequence 1, Appli
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1428	107.5	3.4	374	2	US-09-252-991A-28527	Sequence 28527, A
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1432	107.5	3.4	459	2	US-08-411-295F-225	Sequence 225, App
1433	107.5	3.4	493	2	US-08-467-602-341	Sequence 341, App
1434	107.5	3.4	493	2	US-08-411-295F-267	Sequence 267, App
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1440	107.5	3.4	691	2	US-09-252-991A-31413	Sequence 31413, A
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1443	107.5	3.4	787	2	US-08-252-991A-19991	Sequence 19991, A
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1445	107.5	3.4	832	2	US-09-908-322-6	Sequence 6, Appli
1446	107.5	3.4	984	1	US-08-673-789-9	Sequence 9, Appli
1447	107.5	3.4	998	2	US-09-949-016-6695	Sequence 6695, Ap
1448	107.5	3.4	1001	2	US-10-415-147-3	Sequence 3, Appli
1449	107.5	3.4	1088	2	US-09-233-857-13	Sequence 13, Appli
1450	107.5	3.4	1135	1	US-08-574-959A-7	Sequence 7, Appli
1451	107.5	3.4	1135	2	US-09-357-014-7	Sequence 7, Appli
1452	107.5	3.4	1327	2	US-09-949-016-8412	Sequence 8412, Ap
1453	107	3.4	131	1	US-08-650-598-3	Sequence 3, Appli
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1455	107	3.4	288	2	US-09-252-991A-27676	Sequence 27676, A
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1457	107	3.4	358	2	US-09-949-016-8148	Sequence 8148, Ap
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1459	107	3.4	369	2	US-09-252-991A-29670	Sequence 29670, A
1460	107	3.4	422	2	US-08-252-991A-23619	Sequence 23619, A
1461	107	3.4	500	2	US-09-423-753-2	Sequence 2, Appli
1462	107	3.4	500	3	US-10-241-476-2	Sequence 2, Appli
1463	107	3.4	541	2	US-10-101-464A-913	Sequence 913, App
1464	107	3.4	593	2	US-09-964-899-15	Sequence 15, Appli
1465	107	3.4	615	2	US-09-949-002-301	Sequence 301, App
1466	107	3.4	759	2	US-08-252-991A-18071	Sequence 18071, A
1467	107	3.4	793	2	US-09-252-991A-29395	Sequence 29395, A
1468	107	3.4	806	2	US-08-945-983-2	Sequence 10, Appli
1469	107	3.4	1241	2	US-08-714-741-34	Sequence 34, Appli
1470	107	3.4	1315	2	US-08-899-595-3	Sequence 3, Appli
1471	107	3.4	1315	2	US-08-899-595-3	Sequence 3, Appli
1472	106.5	3.4	157	2	US-08-361-392-68	Sequence 68, Appli
1473	106.5	3.4	157	2	US-09-908-322-68	Sequence 68, Appli
1474	106.5	3.4	157	2	US-09-310-685-20	Sequence 20, Appli
1475	106.5	3.4	176	2	US-09-270-767-32581	Sequence 32581, A
1476	106.5	3.4	176	2	US-09-270-767-47798	Sequence 47798, A
1477	106.5	3.4	247	2	US-08-252-991A-23672	Sequence 23672, A
1478	106.5	3.4	401	2	US-09-248-796A-26759	Sequence 26759, A
1479	106.5	3.4	420	2	US-09-902-540-13993	Sequence 13993, A
1480	106.5	3.4	423	2	US-08-702-665A-5	Sequence 5, Appli
1481	106.5	3.4	464	1	US-08-836-854-19	Sequence 19, Appli
1482	106.5	3.4	464	2	US-09-366-009-7	Sequence 7, Appli
1483	106.5	3.4	464	2	US-08-809-156B-7	Sequence 7, Appli
1484	106.5	3.4	464	2	US-09-775-964-7	Sequence 7, Appli
1485	106.5	3.4	489	2	US-09-366-009-8	Sequence 8, Appli
1486	106.5	3.4	489	2	US-08-809-156B-8	Sequence 8, Appli
1487	106.5	3.4	489	2	US-09-775-964-8	Sequence 8, Appli
1488	106.5	3.4	575	2	US-08-922-865-2	Sequence 2, Appli
1489	106.5	3.4	575	2	US-09-510-949-2	Sequence 2, Appli
1490	106.5	3.4	642	2	US-08-872-855-10	Sequence 10, Appli
1491	106.5	3.4	974	2	US-10-101-464A-921	Sequence 921, App
1492	106.5	3.4	1003	1	US-08-571-758-4	Sequence 4, Appli
1493	106.5	3.4	1003	1	US-08-909-984A-4	Sequence 4, Appli
1494	106.5	3.4	1003	1	US-08-909-984A-4	Sequence 4, Appli
1495	106.5	3.4	1075	5	PCT-US94-07297-41	Sequence 23, Appli
1496	106.5	3.4	1185	2	US-09-041-886-23	Sequence 23, Appli
1497	106.5	3.4	1185	2	US-09-538-092-1209	Sequence 1209, Ap
1498	106.5	3.4	1476	2	US-09-252-991A-29427	Sequence 29427, A
1499	106.5	3.4	1507	2	US-09-914-259-37	Sequence 37, Appli
1500	106.5	3.4	2090	2	US-09-538-092-1081	Sequence 1081, Ap

ALIGNMENTS

RESULT 1

US-09-866-028-69

; Sequence 69, Application US/09866028

; Patent No. 6642360

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin

; APPLICANT: Botstein, David

; APPLICANT: Eaton, Dan

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Gerritsen, Mary

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul

; APPLICANT: Grimaldi, Christopher

; APPLICANT: Gurney, Austin

; APPLICANT: Hillan, Kenneth

; APPLICANT: Kijavini, Ivar

; APPLICANT: Napier, Mary

; APPLICANT: Roy, Margaret

; APPLICANT: Tumas, Daniel

; APPLICANT: Wood, William

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; FILE OF INVENTION: ACIDS ENCODING THE SAME

; FILE REFERENCE: P2548P1C1

; CURRENT APPLICATION NUMBER: US/09/866,028

; CURRENT FILING DATE: 2001-05-25

; Prior application data removed - consult PALM or file wrapper

; NUMBER OF SEQ ID NOS: 120

; SEQ ID NO 69

; LENGTH: 598

; TYPE: PRT

; ORGANISM: Homo Sapien

US-09-866-028-69

Query Match 100.0%; Score 3135; DB 2; Length 598;

Best Local Similarity 100.0%; Pred. No. 7.3e-217;

Matches 598; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCSRVPLLLPLLLALGPGVCGSCGCCSQPQTVCFTARQGTTPRDPVPPDTVGLYVF 60

Db 1 MCSRVPLLLPLLLALGPGVCGSCGCCSQPQTVCFTARQGTTPRDPVPPDTVGLYVF 60

QY 61 ENGITMDASSFAGLPGLQLLDLSQNOIASLRPLRLLLDLSHNSLLALEPGILDITANVE 120

Db 61 ENGITMDASSFAGLPGLQLLDLSQNOIASLRPLRLLLDLSHNSLLALEPGILDITANVE 120

QY 121 ALRLAGLGLQQLDEGLFSRLRNHLHDLDVSDNQLRVPVIRGLRGLTRLRAGNTRIAQL 180

Db 121 ALRLAGLGLQQLDEGLFSRLRNHLHDLDVSDNQLRVPVIRGLRGLTRLRAGNTRIAQL 180

QY 181 RPEDLAGLAAQLQELDVSNLSLQALPGDLSGLFPRLLELLAAARNPNCVCLSFSGFWGVRE 240

Db 181 RPEDLAGLAAQLQELDVSNLSLQALPGDLSGLFPRLLELLAAARNPNCVCLSFSGFWGVRE 240

QY 241 SHVTLASPETRCHFPKKNAGRLLELDVADFCGCPATTTTATVPTTRPVVRPTALSSSL 300
Db 241 SHVTLASPETRCHFPKKNAGRLLELDVADFCGCPATTTTATVPTTRPVVRPTALSSSL 300
QY 301 APTWLSPTAPATAPSPPTAPTVGVPOQDCPPSTCLNGCTCHLGRHHLACLCPG 360
Db 301 APTWLSPTAPATAPSPPTAPTVGVPOQDCPPSTCLNGCTCHLGRHHLACLCPG 360
QY 361 FTGLYCESQMGQTRSPTPTPRPSRLTLGTEPVSPSLRVGLORYLOGSSVQLRSR 420
Db 361 FTGLYCESQMGQTRSPTPTPRPSRLTLGTEPVSPSLRVGLORYLOGSSVQLRSR 420
QY 421 LTYRNLSGDPKRLVTLRLPASLAEYTVTLRPNATYSVCVMPPLGPGRVPEGEACGEAHT 480
Db 421 LTYRNLSGDPKRLVTLRLPASLAEYTVTLRPNATYSVCVMPPLGPGRVPEGEACGEAHT 480
QY 481 PPAVSHNHAVTQAREGNLPLLIAPALAAVLLAALAAVGAAYCVRRGRAMAAAAQDKGV 540
Db 481 PPAVSHNHAVTQAREGNLPLLIAPALAAVLLAALAAVGAAYCVRRGRAMAAAAQDKGV 540
QY 541 GPGAGPLELGVKVPLEPGPKATEGGGEALPSGSECEVPLMGPPGLOSPLHAKPYI 598
Db 541 GPGAGPLELGVKVPLEPGPKATEGGGEALPSGSECEVPLMGPPGLOSPLHAKPYI 598

RESULT 2

US-09-944-457-69
; Sequence 69, Application US/09944457
; Patent No. 6734288
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerriksen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/944,457
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069335
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,278
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,425
; PRIOR FILING DATE: December 12, 1997
; PRIOR APPLICATION NUMBER: 60/069,696
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,694
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,702
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,870
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/069,873
; PRIOR FILING DATE: December 17, 1997

; PRIOR APPLICATION NUMBER: 60/068,017
; PRIOR FILING DATE: December 18, 1997
; PRIOR APPLICATION NUMBER: 60/070,440
; PRIOR FILING DATE: January 5, 1998
; PRIOR APPLICATION NUMBER: 60/074,086
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/074,092
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/075,945
; PRIOR FILING DATE: February 25, 1998
; PRIOR APPLICATION NUMBER: 60/112,850
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 60/113,296
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 60/146,222
; PRIOR FILING DATE: July 28, 1999
; PRIOR APPLICATION NUMBER: PCT/US98/19330
; PRIOR FILING DATE: September 16, 1998
; PRIOR APPLICATION NUMBER: PCT/US98/25108
; PRIOR FILING DATE: December 1, 1998
; PRIOR APPLICATION NUMBER: 09/216,021
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 09/218,517
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 09/254,311
; PRIOR FILING DATE: March 3, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: June 22, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: September 15, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28409
; PRIOR FILING DATE: No. 6734288ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: No. 6734288ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28301
; PRIOR FILING DATE: December 1, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: December 16, 1999
; PRIOR APPLICATION NUMBER: PCT/US00/03565
; PRIOR FILING DATE: February 11, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: February 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: March 2, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: March 30, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: May 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: July 28, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: December 1, 2000
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: February 28, 2001
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 69
; LENGTH: 598
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-944-457-69

Query Match 100.0%; Score 3135; DB 2; Length 598;
Best Local Similarity 100.0%; Pred. No. 7.3e-217;
Matches 599; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCSRVPLLLPLLLLLALGPGVQGCPCGCGCQSQPQTVFCTARQGTTPRDPVPPDTVGLYVF 60
Db 1 MCSRVPLLLPLLLLLALGPGVQGCPCGCGCQSQPQTVFCTARQGTTPRDPVPPDTVGLYVF 60
QY 61 ENGITMLDASSFAGLPGQLQLLDLSQNOIASIRLPRLLILLDLSHNSILALBPGILDTANVE 120
Db 61 ENGITMLDASSFAGLPGQLQLLDLSQNOIASIRLPRLLILLDLSHNSILALBPGILDTANVE 120

QY 121 ALRLAGLGLQOQDEGLFSLRLNHLHDVSDNQLERVPVIRGLRGLTRLRLAGNTRIAQL 180
DB 121 ALRLAGLGLQOQDEGLFSLRLNHLHDVSDNQLERVPVIRGLRGLTRLRLAGNTRIAQL 180
QY 181 RPEDLAGLAALQELDVSNLSLOALPGDLISGLFRLRLAAARNPNCVCPPLSWFGFWVRE 240
DB 181 RPEDLAGLAALQELDVSNLSLOALPGDLISGLFRLRLAAARNPNCVCPPLSWFGFWVRE 240
QY 241 SHVTLASPETRCHFPKKNAGRLLELDYADGCGPATTTATVTRPVVREPTALSSSL 300
DB 241 SHVTLASPETRCHFPKKNAGRLLELDYADGCGPATTTATVTRPVVREPTALSSSL 300
QY 301 APTWLSPTAPATEAPSPSTAPTGTGVPVPOQDCPSTCLNGSTCHLGRHHLACLCPGG 360
DB 301 APTWLSPTAPATEAPSPSTAPTGTGVPVPOQDCPSTCLNGSTCHLGRHHLACLCPGG 360
QY 361 FTGLCESQMGOGTRPSPTPTVTRPRPSRLTLGIEPVSPSLRVGLQRYLQSSVQLRSRL 420
DB 361 FTGLCESQMGOGTRPSPTPTVTRPRPSRLTLGIEPVSPSLRVGLQRYLQSSVQLRSRL 420
QY 421 LTYRNLSGDKRLVTLRLPASLAETVTLQLRPNATYSVCVMPPLGCRVPEGEACEAHT 480
DB 421 LTYRNLSGDKRLVTLRLPASLAETVTLQLRPNATYSVCVMPPLGCRVPEGEACEAHT 480
QY 481 PPAVSHSNHAPVTOAREGNLPLLIAPALAAVLAALAAVCAAYCVRRGRAMAAAOQKGV 540
DB 481 PPAVSHSNHAPVTOAREGNLPLLIAPALAAVLAALAAVCAAYCVRRGRAMAAAOQKGV 540
QY 541 GFGAGPLELEGVKVPLEPGPKATEGGEGALPGSGSECEVPLMGFPGLQSPHAKPYI 598
DB 541 GFGAGPLELEGVKVPLEPGPKATEGGEGALPGSGSECEVPLMGFPGLQSPHAKPYI 598

RESULT 3
US-09-945-584-69
; Sequence 69, Application US/09945584
; Patent No. 6908993
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/945,584
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,335
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,278
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,425
; PRIOR FILING DATE: December 12, 1997
; PRIOR APPLICATION NUMBER: 60/069,696
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; PRIOR APPLICATION NUMBER: 60/069,694
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,702
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,870
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/069,873
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/068,017
; PRIOR FILING DATE: December 18, 1997
; PRIOR APPLICATION NUMBER: 60/070,440
; PRIOR FILING DATE: January 5, 1998
; PRIOR APPLICATION NUMBER: 60/074,086
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/074,092
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/075,945
; PRIOR FILING DATE: February 25, 1998
; PRIOR APPLICATION NUMBER: 60/112,850
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 60/113,296
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 60/146,222
; PRIOR FILING DATE: July 28, 1999
; PRIOR APPLICATION NUMBER: PCT/US98/19330
; PRIOR FILING DATE: September 16, 1998
; PRIOR APPLICATION NUMBER: PCT/US98/25108
; PRIOR FILING DATE: December 1, 1998
; PRIOR APPLICATION NUMBER: 09/216,021
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 09/216,517
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 09/254,311
; PRIOR FILING DATE: March 3, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: June 22, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: September 15, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28409
; PRIOR FILING DATE: No. 6908993ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: No. 6908993ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28301
; PRIOR FILING DATE: December 1, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: December 16, 1999
; PRIOR APPLICATION NUMBER: PCT/US00/03565
; PRIOR FILING DATE: February 11, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: February 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: March 2, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: March 30, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: May 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: July 28, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: December 1, 2000
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: February 28, 2001
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 69
; LENGTH: 598
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-945-584-69

Query Match 100.0%; Score 3135; DB 2: Length 598;
Best Local Similarity 100.0%; Pred. No. 7.3e-217;
Matches 598; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCSRVPLLLPLLLLLALGFGVGCSPGCGCQSQPQTVFCTARQTTVPDRDPTVGLVVF 60
DB 1 MCSRVPLLLPLLLLLALGFGVGCSPGCGCQSQPQTVFCTARQTTVPDRDPTVGLVVF 60
QY 61 ENGITWLDASSFAGLPGLQLLDLSQNTASLRPLRLLLLDLSHNLLALEPGILDITANVE 120
DB 61 ENGITWLDASSFAGLPGLQLLDLSQNTASLRPLRLLLLDLSHNLLALEPGILDITANVE 120
QY 121 ALRLAGLGOQDEGLFSRLNHLDDLVDSDNOLERVPPVIRGLRGLTRLRLAGNTRIAQL 180
DB 121 ALRLAGLGOQDEGLFSRLNHLDDLVDSDNOLERVPPVIRGLRGLTRLRLAGNTRIAQL 180
QY 181 RPEDLAGLAALQELDVSNLSLOALPCLDLSGLFPRLRLAAAARNPNCVPLSWFGFVWRE 240
DB 181 RPEDLAGLAALQELDVSNLSLOALPCLDLSGLFPRLRLAAAARNPNCVPLSWFGFVWRE 240
QY 241 SHVTLASPETHCHPPKKNAGRLLELDVADFGCPATTTTATVTPTRPVVREPTALSSSL 300
DB 241 SHVTLASPETHCHPPKKNAGRLLELDVADFGCPATTTTATVTPTRPVVREPTALSSSL 300
QY 301 APTWLSPTAPATEAPSPSTAPPTVGPVPODCCPSTCLNGTCHLGRHHLACLCPBG 360
DB 301 APTWLSPTAPATEAPSPSTAPPTVGPVPODCCPSTCLNGTCHLGRHHLACLCPBG 360
QY 361 FTGLYCESQMGQCTRPSTPTVTPRPPRSLTLGIEPVSPSTSLRVGLQRYLQSSVQLRSUR 420
DB 361 FTGLYCESQMGQCTRPSTPTVTPRPPRSLTLGIEPVSPSTSLRVGLQRYLQSSVQLRSUR 420
QY 421 LTVRNLSGDPKRLVTLURLPASLAETVTLRPNATYSVCVMPDGPGRVPEGEACEAHT 480
DB 421 LTVRNLSGDPKRLVTLURLPASLAETVTLRPNATYSVCVMPDGPGRVPEGEACEAHT 480
QY 481 PPAVHSHNAPVTOAREGNPLLLTAPALAAVLAALAAVGAAYCVRGRMAAAAOBKGV 540
DB 481 PPAVHSHNAPVTOAREGNPLLLTAPALAAVLAALAAVGAAYCVRGRMAAAAOBKGV 540
QY 541 GPAGGLEGVKVPLEPGPKATEGGGEALPSGSECEVPLMGFPGLQSPHAKPYI 598
DB 541 GPAGGLEGVKVPLEPGPKATEGGGEALPSGSECEVPLMGFPGLQSPHAKPYI 598
RESULT 4
US-09-944-944-69
Sequence 69, Application US/09944944
Patent No. 6929947
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul
APPLICANT: Grimaldi, Christopher
APPLICANT: Gurney, Austin
APPLICANT: Hillan, Kenneth
APPLICANT: Kijavini, Ivar
APPLICANT: Napier, Mary
APPLICANT: Roy, Margaret
APPLICANT: Tumas, Daniel
APPLICANT: Wood, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P2548P1C1
CURRENT APPLICATION NUMBER: US/09/944, 944
CURRENT FILING DATE: 2001-09-26
PRIORITY FILING DATE: 09/866, 028
PRIORITY FILING DATE: 2001-05-25
PRIORITY FILING DATE: 09/067, 411
PRIORITY FILING DATE: December 3, 1997
PRIORITY FILING DATE: 60/069, 334
PRIORITY FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069, 335
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069, 278
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069, 425
PRIOR FILING DATE: December 12, 1997
PRIOR APPLICATION NUMBER: 60/069, 686
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069, 694
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069, 702
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069, 870
PRIOR FILING DATE: December 17, 1997
PRIOR APPLICATION NUMBER: 60/069, 873
PRIOR FILING DATE: December 17, 1997
PRIOR APPLICATION NUMBER: 60/068, 017
PRIOR FILING DATE: December 18, 1997
PRIOR APPLICATION NUMBER: 60/070, 440
PRIOR FILING DATE: January 5, 1998
PRIOR APPLICATION NUMBER: 60/074, 086
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/074, 092
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/075, 945
PRIOR FILING DATE: February 25, 1998
PRIOR APPLICATION NUMBER: 60/112, 850
PRIOR FILING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 60/113, 296
PRIOR FILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 60/146, 222
PRIOR FILING DATE: July 28, 1999
PRIOR APPLICATION NUMBER: PCT/US98/19330
PRIOR FILING DATE: September 16, 1998
PRIOR APPLICATION NUMBER: PCT/US98/25108
PRIOR FILING DATE: December 1, 1998
PRIOR APPLICATION NUMBER: 09/216, 021
PRIOR FILING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 09/218, 517
PRIOR FILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 09/254, 311
PRIOR FILING DATE: March 3, 1999
PRIOR APPLICATION NUMBER: PCT/US99/12252
PRIOR FILING DATE: June 22, 1999
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: September 15, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28409
PRIOR FILING DATE: No. 6929947ember 30, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: No. 6929947ember 30, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28301
PRIOR FILING DATE: December 1, 1999
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: December 16, 1999
PRIOR APPLICATION NUMBER: PCT/US00/03565
PRIOR FILING DATE: February 11, 2000
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: February 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/05841
PRIOR FILING DATE: March 2, 2000
PRIOR APPLICATION NUMBER: PCT/US00/08439
PRIOR FILING DATE: March 30, 2000
PRIOR APPLICATION NUMBER: PCT/US00/14042
PRIOR FILING DATE: May 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/20710
PRIOR FILING DATE: July 28, 2000
PRIOR APPLICATION NUMBER: PCT/US00/32678
PRIOR FILING DATE: December 1, 2000
PRIOR APPLICATION NUMBER: PCT/US01/06520
PRIOR FILING DATE: February 28, 2001
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 69
LENGTH: 598

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; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-944-944-69

Query Match          100.0%; Score 3135; DB 2; Length 598;
Best Local Similarity 100.0%; Pred. No. 7,3e-217;
Matches 598; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCSRVPLLLPLLLLLALGFGVGCPCGQCQSQPQTVECTARQGTTVPRDVPDPTVGLYVF 60
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DB 1 MCSRVPLLLPLLLLLALGFGVGCPCGQCQSQPQTVECTARQGTTVPRDVPDPTVGLYVF 60
    |||||
QY 61 ENGITWLDASSFAGLPGIQLLDLSQNIASRLRLPRLLLDLSHNSLLALEPGLDITANVE 120
    |||||
DB 61 ENGITWLDASSFAGLPGIQLLDLSQNIASRLRLPRLLLDLSHNSLLALEPGLDITANVE 120
    |||||
QY 121 ALRLAGLGLQQLDEGLFSRLNHLHDVSDNOLERVPPVIRGLRGLTRLRLAGNTRIAQL 180
    |||||
DB 121 ALRLAGLGLQQLDEGLFSRLNHLHDVSDNQLERVPPVIRGLRGLTRLRLAGNTRIAQL 180
    |||||
QY 181 RPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLLRLAAARNPNCVCLSMFGPWVRE 240
    |||||
DB 181 RPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLLRLAAARNPNCVCLSMFGPWVRE 240
    |||||
QY 241 SHVTLASPRETRCHFPKKNAGRLLELDYADFGCPATTTTATVPTTRPVVREPTALSSSL 300
    |||||
DB 241 SHVTLASPRETRCHFPKKNAGRLLELDYADFGCPATTTTATVPTTRPVVREPTALSSSL 300
    |||||
QY 301 APTWLSPTAPATEAPSPPTAPTPTGVPQPODCPESTCLNGTCHLGRHHLACLCPEG 360
    |||||
DB 301 APTWLSPTAPATEAPSPPTAPTPTGVPQPODCPESTCLNGTCHLGRHHLACLCPEG 360
    |||||
QY 361 FTGLYCESQMGQGTSPPTVTPRPRSLTLGTEPVSPTSLSRVGLQRYLQSSVQLRSLSR 420
    |||||
DB 361 FTGLYCESQMGQGTSPPTVTPRPRSLTLGTEPVSPTSLSRVGLQRYLQSSVQLRSLSR 420
    |||||
QY 421 LTYRNLSGDPKRLVTLRLPASLAETVTOIRPNATYSVCVMPILGPRVPEGEACEAHT 480
    |||||
DB 421 LTYRNLSGDPKRLVTLRLPASLAETVTOIRPNATYSVCVMPILGPRVPEGEACEAHT 480
    |||||
QY 481 PPAVSHNHPVTVQAREGNPLLIAPALAAVLAALAAVGAACVRRGRAMAAADKGOV 540
    |||||
DB 481 PPAVSHNHPVTVQAREGNPLLIAPALAAVLAALAAVGAACVRRGRAMAAADKGOV 540
    |||||
QY 541 GFGAGPLEGKVKVPLEPGPKATEGGEALPGSSECEVPLMGFPGLQSPHLHAKPYI 598
    |||||
DB 541 GFGAGPLEGKVKVPLEPGPKATEGGEALPGSSECEVPLMGFPGLQSPHLHAKPYI 598
    |||||

RESULT 5
US-09-945-587-69
; Sequence 69, Application US/09945587
; Patent No. 6936254
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P2548P1C1

; CURRENT APPLICATION NUMBER: US/09/945,587
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,335
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,278
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,425
; PRIOR FILING DATE: December 12, 1997
; PRIOR APPLICATION NUMBER: 60/069,696
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,694
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,702
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,870
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/069,873
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/068,017
; PRIOR FILING DATE: December 18, 1997
; PRIOR APPLICATION NUMBER: 60/070,440
; PRIOR FILING DATE: January 5, 1998
; PRIOR APPLICATION NUMBER: 60/074,086
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/074,092
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/075,945
; PRIOR FILING DATE: February 25, 1998
; PRIOR APPLICATION NUMBER: 60/112,850
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 60/113,296
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 60/146,222
; PRIOR FILING DATE: July 28, 1999
; PRIOR APPLICATION NUMBER: PCT/US98/19330
; PRIOR FILING DATE: September 16, 1998
; PRIOR APPLICATION NUMBER: PCT/US98/25108
; PRIOR FILING DATE: December 1, 1998
; PRIOR APPLICATION NUMBER: 09/216,021
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 09/218,517
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 09/254,311
; PRIOR FILING DATE: March 3, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: June 22, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: September 15, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28409
; PRIOR FILING DATE: No. 6936254ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: No. 6936254ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28301
; PRIOR FILING DATE: December 1, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: December 16, 1999
; PRIOR APPLICATION NUMBER: PCT/US00/03565
; PRIOR FILING DATE: February 11, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: February 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: March 2, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: March 30, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: May 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/20710
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; PRIOR FILING DATE: July 28, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: December 1, 2000
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: February 28, 2001
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 69
; LENGTH: 598
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-945-587-69

Query Match      100.0%; Score 3135; DB 2; Length 598;
Best Local Similarity 100.0%; Pred. No. 7.3e-217;
Matches 598; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCSRVP LLLP LLL L L L L L A L G P G V Q C P S G C C Q S Q P Q T V F C T A R Q G T T V P R D V P D P T V G L Y V F 60
Db 1 MCSRVP LLLP LLL L L L L L A L G P G V Q C P S G C C Q S Q P Q T V F C T A R Q G T T V P R D V P D P T V G L Y V F 60
QY 61 ENGITWLDASSFAGLPGLQLLDLSQNQIASRLPRLLDLSHNSLLALEPGILDITANVE 120
Db 61 ENGITWLDASSFAGLPGLQLLDLSQNQIASRLPRLLDLSHNSLLALEPGILDITANVE 120
QY 121 ALRLAGLGLQQLDEGLFSRLRNLDLSDNQLERVPVIRGLRGLRRLRAGNTRIAQL 180
Db 121 ALRLAGLGLQQLDEGLFSRLRNLDLSDNQLERVPVIRGLRGLRRLRAGNTRIAQL 180
QY 181 RPEDLAGLAALQBELDVNSLSQALPGDLSGLFPRLLRLLAAARNPFCVCLSWFGPWVRE 240
Db 181 RPEDLAGLAALQBELDVNSLSQALPGDLSGLFPRLLRLLAAARNPFCVCLSWFGPWVRE 240
QY 241 SHVTLASPEETRCHFPFKNAGRLLELDYADFCGCPATTTTATVPTTRPVVREPTALSSSL 300
Db 241 SHVTLASPEETRCHFPFKNAGRLLELDYADFCGCPATTTTATVPTTRPVVREPTALSSSL 300
QY 301 APTWLSPTAPATEAPSPSTAPPTVGPVQPCPPSTCLNGGTCHLGRHHLACLCPG 360
Db 301 APTWLSPTAPATEAPSPSTAPPTVGPVQPCPPSTCLNGGTCHLGRHHLACLCPG 360
QY 361 FTGLYCESQMGQTRPSPTVTPRPRSLTLGIEPVSPSLRVGLQRYLOGSSVQLRSLR 420
Db 361 FTGLYCESQMGQTRPSPTVTPRPRSLTLGIEPVSPSLRVGLQRYLOGSSVQLRSLR 420
QY 421 LTVRNLSGPDKRLVTLRLPASLAEYTVTLRPNATYSVCVMPGLGPRVPEGEACGEAHT 480
Db 421 LTVRNLSGPDKRLVTLRLPASLAEYTVTLRPNATYSVCVMPGLGPRVPEGEACGEAHT 480
QY 481 PPAVHSNHAPVTOAREGNLPLLIAPALAAVLLAALAAVGAAYCVRGRGMAAAADKQGV 540
Db 481 PPAVHSNHAPVTOAREGNLPLLIAPALAAVLLAALAAVGAAYCVRGRGMAAAADKQGV 540
QY 541 GPGAGPLEGKVKVPLEPGPKATEGGGEALPSGSECEVPLMGPPGPGQLSQPLHAKPYI 598
Db 541 GPGAGPLEGKVKVPLEPGPKATEGGGEALPSGSECEVPLMGPPGPGQLSQPLHAKPYI 598

RESULT 6
US-09-944-884-69
; Sequence 69, Application US/09944884
; Patent No. 7018837
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth

; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P2548PICI
; CURRENT APPLICATION NUMBER: US/09/944,884
; CURRENT FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 69
; LENGTH: 598
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-944-884-69

Query Match      100.0%; Score 3135; DB 3; Length 598;
Best Local Similarity 100.0%; Pred. No. 7.3e-217;
Matches 598; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCSRVP LLLP LLL L L L L L A L G P G V Q C P S G C C Q S Q P Q T V F C T A R Q G T T V P R D V P D P T V G L Y V F 60
Db 1 MCSRVP LLLP LLL L L L L L A L G P G V Q C P S G C C Q S Q P Q T V F C T A R Q G T T V P R D V P D P T V G L Y V F 60
QY 61 ENGITWLDASSFAGLPGLQLLDLSQNQIASRLPRLLDLSHNSLLALEPGILDITANVE 120
Db 61 ENGITWLDASSFAGLPGLQLLDLSQNQIASRLPRLLDLSHNSLLALEPGILDITANVE 120
QY 121 ALRLAGLGLQQLDEGLFSRLRNLDLSDNQLERVPVIRGLRGLRRLRAGNTRIAQL 180
Db 121 ALRLAGLGLQQLDEGLFSRLRNLDLSDNQLERVPVIRGLRGLRRLRAGNTRIAQL 180
QY 181 RPEDLAGLAALQBELDVNSLSQALPGDLSGLFPRLLRLLAAARNPFCVCLSWFGPWVRE 240
Db 181 RPEDLAGLAALQBELDVNSLSQALPGDLSGLFPRLLRLLAAARNPFCVCLSWFGPWVRE 240
QY 241 SHVTLASPEETRCHFPFKNAGRLLELDYADFCGCPATTTTATVPTTRPVVREPTALSSSL 300
Db 241 SHVTLASPEETRCHFPFKNAGRLLELDYADFCGCPATTTTATVPTTRPVVREPTALSSSL 300
QY 301 APTWLSPTAPATEAPSPSTAPPTVGPVQPCPPSTCLNGGTCHLGRHHLACLCPG 360
Db 301 APTWLSPTAPATEAPSPSTAPPTVGPVQPCPPSTCLNGGTCHLGRHHLACLCPG 360
QY 361 FTGLYCESQMGQTRPSPTVTPRPRSLTLGIEPVSPSLRVGLQRYLOGSSVQLRSLR 420
Db 361 FTGLYCESQMGQTRPSPTVTPRPRSLTLGIEPVSPSLRVGLQRYLOGSSVQLRSLR 420
QY 421 LTVRNLSGPDKRLVTLRLPASLAEYTVTLRPNATYSVCVMPGLGPRVPEGEACGEAHT 480
Db 421 LTVRNLSGPDKRLVTLRLPASLAEYTVTLRPNATYSVCVMPGLGPRVPEGEACGEAHT 480
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Db 481 PPAVHSNHAPVTOAREGNLPLLIAPALAAVLLAALAAVGAAYCVRGRGMAAAADKQGV 540
QY 541 GPGAGPLEGKVKVPLEPGPKATEGGGEALPSGSECEVPLMGPPGPGQLSQPLHAKPYI 598
Db 541 GPGAGPLEGKVKVPLEPGPKATEGGGEALPSGSECEVPLMGPPGPGQLSQPLHAKPYI 598

RESULT 7
US-09-063-950-2
; Sequence 2, Application US/09063950C
; Patent No. 6225085
; GENERAL INFORMATION:
; APPLICANT: Holtzman, Douglas A.
; TITLE OF INVENTION: NOVEL LRSG PROTEIN AND NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: MEI-019
```

; CURRENT APPLICATION NUMBER: US/09/063,950C
; CURRENT FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 673
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-063-950-2

Query Match		98.4%;	Score 3083.5;	DB 2;	Length 673;
Best Local Similarity		88.7%;	Pred. No. 4.2e-213;		
Matches	597;	Conservative	0;	Mismatches	1;
				Indels	75;
				Gaps	1;

QY	1	MCSRVLLP	LLLLLALGFGVQCPCGQCQSQPTVFCTARQGTTPRDPVDPDTGLGYVF	60
DB	1	MCSRVLLP	LLLLLALGFGVQCPCGQCQSQPTVFCTARQGTTPRDPVDPDTGLGYVF	60
QY	61	ENGITMLDASSFAGLPGIQLLDLSQNIAS	-----LRLPRLLLLDLSHNS	105
DB	61	ENGITMLDAGSFAGLPGIQLLDLSQNIAS	-----LRLPRLLLLDLSHNS	120
QY	91	-----LRLPRLLLLDLSHNS	105	
DB	121	RGURRLRLYLGKRRTHIQPGAFDRLRLLELKLQDNEURLPRLPRLLLLDLSHNS	180	
QY	106	LLALEPGILDTANVEALRLAGLQQLDEGLFSRLRNLDHLDVSDNQLRVPVPIRGLRG	165	
DB	181	LLALEPGILDTANVEALRLAGLQQLDEGLFSRLRNLDHLDVSDNQLRVPVPIRGLRG	240	
QY	166	LTRLRAGNTRIAQLRPEDLAGLALQELDVSNLSLQALPGDLSGLFPRLRLIAAARNPF	225	
DB	241	LTRLRAGNTRIAQLRPEDLAGLALQELDVSNLSLQALPGDLSGLFPRLRLIAAARNPF	300	
QY	226	NCVCPLSFGPWPVRESHVTLASPEETRCHEPPKNAGRLLELDYADPGCPATTTATVPT	285	
DB	301	NCVCPLSFGPWPVRESHVTLASPEETRCHEPPKNAGRLLELDYADPGCPATTTATVPT	360	
QY	286	TRPVREPTALSSSLAPTWSLPATAPATEAPSPSTAPPTVGPVPQDPPSTCLNGGTC	345	
DB	361	TRPVREPTALSSSLAPTWSLPATAPATEAPSPSTAPPTVGPVPQDPPSTCLNGGTC	420	
QY	346	HLGTRHHLACLCEPGTGLYCESQMGQTRPSTPTVTPRPSLTGLGIEVPSTSLRVGL	405	
DB	421	HLGTRHHLACLCEPGTGLYCESQMGQTRPSTPTVTPRPSLTGLGIEVPSTSLRVGL	480	
QY	406	QRYLGSSVQLRSLRITYNLSPDKRLVTLRLPASIAEYVTVQLRPNATYSVCVMPGLP	465	
DB	481	QRYLGSSVQLRSLRITYNLSPDKRLVTLRLPASIAEYVTVQLRPNATYSVCVMPGLP	540	
QY	466	GRVPEGEACGEAHTPPAVHSNHAPVTQAREGNLPLLIAPALAAVLLAALAAVGAAYCVR	525	
DB	541	GRVPEGEACGEAHTPPAVHSNHAPVTQAREGNLPLLIAPALAAVLLAALAAVGAAYCVR	600	
QY	526	RGMAAAAQDKQGVGAGLEGVKVPLEPGPKATEGGALPGSGCEVPLMGFPFG	585	
DB	601	RGMAAAAQDKQGVGAGLEGVKVPLEPGPKATEGGALPGSGCEVPLMGFPFG	660	
QY	586	PGLOSLHAKPYI	598	
DB	661	PGLOSLHAKPYI	673	

RESULT 8
US-09-391-181-52
; Sequence 52, Application US/09991181
; Patent No. 6913919
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Baton, Dan L.

;	APPLICANT:	Ferrara, Napoleone
;	APPLICANT:	Fong, Sherman
;	APPLICANT:	Gerber, Hanspeter
;	APPLICANT:	Gerritsen, Mary E.
;	APPLICANT:	Goddard, Audrey
;	APPLICANT:	Godowski, Paul J.
;	APPLICANT:	Grimaldi, J. Christopher
;	APPLICANT:	Gurney, Austin L.
;	APPLICANT:	Klavin, Ivar J.
;	APPLICANT:	Napier, Mary A.
;	APPLICANT:	Paoni, Nicholas F.
;	APPLICANT:	Roy, Margaret Ann
;	APPLICANT:	Stewart, Timothy A.
;	APPLICANT:	Tumas, Daniel
;	APPLICANT:	Watanabe, Colin K.
;	APPLICANT:	Williams, P. Mickey
;	APPLICANT:	Wood, William I.
;	APPLICANT:	Zhang, Zemin
;	TITLE OF INVENTION:	Secreted and Transmembrane Polypeptides and Nucleic
;	TITLE OF INVENTION:	Acids Encoding the Same
;	FILE REFERENCE:	P2730PIC53
;	CURRENT APPLICATION NUMBER:	US/09/991,181
;	CURRENT FILING DATE:	2001-11-16
;	PRIOR APPLICATION NUMBER:	60/049787
;	PRIOR FILING DATE:	1997-06-16
;	PRIOR APPLICATION NUMBER:	60/062250
;	PRIOR FILING DATE:	1997-10-17
;	PRIOR APPLICATION NUMBER:	60/065186
;	PRIOR FILING DATE:	1997-11-12
;	PRIOR APPLICATION NUMBER:	60/065311
;	PRIOR FILING DATE:	1997-11-13
;	PRIOR APPLICATION NUMBER:	60/066770
;	PRIOR FILING DATE:	1997-11-24
;	PRIOR APPLICATION NUMBER:	60/075945
;	PRIOR FILING DATE:	1998-02-25
;	PRIOR APPLICATION NUMBER:	60/078910
;	PRIOR FILING DATE:	1998-03-20
;	PRIOR APPLICATION NUMBER:	60/083322
;	PRIOR FILING DATE:	1998-04-28
;	PRIOR APPLICATION NUMBER:	60/084600
;	PRIOR FILING DATE:	1998-05-07
;	PRIOR APPLICATION NUMBER:	60/087106
;	PRIOR FILING DATE:	1998-05-28
;	PRIOR APPLICATION NUMBER:	60/087607
;	PRIOR FILING DATE:	1998-06-02
;	PRIOR APPLICATION NUMBER:	60/087609
;	PRIOR FILING DATE:	1998-06-02
;	PRIOR APPLICATION NUMBER:	60/087759
;	PRIOR FILING DATE:	1998-06-02
;	PRIOR APPLICATION NUMBER:	60/087827
;	PRIOR FILING DATE:	1998-06-03
;	PRIOR APPLICATION NUMBER:	60/088021
;	PRIOR FILING DATE:	1998-06-04
;	PRIOR APPLICATION NUMBER:	60/088025
;	PRIOR FILING DATE:	1998-06-04
;	PRIOR APPLICATION NUMBER:	60/088026
;	PRIOR FILING DATE:	1998-06-04
;	PRIOR APPLICATION NUMBER:	60/088028
;	PRIOR FILING DATE:	1998-06-04
;	PRIOR APPLICATION NUMBER:	60/088029
;	PRIOR FILING DATE:	1998-06-04
;	PRIOR APPLICATION NUMBER:	60/088030
;	PRIOR FILING DATE:	1998-06-04
;	PRIOR APPLICATION NUMBER:	60/088033
;	PRIOR FILING DATE:	1998-06-04
;	PRIOR APPLICATION NUMBER:	60/088326
;	PRIOR FILING DATE:	1998-06-04
;	PRIOR APPLICATION NUMBER:	60/088167
;	PRIOR FILING DATE:	1998-06-05
;	PRIOR APPLICATION NUMBER:	60/088202
;	PRIOR FILING DATE:	1998-06-05
;	PRIOR APPLICATION NUMBER:	60/088212

;
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088217
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088655
; PRIOR FILING DATE: 1998-06-09
; PRIOR APPLICATION NUMBER: 60/088734
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088738
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088742
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088810
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088824
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088826
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088858
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; PRIOR APPLICATION NUMBER: 60/088861
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/088876
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/089105
; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: 60/089440
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089512
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089514
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089532
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089538
; PRIOR FILING DATE: 1998-06-17
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; PRIOR FILING DATE: 1998-06-17
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; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089600
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089653
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089801
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; PRIOR FILING DATE: 1998-07-09

Query Match 98.4%; Score 3083.5; DB 2; Length 673;
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Matches 597; Conservative 0; Mismatches 1; Indels 75; Gaps 1;

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Qy 61 ENGITMLDASSFAGLPGQLQLLDLSQNQIAS-----LRLPRLLLLDLSHNS 105
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Qy 91 -----LRLPRLLLLDLSHNS 105
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Qy 166 L T R L R L A G N T R I A Q L R P E D L A G L A A Q E L D V S N L S Q A L P G D L S G L F P R L R L L A A A R N P F 225
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RESULT 9

US-09-990-444-52
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; Patent No. 6930170
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Baton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
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; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
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; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
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; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secured and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C19
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APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
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; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 98.4%; Score 3083.5; DB 2; Length 673;
Best Local Similarity 88.7%; Pred. No. 4.2e-213;
Matches 597; Conservative 0; Mismatches 1; Indels 75; Gaps 1;

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Db 1 MCSRVPLLLPLLLLLALGPGVQCGPCGCCSQPQTVFCTARQGTTPRDVPPDTVGLYVF 60
Qy 61 ENGITMLDASSFAGLPGLQLLDLSQNOIAS----- 90
Db 61 ENGITMLDAGSFAGLPGLQLLDLSQNOIASLPSGVFOPLANLNLDLTANRLHEITNETF 120
Qy 91 -----LRLPRLLLLDLSHNS 105
Db 121 RGLRRLRLYLGNRIHQPAGAFDTLDRLLLEKLQDNELRALPPLRLPRLLLLDLSHNS 180
Qy 106 LLALEPGILDTANVEALRLAGLQQLDEGLFSRLNLHDLVDSDNQLSERVPPVIGLRG 165
Db 181 LLALEPGILDTANVEALRLAGLQQLDEGLFSRLNLHDLVDSDNQLSERVPPVIGLRG 240
Qy 166 LTRRLAGNTRIAQRPELALQELDVSNLSQALPGDLGSLFPRLLRLAAARNPF 225
Db 241 LTRRLAGNTRIAQRPELALQELDVSNLSQALPGDLGSLFPRLLRLAAARNPF 300

QY 226 NCVCPLSWFGPWVRESHVTLASPEETRCHFPKAGRLLELDYADFGCPATTTATVPT 285
 DB 301 NCVCPLSWFGPWVRESHVTLASPEETRCHFPKAGRLLELDYADFGCPATTTATVPT 360
 QY 286 TRVVREPTALSSSLAPTWSPTAPATEAPSPSTAPPTVGPVPOQDCPPSTCLNGGTC 345
 DB 361 TRVVREPTALSSSLAPTWSPTAPATEAPSPSTAPPTVGPVPOQDCPPSTCLNGGTC 420
 QY 346 HLGTRHHLACLCEGTGLGYCESQMGQGRPSPTVTPRPRSLTLGIEPVSPTSRLVGL 405
 DB 421 HLGTRHHLACLCEGTGLGYCESQMGQGRPSPTVTPRPRSLTLGIEPVSPTSRLVGL 480
 QY 406 QRYLOGSSVQLRSLRITYRNLSGDKRLVTLRPLASLAETVTLQRPNATYSVCVMPPLGP 465
 DB 481 QRYLOGSSVQLRSLRITYRNLSGDKRLVTLRPLASLAETVTLQRPNATYSVCVMPPLGP 540
 QY 466 GRVPEGEACEAHTTPAVHSHNAPVTOAREGNLPLLIAPALAAVLLAALAAVGAAYCYVR 525
 DB 541 GRVPEGEACEAHTTPAVHSHNAPVTOAREGNLPLLIAPALAAVLLAALAAVGAAYCYVR 600
 QY 526 RGRAMAAAQDKQVGFAGGLEGVKVPLEPGPKATEGGSEALPSGSECEVPLMGFP 585
 DB 601 RGRAMAAAQDKQVGFAGGLEGVKVPLEPGPKATEGGSEALPSGSECEVPLMGFP 660
 QY 586 PGLQSLHAKPYI 598
 DB 661 PGLQSLHAKPYI 673

RESULT 13

US-09-989-726-52

; Sequence 52, Application US/09989726

; Patent No. 7018811

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Fong, Sherman

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Kljavin, Ivar J.

; APPLICANT: Napier, Mary A.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; FILE REFERENCE: P2730PIC60

; CURRENT APPLICATION NUMBER: US/09/989, 726

; CURRENT FILING DATE: 2001-11-19

; PRIOR APPLICATION NUMBER: 60/049787

; PRIOR FILING DATE: 1997-06-16

; PRIOR APPLICATION NUMBER: 60/062250

; PRIOR FILING DATE: 1997-10-17

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; PRIOR FILING DATE: 1998-07-09

Query Match 98.4%; Score 3083.5; DB 3; Length 673;
Best Local Similarity 88.7%; Pred. No. 4.2e-213;
Matches 597; Conservative 0; Mismatches 1; Indels 75; Caps 1;

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DB 421 HLGTRHHLACLCEGFTGLYCESQMGQTRPGPTVTPRPRSLTLGIEPVSPTSURVGL 480
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DB 541 GRVPEGEACGEAHTPPAVHSHNAPVTOAREGNLPLLIAPALAAVLLAALAAVGAAYCVR 600
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DB 601 RGRAMAAAQDKGVGPGAGPLEGKVPLEPGPKATGGGALPSGSECEVPLMGFP 660
QY 586 PGLQSPHAKPYI 598
DB 661 PGLQSPHAKPYI 673

RESULT 14
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; Sequence 52, Application US/09997514
; Patent No. 7019116
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.

APPLICANT: Botstein, David
APPLICANT: Desmoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PIC46
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CURRENT FILING DATE: 2001-11-15
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QY	91	-----	-----	-----
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257	3083.5	98.4	673	4	US-10-063-694-16	Sequence 16, Appl	330	3083.5	98.4	673	4	US-10-063-653-16	Sequence 16, Appl
258	3083.5	98.4	673	4	US-10-063-698-16	Sequence 16, Appl	331	3083.5	98.4	673	4	US-10-063-660-16	Sequence 16, Appl
259	3083.5	98.4	673	4	US-10-063-699-16	Sequence 16, Appl	332	3083.5	98.4	673	4	US-10-063-665-16	Sequence 16, Appl
260	3083.5	98.4	673	4	US-10-063-702-16	Sequence 16, Appl	333	3083.5	98.4	673	4	US-10-063-584-16	Sequence 16, Appl
261	3083.5	98.4	673	4	US-10-063-705-16	Sequence 16, Appl	334	3083.5	98.4	673	4	US-10-063-536-16	Sequence 16, Appl
262	3083.5	98.4	673	4	US-10-063-707-16	Sequence 16, Appl	335	3083.5	98.4	673	4	US-10-063-563-16	Sequence 16, Appl
263	3083.5	98.4	673	4	US-10-063-709-16	Sequence 16, Appl	336	3083.5	98.4	673	4	US-10-063-638-16	Sequence 16, Appl
264	3083.5	98.4	673	4	US-10-063-713-16	Sequence 16, Appl	337	3083.5	98.4	673	4	US-10-063-666-16	Sequence 16, Appl
265	3083.5	98.4	673	4	US-10-063-724-16	Sequence 16, Appl	338	3083.5	98.4	673	4	US-10-063-672-16	Sequence 16, Appl
266	3083.5	98.4	673	4	US-10-063-727-16	Sequence 16, Appl	339	3083.5	98.4	673	4	US-10-063-682-16	Sequence 16, Appl
267	3083.5	98.4	673	4	US-10-063-730-16	Sequence 16, Appl	340	3083.5	98.4	673	4	US-10-063-721-16	Sequence 16, Appl
268	3083.5	98.4	673	4	US-10-063-734-16	Sequence 16, Appl	341	3083.5	98.4	673	4	US-10-063-723-16	Sequence 16, Appl
269	3083.5	98.4	673	4	US-10-063-736-16	Sequence 16, Appl	342	3083.5	98.4	673	4	US-10-063-514-16	Sequence 16, Appl
270	3083.5	98.4	673	4	US-10-063-742-16	Sequence 16, Appl	343	3083.5	98.4	673	4	US-10-063-516-16	Sequence 16, Appl
271	3083.5	98.4	673	4	US-10-063-743-16	Sequence 16, Appl	344	3083.5	98.4	673	4	US-10-063-529-16	Sequence 16, Appl
272	3083.5	98.4	673	4	US-10-063-744-16	Sequence 16, Appl	345	3083.5	98.4	673	4	US-10-063-684-16	Sequence 16, Appl
273	3083.5	98.4	673	4	US-10-063-565-16	Sequence 16, Appl	346	3083.5	98.4	673	4	US-10-063-688-16	Sequence 16, Appl
274	3083.5	98.4	673	4	US-10-063-577-16	Sequence 16, Appl	347	3083.5	98.4	673	4	US-10-063-520-16	Sequence 16, Appl
275	3083.5	98.4	673	4	US-10-063-591-16	Sequence 16, Appl	348	3083.5	98.4	673	4	US-10-063-647-16	Sequence 16, Appl
276	3083.5	98.4	673	4	US-10-063-610-16	Sequence 16, Appl	349	3083.5	98.4	673	4	US-10-063-548-16	Sequence 16, Appl
277	3083.5	98.4	673	4	US-10-063-673-16	Sequence 16, Appl	350	3083.5	98.4	673	4	US-10-063-578-16	Sequence 16, Appl
278	3083.5	98.4	673	4	US-10-063-710-16	Sequence 16, Appl	351	3083.5	98.4	673	4	US-10-063-648-16	Sequence 16, Appl
279	3083.5	98.4	673	4	US-10-063-711-16	Sequence 16, Appl	352	3083.5	98.4	673	4	US-10-063-717-16	Sequence 16, Appl
280	3083.5	98.4	673	4	US-10-063-712-16	Sequence 16, Appl	353	3083.5	98.4	673	4	US-10-063-678-16	Sequence 16, Appl
281	3083.5	98.4	673	4	US-10-063-714-16	Sequence 16, Appl	354	3083.5	98.4	673	4	US-10-063-741-16	Sequence 16, Appl
282	3083.5	98.4	673	4	US-10-063-715-16	Sequence 16, Appl	355	3083.5	98.4	673	4	US-10-063-617-16	Sequence 16, Appl
283	3083.5	98.4	673	4	US-10-063-716-16	Sequence 16, Appl	356	3083.5	98.4	673	4	US-10-063-664-16	Sequence 16, Appl
284	3083.5	98.4	673	4	US-10-063-717-16	Sequence 16, Appl	357	3083.5	98.4	673	4	US-10-063-561-16	Sequence 16, Appl
285	3083.5	98.4	673	4	US-10-063-720-16	Sequence 16, Appl	358	3083.5	98.4	673	4	US-10-063-618-16	Sequence 16, Appl
286	3083.5	98.4	673	4	US-10-063-722-16	Sequence 16, Appl	359	3083.5	98.4	673	4	US-10-063-657-16	Sequence 16, Appl
287	3083.5	98.4	673	4	US-10-063-726-16	Sequence 16, Appl	360	3083.5	98.4	673	4	US-10-063-668-16	Sequence 16, Appl
288	3083.5	98.4	673	4	US-10-063-728-16	Sequence 16, Appl	361	3083.5	98.4	673	4	US-10-219-538-52	Sequence 52, Appl
289	3083.5	98.4	673	4	US-10-063-731-16	Sequence 16, Appl	362	3083.5	98.4	673	4	US-10-063-743-16	Sequence 16, Appl
290	3083.5	98.4	673	4	US-10-063-732-16	Sequence 16, Appl	363	3083.5	98.4	673	4	US-10-063-745-16	Sequence 16, Appl
291	3083.5	98.4	673	4	US-10-063-523-16	Sequence 16, Appl	364	3083.5	98.4	673	5	US-10-972-317-16	Sequence 16, Appl
292	3083.5	98.4	673	4	US-10-063-527-16	Sequence 16, Appl	365	3083.5	98.4	673	5	US-10-950-374-52	Sequence 52, Appl
293	3083.5	98.4	673	4	US-10-063-579-16	Sequence 16, Appl	366	3083.5	98.4	673	5	US-10-063-703-16	Sequence 16, Appl
294	3083.5	98.4	673	4	US-10-063-581-16	Sequence 16, Appl	367	3083.5	98.4	673	6	US-11-102-240-16	Sequence 16, Appl
295	3083.5	98.4	673	4	US-10-063-583-16	Sequence 16, Appl	368	3083.5	98.4	673	6	US-11-103-193-16	Sequence 16, Appl
296	3083.5	98.4	673	4	US-10-063-589-16	Sequence 16, Appl	369	3078.5	98.2	676	4	US-10-029-386-33083	Sequence 33083, A
297	3083.5	98.4	673	4	US-10-063-593-16	Sequence 16, Appl	370	2935	93.6	672	4	US-10-050-704-99	Sequence 99, Appl
298	3083.5	98.4	673	4	US-10-063-596-16	Sequence 16, Appl	371	2935	93.6	672	4	US-10-798-513-99	Sequence 99, Appl
299	3083.5	98.4	673	4	US-10-063-600-16	Sequence 16, Appl	372	2935	93.6	723	4	US-10-050-704-186	Sequence 186, App
300	3083.5	98.4	673	4	US-10-063-604-16	Sequence 16, Appl	373	2935	93.6	723	4	US-10-798-513-186	Sequence 186, App
301	3083.5	98.4	673	4	US-10-063-612-16	Sequence 16, Appl	374	2490	79.4	673	3	US-09-782-980-68	Sequence 68, Appl
302	3083.5	98.4	673	4	US-10-063-616-16	Sequence 16, Appl	375	2490	79.4	673	4	US-10-806-018-68	Sequence 68, Appl
303	3083.5	98.4	673	4	US-10-063-615-16	Sequence 16, Appl	376	2494	79.2	673	4	US-10-487-421-10	Sequence 10, Appl
304	3083.5	98.4	673	4	US-10-063-640-16	Sequence 16, Appl	377	1178.5	37.6	281	3	US-09-866-050A-648	Sequence 648, App
305	3083.5	98.4	673	4	US-10-063-642-16	Sequence 16, Appl	378	980.5	31.3	207	5	US-10-491-355-18	Sequence 18, Appl
306	3083.5	98.4	673	4	US-10-063-644-16	Sequence 16, Appl	379	360.5	11.5	635	5	US-10-363-374-8	Sequence 8, Appl
307	3083.5	98.4	673	4	US-10-063-649-16	Sequence 16, Appl	380	360.5	11.5	647	4	US-10-093-463-188	Sequence 188, App
308	3083.5	98.4	673	4	US-10-063-650-16	Sequence 16, Appl	381	357.5	11.4	778	4	US-10-093-463-192	Sequence 192, App
309	3083.5	98.4	673	4	US-10-063-652-16	Sequence 16, Appl	382	339	10.8	566	4	US-10-093-463-190	Sequence 190, App
310	3083.5	98.4	673	4	US-10-063-654-16	Sequence 16, Appl	383	338	10.8	551	3	US-09-897-214-8	Sequence 8, Appl
311	3083.5	98.4	673	4	US-10-063-659-16	Sequence 16, Appl	384	337	10.7	553	3	US-09-957-187-10	Sequence 10, Appl
312	3083.5	98.4	673	4	US-10-063-661-16	Sequence 16, Appl	385	337	10.7	653	6	US-11-058-709-10	Sequence 10, Appl
313	3083.5	98.4	673	4	US-10-063-528-16	Sequence 16, Appl	386	333	10.6	590	3	US-09-957-189-12	Sequence 12, Appl
314	3083.5	98.4	673	4	US-10-063-540-16	Sequence 16, Appl	387	333	10.6	590	6	US-11-058-709-12	Sequence 12, Appl
315	3083.5	98.4	673	4	US-10-063-568-16	Sequence 16, Appl	388	332	10.6	526	5	US-10-450-763-35186	Sequence 35186, A
316	3083.5	98.4	673	4	US-10-063-570-16	Sequence 16, Appl	389	330	10.5	653	3	US-09-989-722-229	Sequence 229, App
317	3083.5	98.4	673	4	US-10-063-582-16	Sequence 16, Appl	390	330	10.5	653	3	US-09-989-723-229	Sequence 229, App
318	3083.5	98.4	673	4	US-10-063-587-16	Sequence 16, Appl	391	330	10.5	653	3	US-09-989-279-229	Sequence 229, App
319	3083.5	98.4	673	4	US-10-063-592-16	Sequence 16, Appl	392	330	10.5	653	3	US-09-989-727-229	Sequence 229, App

393	330	10.5	653	3	US-09-989-731-229	Sequence 229, App	466	330	10.5	653	4	US-10-176-918-438	Sequence 438, App
394	330	10.5	653	3	US-09-989-732-229	Sequence 229, App	467	330	10.5	653	4	US-10-176-921-438	Sequence 438, App
395	330	10.5	653	3	US-09-991-073-229	Sequence 229, App	468	330	10.5	653	4	US-10-137-865-438	Sequence 438, App
396	330	10.5	653	3	US-09-990-442-229	Sequence 229, App	469	330	10.5	653	4	US-10-140-474-438	Sequence 438, App
397	330	10.5	653	3	US-09-991-163-229	Sequence 229, App	470	330	10.5	653	4	US-10-142-431-438	Sequence 438, App
398	330	10.5	653	3	US-09-993-604-229	Sequence 229, App	471	330	10.5	653	4	US-10-143-114-438	Sequence 438, App
399	330	10.5	653	3	US-09-990-456-229	Sequence 229, App	472	330	10.5	653	4	US-10-142-419-438	Sequence 438, App
400	330	10.5	653	3	US-09-989-721-229	Sequence 229, App	473	330	10.5	653	4	US-10-123-262-438	Sequence 438, App
401	330	10.5	653	3	US-09-992-598-229	Sequence 229, App	474	330	10.5	653	4	US-10-142-423-438	Sequence 438, App
402	330	10.5	653	3	US-09-989-293A-229	Sequence 229, App	475	330	10.5	653	4	US-10-121-050-438	Sequence 438, App
403	330	10.5	653	3	US-09-989-735-229	Sequence 229, App	476	330	10.5	653	4	US-10-141-755-438	Sequence 438, App
404	330	10.5	653	3	US-09-989-735-229	Sequence 229, App	477	330	10.5	653	4	US-10-143-032-438	Sequence 438, App
405	330	10.5	653	3	US-09-990-444-229	Sequence 229, App	478	330	10.5	653	4	US-10-103-108-438	Sequence 438, App
406	330	10.5	653	3	US-09-991-181-229	Sequence 229, App	479	330	10.5	653	4	US-10-123-236-438	Sequence 438, App
407	330	10.5	653	3	US-09-989-730-229	Sequence 229, App	480	330	10.5	653	4	US-10-123-261-438	Sequence 438, App
408	330	10.5	653	3	US-09-990-436-229	Sequence 229, App	481	330	10.5	653	4	US-10-140-921-438	Sequence 438, App
409	330	10.5	653	3	US-09-993-687-229	Sequence 229, App	482	330	10.5	653	4	US-10-140-928-438	Sequence 438, App
410	330	10.5	653	3	US-09-989-734-229	Sequence 229, App	483	330	10.5	653	4	US-10-121-045-438	Sequence 438, App
411	330	10.5	653	3	US-09-997-653-229	Sequence 229, App	484	330	10.5	653	4	US-10-123-293-438	Sequence 438, App
412	330	10.5	653	3	US-09-989-724-229	Sequence 229, App	485	330	10.5	653	4	US-10-123-903-438	Sequence 438, App
413	330	10.5	653	3	US-09-989-728-229	Sequence 229, App	486	330	10.5	653	4	US-10-124-819-438	Sequence 438, App
414	330	10.5	653	3	US-09-990-441-229	Sequence 229, App	487	330	10.5	653	4	US-10-124-822-438	Sequence 438, App
415	330	10.5	653	3	US-09-993-667-229	Sequence 229, App	488	330	10.5	653	4	US-10-140-925-438	Sequence 438, App
416	330	10.5	653	3	US-09-997-428-229	Sequence 229, App	489	330	10.5	653	4	US-10-160-498-438	Sequence 438, App
417	330	10.5	653	3	US-09-997-666-229	Sequence 229, App	490	330	10.5	653	4	US-10-124-824-438	Sequence 438, App
418	330	10.5	653	3	US-09-990-562-229	Sequence 229, App	491	330	10.5	653	4	US-10-127-825A-438	Sequence 438, App
419	330	10.5	653	3	US-09-990-711-229	Sequence 229, App	492	330	10.5	653	4	US-10-127-829A-438	Sequence 438, App
420	330	10.5	653	3	US-09-989-726-229	Sequence 229, App	493	330	10.5	653	4	US-10-127-835A-438	Sequence 438, App
421	330	10.5	653	3	US-09-998-156-229	Sequence 229, App	494	330	10.5	653	4	US-10-127-839A-438	Sequence 438, App
422	330	10.5	653	3	US-09-990-437-229	Sequence 229, App	495	330	10.5	653	4	US-10-127-901A-438	Sequence 438, App
423	330	10.5	653	3	US-09-991-157-229	Sequence 229, App	496	330	10.5	653	4	US-10-128-693A-438	Sequence 438, App
424	330	10.5	653	3	US-09-997-514-229	Sequence 229, App	497	330	10.5	653	4	US-10-131-813A-438	Sequence 438, App
425	330	10.5	653	3	US-09-997-573-229	Sequence 229, App	498	330	10.5	653	4	US-10-131-818A-438	Sequence 438, App
426	330	10.5	653	3	US-09-991-172-229	Sequence 229, App	499	330	10.5	653	4	US-10-131-823A-438	Sequence 438, App
427	330	10.5	653	3	US-09-990-726-229	Sequence 229, App	500	330	10.5	653	4	US-10-131-824A-438	Sequence 438, App
428	330	10.5	653	3	US-09-997-559-229	Sequence 229, App	501	330	10.5	653	4	US-10-131-830A-438	Sequence 438, App
429	330	10.5	653	3	US-09-997-601-229	Sequence 229, App	502	330	10.5	653	4	US-10-131-837A-438	Sequence 438, App
430	330	10.5	653	3	US-09-990-443-229	Sequence 229, App	503	330	10.5	653	4	US-10-137-872A-438	Sequence 438, App
431	330	10.5	653	3	US-09-991-854-229	Sequence 229, App	504	330	10.5	653	4	US-10-147-500-438	Sequence 438, App
432	330	10.5	653	3	US-09-997-628-229	Sequence 229, App	505	330	10.5	653	4	US-10-147-502-438	Sequence 438, App
433	330	10.5	653	3	US-09-997-683-229	Sequence 229, App	506	330	10.5	653	4	US-10-147-515-438	Sequence 438, App
434	330	10.5	653	3	US-09-989-729A-229	Sequence 229, App	507	330	10.5	653	4	US-10-147-517-438	Sequence 438, App
435	330	10.5	653	3	US-09-997-349-229	Sequence 229, App	508	330	10.5	653	4	US-10-147-526-438	Sequence 438, App
436	330	10.5	653	3	US-09-997-440-229	Sequence 229, App	509	330	10.5	653	4	US-10-147-527-438	Sequence 438, App
437	330	10.5	653	3	US-09-990-440-229	Sequence 229, App	510	330	10.5	653	4	US-10-121-041-438	Sequence 438, App
438	330	10.5	653	3	US-09-997-857-229	Sequence 229, App	511	330	10.5	653	4	US-10-121-043-438	Sequence 438, App
439	330	10.5	653	3	US-09-993-469-229	Sequence 229, App	512	330	10.5	653	4	US-10-121-047-438	Sequence 438, App
440	330	10.5	653	3	US-09-997-542-229	Sequence 229, App	513	330	10.5	653	4	US-10-123-215-438	Sequence 438, App
441	330	10.5	653	3	US-09-993-748-229	Sequence 229, App	514	330	10.5	653	4	US-10-123-902-438	Sequence 438, App
442	330	10.5	653	3	US-09-990-439-229	Sequence 229, App	515	330	10.5	653	4	US-10-123-908-438	Sequence 438, App
443	330	10.5	653	3	US-09-990-427-229	Sequence 229, App	516	330	10.5	653	4	US-10-123-909-438	Sequence 438, App
444	330	10.5	653	3	US-09-989-328-229	Sequence 229, App	517	330	10.5	653	4	US-10-123-910-438	Sequence 438, App
445	330	10.5	653	3	US-09-993-583-229	Sequence 229, App	518	330	10.5	653	4	US-10-124-813-438	Sequence 438, App
446	330	10.5	653	3	US-09-941-992-229	Sequence 229, App	519	330	10.5	653	4	US-10-124-817-438	Sequence 438, App
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448	330	10.5	653	3	US-09-997-333-229	Sequence 229, App	521	330	10.5	653	4	US-10-125-924-438	Sequence 438, App
449	330	10.5	653	3	US-09-997-384-229	Sequence 229, App	522	330	10.5	653	4	US-10-140-860-438	Sequence 438, App
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452	330	10.5	653	3	US-09-997-614-229	Sequence 229, App	525	330	10.5	653	4	US-10-157-782-438	Sequence 438, App
453	330	10.5	653	3	US-09-989-862-229	Sequence 229, App	526	330	10.5	653	4	US-10-152-395-438	Sequence 438, App
454	330	10.5	653	3	US-09-997-529-229	Sequence 229, App	527	330	10.5	653	4	US-10-125-926A-438	Sequence 438, App
455	330	10.5	653	3	US-09-989-725-229	Sequence 229, App	528	330	10.5	653	4	US-10-125-930A-438	Sequence 438, App
456	330	10.5	653	3	US-09-991-150-229	Sequence 229, App	529	330	10.5	653	4	US-10-127-831A-438	Sequence 438, App
457	330	10.5	653	3	US-09-997-641-229	Sequence 229, App	530	330	10.5	653	4	US-10-127-838B-438	Sequence 438, App
458	330	10.5	653	3	US-09-989-733-229	Sequence 229, App	531	330	10.5	653	4	US-10-127-842A-438	Sequence 438, App
459	330	10.5	653	3	US-09-992-643-229	Sequence 229, App	532	330	10.5	653	4	US-10-127-843A-438	Sequence 438, App
460	330	10.5	653	4	US-10-028-072-438	Sequence 438, App	533	330	10.5	653	4	US-10-127-845A-438	Sequence 438, App
461	330	10.5	653	4	US-10-140-808-438	Sequence 438, App	534	330	10.5	653	4	US-10-127-846A-438	Sequence 438, App
462	330	10.5	653	4	US-10-121-049-438	Sequence 438, App	535	330	10.5	653	4	US-10-127-848A-438	Sequence 438, App
463	330	10.5	653	4	US-10-123-904-438	Sequence 438, App	536	330	10.5	653	4	US-10-127-849A-438	Sequence 438, App
464	330	10.5	653	4	US-10-140-470-438	Sequence 438, App	537	330	10.5	653	4	US-10-127-850A-438	Sequence 438, App
465	330	10.5	653	4	US-10-175-746-438	Sequence 438, App	538	330	10.5	653	4		

685	330	10.5	653	4	US-10-145-755-438	Sequence 438, App	758	330	10.5	653	4	US-10-152-373-438	Sequence 438, App
686	330	10.5	653	4	US-10-145-810-438	Sequence 438, App	759	330	10.5	653	4	US-10-121-044-438	Sequence 438, App
687	330	10.5	653	4	US-10-145-820-438	Sequence 438, App	760	330	10.5	653	4	US-10-121-055-438	Sequence 438, App
688	330	10.5	653	4	US-10-145-872-438	Sequence 438, App	761	330	10.5	653	4	US-10-121-057-438	Sequence 438, App
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693	330	10.5	653	4	US-10-147-522-438	Sequence 438, App	766	330	10.5	653	4	US-10-123-154-438	Sequence 438, App
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695	330	10.5	653	4	US-10-157-783-438	Sequence 438, App	768	330	10.5	653	4	US-10-123-906-438	Sequence 438, App
696	330	10.5	653	4	US-10-158-792-438	Sequence 438, App	769	330	10.5	653	4	US-10-124-814-438	Sequence 438, App
697	330	10.5	653	4	US-10-158-827-438	Sequence 438, App	770	330	10.5	653	4	US-10-124-816-438	Sequence 438, App
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757	330	10.5	653	4	US-10-145-750-438	Sequence 438, App	830	330	10.5	653	4	US-10-140-810-438	Sequence 438, App

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836	330	10.5	653	4	US-10-141-762-438	Sequence 438, App	909	330	10.5	653	5	US-10-989-826-30	Sequence 30, Appl
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838	330	10.5	653	4	US-10-142-429-438	Sequence 438, App	911	330	10.5	653	5	US-10-917-905-2	Sequence 2, Appl
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841	330	10.5	653	4	US-10-143-115-438	Sequence 438, App	914	330	10.5	653	5	US-10-152-370-438	Sequence 438, App
842	330	10.5	653	4	US-10-144-956-438	Sequence 438, App	915	330	10.5	653	6	US-11-135-855-25	Sequence 25, Appl
843	330	10.5	653	4	US-10-144-958-438	Sequence 438, App	916	330	10.5	653	6	US-11-290-153-438	Sequence 438, App
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903	330	10.5	653	5	US-10-147-488-438	Sequence 438, App	976	328.5	10.5	627	4	US-10-245-899-100	Sequence 100, App

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1487	320	10.2	660	4	US-10-156-844-350	Sequence 350, App
1488	320	10.2	660	4	US-10-156-845-350	Sequence 350, App
1489	320	10.2	660	4	US-10-156-846-350	Sequence 350, App
1490	320	10.2	660	4	US-10-121-048-350	Sequence 350, App
1491	320	10.2	660	4	US-10-121-052-350	Sequence 350, App
1492	320	10.2	660	4	US-10-121-053-350	Sequence 350, App
1493	320	10.2	660	4	US-10-121-054-350	Sequence 350, App
1494	320	10.2	660	4	US-10-121-063-350	Sequence 350, App
1495	320	10.2	660	4	US-10-123-212-350	Sequence 350, App
1496	320	10.2	660	4	US-10-123-213-350	Sequence 350, App
1497	320	10.2	660	4	US-10-123-291-350	Sequence 350, App
1498	320	10.2	660	4	US-10-123-322-350	Sequence 350, App
1499	320	10.2	660	4	US-10-123-771-350	Sequence 350, App
1500	320	10.2	660	4	US-10-123-911-350	Sequence 350, App
ALIGNMENTS						
RESULT 1						
US-09-866-028-69						
; Sequence 69, Application US/09866028						
; Patent No. US20020058309A1						
; GENERAL INFORMATION:						
; APPLICANT: Baker, Kevin						
; APPLICANT: Botstein, David						
; APPLICANT: Eaton, Dan						
; APPLICANT: Ferrara, Napoleone						
; APPLICANT: Filvaroff, Ellen						
; APPLICANT: Gerritsen, Mary						
; APPLICANT: Goddard, Audrey						
; APPLICANT: Godowski, Paul						
; APPLICANT: Grimaldi, Christopher						
; APPLICANT: Gurney, Austin						
; APPLICANT: Hillan, Kenneth						
; APPLICANT: Kljavin, Ivar						
; APPLICANT: Napier, Mary						
; APPLICANT: Roy, Margaret						
; APPLICANT: Tumas, Daniel						
; APPLICANT: Wood, William						
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC						
; FILE REFERENCE: P2548P1C1						
; CURRENT APPLICATION NUMBER: US/09/866,028						
; CURRENT FILING DATE: 2001-05-25						
; Prior application data removed - consult PALM or file wrapper						
; NUMBER OF SEQ ID NOS: 120						
; SEQ ID NO 69						
; LENGTH: 598						
; TYPE: PRT						
; ORGANISM: Homo Sapien						
US-09-866-028-69						
Query Match 100.0%; Score 3135; DB 3; Length 598;						
Best Local Similarity 100.0%; Pred. No. 2.4e-194;						
Matches 598; Conservative 0; Mismatches 0; Indels 0; Gaps 0;						
Qy	1	MCSRVP	LLPL	LLPL	LLAL	GGVQC
Db	1	MCSRVP	LLPL	LLPL	LLAL	GGVQC
Qy	61	ENGITM	DASS	PAGL	PGLQL	LDLS
Db	61	ENGITM	DASS	PAGL	PGLQL	LDLS
Qy	121	ALRLAG	LQIQ	DEGL	FSRL	NLHDL
Db	121	ALRLAG	LQIQ	DEGL	FSRL	NLHDL
Qy	181	RPEDLAG	LAAL	QELD	VSNLS	LQAL
Db	181	RPEDLAG	LAAL	QELD	VSNLS	LQAL
Qy	241	SHVTLAS	PEET	RCHP	PPNN	AGRL
Db	241	SHVTLAS	PEET	RCHP	PPNN	AGRL

Db 241 SHVTLASPEETRCHFPKNAKRLLELDYADFCCPATTATVTRPVRREPTALSSSL 300
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Db 301 APTWLSPTAPATEAPSPSTAPTVGVFPQDQCPSTCLNGTCHLGRHHLACLCPG 360
QY 361 FTGLYCESQMGQTRSPPTVPRPRSLTLGIEPVSPSLRVLQRYLQGSVQLRSUR 420
Db 361 FTGLYCESQMGQTRSPPTVPRPRSLTLGIEPVSPSLRVLQRYLQGSVQLRSUR 420
QY 421 LTVRNLSGDPKRLVTLURLPASLAEYTVTLRPNATYSVCMPLGRCRVEGEACEAHT 480
Db 421 LTVRNLSGDPKRLVTLURLPASLAEYTVTLRPNATYSVCMPLGRCRVEGEACEAHT 480
QY 481 PPAVHSHAFVTOAREGNLPLLIAPALAAVLLAALAAVGAAYCVRGRMAAAQDKGV 540
Db 481 PPAVHSHAFVTOAREGNLPLLIAPALAAVLLAALAAVGAAYCVRGRMAAAQDKGV 540
QY 541 GPAGBLEGVKVPLEPGPKATEGGGEALPSGSECEVPLMGPPGLQSPHAKPYI 598
Db 541 GPAGBLEGVKVPLEPGPKATEGGGEALPSGSECEVPLMGPPGLQSPHAKPYI 598

RESULT 2

US-09-944-449-69
; Sequence 69, Application US/09944449
; Patent No. US20020102647A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Saton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/944,449
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,335
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,278
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,425
; PRIOR FILING DATE: December 12, 1997
; PRIOR APPLICATION NUMBER: 60/069,696
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,694
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,702
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,870
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/069,873
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/068,017

; PRIOR FILING DATE: December 18, 1997
; PRIOR APPLICATION NUMBER: 60/070,440
; PRIOR FILING DATE: January 5, 1998
; PRIOR APPLICATION NUMBER: 60/074,086
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/074,092
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/075,945
; PRIOR FILING DATE: February 25, 1998
; PRIOR APPLICATION NUMBER: 60/112,850
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 60/113,296
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 60/146,222
; PRIOR FILING DATE: July 28, 1999
; PRIOR APPLICATION NUMBER: PCT/US98/19330
; PRIOR FILING DATE: September 16, 1998
; PRIOR APPLICATION NUMBER: PCT/US98/25108
; PRIOR FILING DATE: December 1, 1998
; PRIOR APPLICATION NUMBER: 09/216,021
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 09/218,517
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 09/254,311
; PRIOR FILING DATE: March 3, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: June 22, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: September 15, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28409
; PRIOR FILING DATE: No. US20020102647A1ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: No. US20020102647A1ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28301
; PRIOR FILING DATE: December 1, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: December 16, 1999
; PRIOR APPLICATION NUMBER: PCT/US00/03565
; PRIOR FILING DATE: February 11, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: February 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: March 2, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: March 30, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: May 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: July 28, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: December 1, 2000
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 69
; LENGTH: 598
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-944-449-69
Query Match 100.0%; Score 3135; DB 3; Length 598;
Best Local Similarity 100.0%; Pred No. 2 4e-194;
Matches 598; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MCSRVPLLLPLLLLLALGPGVQCPSGQCQSQPQTVFCTARQGTTPRDPVPPDTVGLYVF 60
Db 1 MCSRVPLLLPLLLLLALGPGVQCPSGQCQSQPQTVFCTARQGTTPRDPVPPDTVGLYVF 60
QY 61 ENGITMLDASSFAGLPGQLQLLDLSQNIASRLPRLLLDLSHNSLLALESPGILDTANVE 120
Db 61 ENGITMLDASSFAGLPGQLQLLDLSQNIASRLPRLLLDLSHNSLLALESPGILDTANVE 120
QY 121 ALRLAGLGLQQLDEGLFSRLNLHDLVDSDNQLRPPVPIRGLRGLTRLRAGNTRIAQL 180

Db 121 ALRLAGLQQLDEGLSRLNLDVSDNQLERVPVIRGLRGLTRLRAGNTRIQAOL 180
QY 181 RPEDLAGLAALQELDVSNLSLOALPGDLSGLPRLRLAAARNPNCVPLSWFGPWVRE 240
Db 181 RPEDLAGLAALQELDVSNLSLOALPGDLSGLPRLRLAAARNPNCVPLSWFGPWVRE 240
QY 241 SHVTLASPETRCHFPFKNAGRLLLLDYADFCGCPATTTATVTPTRPVVREPTALSSSL 300
Db 241 SHVTLASPETRCHFPFKNAGRLLLLDYADFCGCPATTTATVTPTRPVVREPTALSSSL 300
QY 301 APTWLSPTAPATEAPSPSTAPPTGVPQPODCPSTCLNGTCHLGRHLACLCPG 360
Db 301 APTWLSPTAPATEAPSPSTAPPTGVPQPODCPSTCLNGTCHLGRHLACLCPG 360
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Db 361 FTGLYCESQMGQTRSPPTVTPRPRSLTLGIEPVSPSLRVLQRYLQGSVQLRSLR 420
QY 421 LTYRNLSGDPKRLVTURLPASLAETVTLQRPNATYSVCVMPILGPGRVPEGEACGEAHT 480
Db 421 LTYRNLSGDPKRLVTURLPASLAETVTLQRPNATYSVCVMPILGPGRVPEGEACGEAHT 480
QY 481 PRAVHNSHAPVTOAREGNLPLLIAPALAAVLLAALAAVGAACVREGRAWAAADKGOV 540
Db 481 PRAVHNSHAPVTOAREGNLPLLIAPALAAVLLAALAAVGAACVREGRAWAAADKGOV 540
QY 541 GPGAGPLEGKVKVPLEPGPKATEGGEALPGSGECEVPLMGPGGLQSPHAKPIYI 598
Db 541 GPGAGPLEGKVKVPLEPGPKATEGGEALPGSGECEVPLMGPGGLQSPHAKPIYI 598

RESULT 3

US-09-944-457-69
; Sequence 69, Application US/09944457
; Patent No. US20020110859A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kijavini, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548P1C1
; CURRENT FILING DATE: 2001-09-26
; CURRENT APPLICATION NUMBER: US/09/944,457
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,335
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,278
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,425
; PRIOR FILING DATE: December 12, 1997
; PRIOR APPLICATION NUMBER: 60/069,696
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,694

; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,702
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,870
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/069,873
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/068,017
; PRIOR FILING DATE: December 18, 1997
; PRIOR APPLICATION NUMBER: 60/070,440
; PRIOR FILING DATE: January 5, 1998
; PRIOR APPLICATION NUMBER: 60/074,086
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/074,092
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/075,945
; PRIOR FILING DATE: February 25, 1998
; PRIOR APPLICATION NUMBER: 60/112,850
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 60/113,296
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 60/146,222
; PRIOR FILING DATE: July 28, 1999
; PRIOR APPLICATION NUMBER: PCT/US98/19330
; PRIOR FILING DATE: September 16, 1998
; PRIOR APPLICATION NUMBER: PCT/US98/25108
; PRIOR FILING DATE: December 1, 1998
; PRIOR APPLICATION NUMBER: 09/216,021
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 09/218,517
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 09/254,311
; PRIOR FILING DATE: March 3, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: June 22, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: September 15, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28409
; PRIOR FILING DATE: No. US20020110859A1ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: No. US20020110859A1ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28301
; PRIOR FILING DATE: December 1, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: December 16, 1999
; PRIOR APPLICATION NUMBER: PCT/US00/03565
; PRIOR FILING DATE: February 11, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: February 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: March 2, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: March 30, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: May 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: July 28, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: December 1, 2000
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 69
; LENGTH: 598
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-944-457-69

Query Match 100.0%; Score 3135; DB 3; Length 598;
Best Local Similarity 100.0%; Pred. No. 2.4e-194;
Matches 598; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MCSRVPLLLPLLLALLGAGVGCSCGCCSQPQVCTARQTTVPDPVDTVGLYVF 60
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Db 61 ENGITWLDASSFAGLPGLQLDLSONQIASRLPRLLDLDSHNSLLALEPGLDTANVE 120
QY 121 ALRLAGLGLQDLDEGLFSLRNLHDLVDSDNQLRVPVIRGLRGITRLRLAGNTRIAQL 180
Db 121 ALRLAGLGLQDLDEGLFSLRNLHDLVDSDNQLRVPVIRGLRGITRLRLAGNTRIAQL 180
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Db 181 RPEDLAGLALQELDVSNLSLQALPGDLISGLPRRLRLAAARNPNCVCPISWFGPWVRE 240
QY 241 SHVTLASPBETRCHFFPKNAGRLLELDYADFGCPATTTTATVPTTRPVVREPTALSSSL 300
Db 241 SHVTLASPBETRCHFFPKNAGRLLELDYADFGCPATTTTATVPTTRPVVREPTALSSSL 300
QY 301 APTWLSPTAPATAPSPPTAPPTVGPVQPDQCPSTCLNGTCHLGRHHLACLCPRG 360
Db 301 APTWLSPTAPATAPSPPTAPPTVGPVQPDQCPSTCLNGTCHLGRHHLACLCPRG 360
QY 361 FTGLYCESQMGQTRSPTPTPRPSRLTLGIEPVSPSLRVLQRYLQGSVQLRSRLR 420
Db 361 FTGLYCESQMGQTRSPTPTPRPSRLTLGIEPVSPSLRVLQRYLQGSVQLRSRLR 420
QY 421 LTVRNLSGDPKRLVTLRLPASLAEYTVTLQRPNATYSVCVMPILGPGKVPGEBAEAGEAHT 480
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Db 481 PPAVHNSHAPVTOAREGNPLLIAPALAAVLLAALAAVGAAYCVRGRMAAAADKQGV 540
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RESULT 4

US-09-944-862-69
; Sequence 69, Application US/09944862
; Patent No. US20020115145A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/944,862
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,335

; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,278
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,425
; PRIOR FILING DATE: December 12, 1997
; PRIOR APPLICATION NUMBER: 60/069,696
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,694
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,702
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,870
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/069,873
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/068,017
; PRIOR FILING DATE: December 18, 1997
; PRIOR APPLICATION NUMBER: 60/070,440
; PRIOR FILING DATE: January 5, 1998
; PRIOR APPLICATION NUMBER: 60/074,086
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/074,092
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/075,945
; PRIOR FILING DATE: February 25, 1998
; PRIOR APPLICATION NUMBER: 60/112,850
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 60/113,296
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 60/146,222
; PRIOR FILING DATE: July 28, 1999
; PRIOR APPLICATION NUMBER: PCT/US98/19330
; PRIOR FILING DATE: September 16, 1998
; PRIOR APPLICATION NUMBER: PCT/US98/25108
; PRIOR FILING DATE: December 1, 1998
; PRIOR APPLICATION NUMBER: 09/216,021
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 09/218,517
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 09/254,311
; PRIOR FILING DATE: March 3, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: June 22, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: September 15, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28409
; PRIOR FILING DATE: No. US20020115145A1
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: No. US20020115145A1
; PRIOR APPLICATION NUMBER: PCT/US99/28301
; PRIOR FILING DATE: December 1, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: December 16, 1999
; PRIOR APPLICATION NUMBER: PCT/US00/03565
; PRIOR FILING DATE: February 11, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: February 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: March 2, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: March 30, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: May 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: July 28, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: December 1, 2000
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: February 28, 2001
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 69
; LENGTH: 598
; TYPE: PRT

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; ORGANISM: Homo Sapien
US-09-944-862-69

Query Match
Best Local Similarity 100.0%; Score 3135; DB 3; Length 598;
Matches 598; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MCSRVPLLLPLLLLLALGFGVGCPCGCGCQSQPQTVECTARQGTTPRDPVDPDTVGLYVP 60

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DB 61 ENGITWLDASSFAGLPGQLQDLDSQNOIASRLPRILLDLDSHNSLLALEPGLDTPANVE 120

QY 121 ALRLAGLGLQQLDEGLFSRLRNLDHLDVSDNQLERVPVIRGLRGLTRLRLAGNTRIAQL 180
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DB 181 RPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLRLAAARNPFCVCPLSWFGPWVRE 240

QY 241 SHVTLASPESTRCHFPKKNAGRLILLELDYADFGCPATTTTATVPTTRPVVREPTALSSSL 300
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QY 301 APTWLSPTAPATEAPSPPTAPTGVGPVQPODCPPSTCLNGTCHLGRHHLACLCPBG 360
DB 301 APTWLSPTAPATEAPSPPTAPTGVGPVQPODCPPSTCLNGTCHLGRHHLACLCPBG 360

QY 361 FTGLYCESQMGQGTSPPTVTPRPRSLTLGIEPVSPVSLRVGLQRYLQSGSVQLRSLR 420
DB 361 FTGLYCESQMGQGTSPPTVTPRPRSLTLGIEPVSPVSLRVGLQRYLQSGSVQLRSLR 420

QY 421 LTYRNLSGDPKRLVTLRLPASLAETVTVQIRPNATYSVCVMPGLGPRVPEGEACEAHT 480
DB 421 LTYRNLSGDPKRLVTLRLPASLAETVTVQIRPNATYSVCVMPGLGPRVPEGEACEAHT 480

QY 481 PPAVSHNHAPVTQAREGNPLLIAPALAAVLAALAAVGAACVRRGRAMAAADKGOV 540
DB 481 PPAVSHNHAPVTQAREGNPLLIAPALAAVLAALAAVGAACVRRGRAMAAADKGOV 540

QY 541 GFGAGPLELEGVKVPLPEPGKATEGGEALPGSCECEVPLMGFPGLQSPHLHAKPYI 598
DB 541 GFGAGPLELEGVKVPLPEPGKATEGGEALPGSCECEVPLMGFPGLQSPHLHAKPYI 598

RESULT 5
US-09-945-587-69
; Sequence 69, Application US/09945587
; Patent No. US20020127643A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Nary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/945,587
;
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,335
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,278
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,425
; PRIOR FILING DATE: December 12, 1997
; PRIOR APPLICATION NUMBER: 60/069,696
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,694
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,702
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,870
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/069,873
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/068,017
; PRIOR FILING DATE: December 18, 1997
; PRIOR APPLICATION NUMBER: 60/070,440
; PRIOR FILING DATE: January 5, 1998
; PRIOR APPLICATION NUMBER: 60/074,086
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/074,092
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/075,945
; PRIOR FILING DATE: February 25, 1998
; PRIOR APPLICATION NUMBER: 60/112,850
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 60/113,296
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 60/146,222
; PRIOR FILING DATE: July 28, 1999
; PRIOR APPLICATION NUMBER: PCT/US98/19330
; PRIOR FILING DATE: September 16, 1998
; PRIOR APPLICATION NUMBER: PCT/US98/25108
; PRIOR FILING DATE: December 1, 1998
; PRIOR APPLICATION NUMBER: 09/216,021
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 09/218,517
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 09/254,311
; PRIOR FILING DATE: March 3, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: June 22, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: September 15, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28409
; PRIOR FILING DATE: No. US20020127643A1, September 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: No. US20020127643A1, September 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28301
; PRIOR FILING DATE: December 1, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: December 16, 1999
; PRIOR APPLICATION NUMBER: PCT/US00/03565
; PRIOR FILING DATE: February 11, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: February 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: March 2, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: March 30, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: May 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: July 28, 2000
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; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: December 1, 2000
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: February 28, 2001
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 69
; LENGTH: 598
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-945-587-69

Query Match      100.0%; Score 3135; DB 3; Length 598;
Best Local Similarity 100.0%; Pred. No. 2.4e-194;
Matches 598; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MCSRVPLLLPLLLLALGPGVQCPCSCCQSQPOTVCTARQTTVPDVPDPTVGLYVF 60
Db 1 MCSRVPLLLPLLLLALGPGVQCPCSCCQSQPOTVCTARQTTVPDVPDPTVGLYVF 60
Qy 61 ENGITMDASSFAGLPGQLDLSQNIASRLPRLLLDLSHNSLLALEPGILDPTANVE 120
Db 61 ENGITMDASSFAGLPGQLDLSQNIASRLPRLLLDLSHNSLLALEPGILDPTANVE 120
Qy 121 ALRLAGLQQLDEGLFSRLRNHLDDVSDNQLERVPPVIRGLRGLTRLAGNTRIAQL 180
Db 121 ALRLAGLQQLDEGLFSRLRNHLDDVSDNQLERVPPVIRGLRGLTRLAGNTRIAQL 180
Qy 181 RPEDLAGLAALQELDVSNLSQALPGDLSGLFPRLLRLAAARNPFCVPLSMFGPWVRE 240
Db 181 RPEDLAGLAALQELDVSNLSQALPGDLSGLFPRLLRLAAARNPFCVPLSMFGPWVRE 240
Qy 241 SHVTLASPEETRCHFPKNAKRLLELDYADFQCPATTTTATVTPTRPVVREPTALSSSL 300
Db 241 SHVTLASPEETRCHFPKNAKRLLELDYADFQCPATTTTATVTPTRPVVREPTALSSSL 300
Qy 301 APTWLSPTAPATAPSPPTAPTVGVPOQPCPSTCLNGTCHLGRHHLACLCPEG 360
Db 301 APTWLSPTAPATAPSPPTAPTVGVPOQPCPSTCLNGTCHLGRHHLACLCPEG 360
Qy 361 FTGLYCESQMGQTRSPPTVTPRPRSLTLGTEPVSPSTSLRVGLQRYLGSSVQLRSLR 420
Db 361 FTGLYCESQMGQTRSPPTVTPRPRSLTLGTEPVSPSTSLRVGLQRYLGSSVQLRSLR 420
Qy 421 LTYRNLGGPKRLVTLRLPASLAETVTLQRPNATYSVCVMPPLGPGRVPEGEACGEAHT 480
Db 421 LTYRNLGGPKRLVTLRLPASLAETVTLQRPNATYSVCVMPPLGPGRVPEGEACGEAHT 480
Qy 481 PPAVHSHNAPVTOAREGNLPLLIAPALAAVLLAALAAVGAAYCVRGRGMAAAQDKGV 540
Db 481 PPAVHSHNAPVTOAREGNLPLLIAPALAAVLLAALAAVGAAYCVRGRGMAAAQDKGV 540
Qy 541 GPAGAPLELGGVKVPLEPGBKATGGGGEALPSGSECEVPLMGFPGLQSLPHAKPYI 598
Db 541 GPAGAPLELGGVKVPLEPGBKATGGGGEALPSGSECEVPLMGFPGLQSLPHAKPYI 598

RESULT 6
US-09-945-015-69
; Sequence 69, Application US/09945015
; Patent No. US20020132768A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
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```
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/945,015
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,335
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,278
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,425
; PRIOR FILING DATE: December 12, 1997
; PRIOR APPLICATION NUMBER: 60/069,696
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,694
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,702
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,870
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/069,873
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/068,017
; PRIOR FILING DATE: December 18, 1997
; PRIOR APPLICATION NUMBER: 60/070,440
; PRIOR FILING DATE: January 5, 1998
; PRIOR APPLICATION NUMBER: 60/074,086
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/074,092
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/075,945
; PRIOR FILING DATE: February 25, 1998
; PRIOR APPLICATION NUMBER: 60/112,850
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 60/113,296
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 60/146,222
; PRIOR FILING DATE: July 28, 1999
; PRIOR APPLICATION NUMBER: PCT/US98/19330
; PRIOR FILING DATE: September 16, 1998
; PRIOR APPLICATION NUMBER: PCT/US98/25108
; PRIOR FILING DATE: December 1, 1998
; PRIOR APPLICATION NUMBER: 09/216,021
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 09/218,517
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 09/254,311
; PRIOR FILING DATE: March 3, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: June 22, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: September 15, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28409
; PRIOR FILING DATE: No. US20020132768A1ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: No. US20020132768A1ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28301
; PRIOR FILING DATE: December 1, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: December 16, 1999
; PRIOR APPLICATION NUMBER: PCT/US00/03565
; PRIOR FILING DATE: February 11, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: February 22, 2000
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; PRIOR APPLICATION NUMBER: PCT/US99/28301
; PRIOR FILING DATE: December 1, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: December 16, 1999
; PRIOR APPLICATION NUMBER: PCT/US00/03565
; PRIOR FILING DATE: February 11, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: February 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: March 2, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: March 30, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: May 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: July 28, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: December 1, 2000
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: February 28, 2001
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 69
; LENGTH: 598
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-944-396-69

Query Match 100.0%; Score 3135; DB 3; Length 598;
Best Local Similarity 100.0%; Pred. No. 2.4e-194;
Matches 598; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCSRVPLLLPLLLALGPGVQCPCGQCQSQPTVCTARQTTVPDRVPPDTVGLYVF 60
Db 1 MCSRVPLLLPLLLALGPGVQCPCGQCQSQPTVCTARQTTVPDRVPPDTVGLYVF 60

QY 61 ENGITMLDASSFAGLPGQLLDLSQNOIASLRPLRLLDLSHNSLLALEPGILDTANVE 120
Db 61 ENGITMLDASSFAGLPGQLLDLSQNOIASLRPLRLLDLSHNSLLALEPGILDTANVE 120

QY 121 ALRLAGLQOOLDEGLFSRLNHLDDVSDNQLERVPPVIRGLTRLRACNTRIAQL 180
Db 121 ALRLAGLQOOLDEGLFSRLNHLDDVSDNQLERVPPVIRGLTRLRACNTRIAQL 180

QY 181 RPEDLAGLAALQELDVSNLSQALPGDLSGLFPRLLRLAAARNPFCVPLSFGPWVRE 240
Db 181 RPEDLAGLAALQELDVSNLSQALPGDLSGLFPRLLRLAAARNPFCVPLSFGPWVRE 240

QY 241 SHVTLASPESTRCHFPKXAGRLLELDYADFCGPATTTTATVPTTRPVVREPTALSSSL 300
Db 241 SHVTLASPESTRCHFPKXAGRLLELDYADFCGPATTTTATVPTTRPVVREPTALSSSL 300

QY 301 APTWLSPTAPATEAPSPSTAPPTVPVPOQDCPBSTCLNGGTCHLGRHHLACLCPEG 360
Db 301 APTWLSPTAPATEAPSPSTAPPTVPVPOQDCPBSTCLNGGTCHLGRHHLACLCPEG 360

QY 361 FTGLYCSQMGQGRPSPTPTVTPRPSRLTLGIEPVPSPTSLRVGLQRYLQSSSVQLRSRL 420
Db 361 FTGLYCSQMGQGRPSPTPTVTPRPSRLTLGIEPVPSPTSLRVGLQRYLQSSSVQLRSRL 420

QY 421 LTVRNLSGPDKRLVTLRLPLASLAEYTVTQLRPNATYSCVMPGLPGRVPEGEACGGAHT 480
Db 421 LTVRNLSGPDKRLVTLRLPLASLAEYTVTQLRPNATYSCVMPGLPGRVPEGEACGGAHT 480

QY 481 PPAVHSHNAPVTQAREGNPLLIAPALAAVLAALAAVGAAYCVRGRGMAAAADKGQV 540
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QY 541 GPGAGPLEGKVPLPGPKATGEGGALPGSGECEVPLMGFPGLQSPPLHAKPYI 598
Db 541 GPGAGPLEGKVPLPGPKATGEGGALPGSGECEVPLMGFPGLQSPPLHAKPYI 598

US-09-944-432-69
; Sequence 69, Application US/09944432
; Patent No. US20020142419A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548PIC1
; CURRENT APPLICATION NUMBER: US/09/944,432
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,335
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,278
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,425
; PRIOR FILING DATE: December 12, 1997
; PRIOR APPLICATION NUMBER: 60/069,696
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,694
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,702
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,870
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/069,873
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/068,017
; PRIOR FILING DATE: December 18, 1997
; PRIOR APPLICATION NUMBER: 60/070,440
; PRIOR FILING DATE: January 5, 1998
; PRIOR APPLICATION NUMBER: 60/074,086
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/074,092
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/075,945
; PRIOR FILING DATE: February 25, 1998
; PRIOR APPLICATION NUMBER: 60/112,850
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 60/113,296
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 60/146,222
; PRIOR FILING DATE: July 28, 1999
; PRIOR APPLICATION NUMBER: PCT/US98/19330
; PRIOR FILING DATE: September 16, 1998
; PRIOR APPLICATION NUMBER: PCT/US98/25108
; PRIOR FILING DATE: December 1, 1998
; PRIOR APPLICATION NUMBER: 09/216,021
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 09/218,517
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 09/254,311
; PRIOR FILING DATE: March 3, 1999

; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: June 22, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: September 15, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28409
; PRIOR FILING DATE: No. US20020142419A1ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: No. US20020142419A1ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28301
; PRIOR FILING DATE: December 1, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: December 16, 1999
; PRIOR APPLICATION NUMBER: PCT/US00/03565
; PRIOR FILING DATE: February 11, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: February 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: March 2, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: March 30, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: May 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: July 28, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: December 1, 2000
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: February 28, 2001
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 69
; LENGTH: 598
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-944-432-69

Query Match
Best Local Similarity 100.0%; Score 3135; DB 3; Length 598;
Matches 598; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCSRVPLLLPLLLLLALGFGVGCSPGCGSQCPQVCTAROGTTVPDRVPPDTVGLYVF 60
Db 1 MCSRVPLLLPLLLLLALGFGVGCSPGCGSQCPQVCTAROGTTVPDRVPPDTVGLYVF 60

QY 61 ENGITMLDASSPAGLPGQLLDLSNQIASLRPLRLDLLSHNSLLALEPGILDTANVE 120
Db 61 ENGITMLDASSPAGLPGQLLDLSNQIASLRPLRLDLLSHNSLLALEPGILDTANVE 120

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Db 121 ALRLAGLGLQQLDEGLFSLRLNHLDDLVDSDNQLERVPVIRGLRGLTRLRAGNTRIAQL 180

QY 181 RPEDLAGLAALQELDVSNLSLQALPGDLISGLPFLRLLLAAARNPNCVCLSWFGPWVRE 240
Db 181 RPEDLAGLAALQELDVSNLSLQALPGDLISGLPFLRLLLAAARNPNCVCLSWFGPWVRE 240

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Db 241 SHVTLASPEETRCHFPKKNAGRLLELDYADGCGPATTTTATVPTTRPVVREPTALSSSL 300

QY 301 APTWLSPTAPATEASPSSTAPTGVPOPODCPPSTCLNGCTCHLGRHHLACLCPG 360
Db 301 APTWLSPTAPATEASPSSTAPTGVPOPODCPPSTCLNGCTCHLGRHHLACLCPG 360

QY 361 FTGLYCESOMGGTTPSPPTVTPRPSRLTLGIEPVSPSTSLRVGLQRYLQSSVOLRSRL 420
Db 361 FTGLYCESOMGGTTPSPPTVTPRPSRLTLGIEPVSPSTSLRVGLQRYLQSSVOLRSRL 420

QY 421 LTYRNLSPGDKRLVTLRLPASLAETVTLQLRNATYSCVMPPLGPRVPEGEACGEAHT 480
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Db 541 GFGAGPLELEGVKVPLEPGPKATEGGGEALPGSGSECEVPLMGFPFGGLQSLHAKPYI 598

RESULT 9
US-09-943-762-69
; Sequence 69, Application US/09943762
; Patent No. US20020142958A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tomas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548PIC1
; CURRENT APPLICATION NUMBER: US/09/943,762
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,335
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,278
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,425
; PRIOR FILING DATE: December 12, 1997
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; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,694
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,702
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,870
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/069,873
; PRIOR FILING DATE: December 17, 1997
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; PRIOR FILING DATE: January 5, 1998
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; PRIOR APPLICATION NUMBER: 60/074,092
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; PRIOR FILING DATE: February 25, 1998
; PRIOR APPLICATION NUMBER: 60/112,850
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 60/113,296
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 60/146,222
; PRIOR FILING DATE: July 28, 1999
; PRIOR APPLICATION NUMBER: PCT/US98/19330
; PRIOR FILING DATE: September 16, 1998

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; PRIOR APPLICATION NUMBER: PCT/US98/25108
; PRIOR FILING DATE: December 1, 1998
; PRIOR APPLICATION NUMBER: 09/216,021
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 09/218,517
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 09/254,311
; PRIOR FILING DATE: March 3, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: June 22, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: September 15, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28409
; PRIOR FILING DATE: No. US20020142958A1ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: No. US20020142958A1ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28301
; PRIOR FILING DATE: December 1, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: December 16, 1999
; PRIOR APPLICATION NUMBER: PCT/US00/03565
; PRIOR FILING DATE: February 11, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: February 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: March 2, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: March 30, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: May 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: July 28, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: December 1, 2000
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: February 28, 2001
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 69
; LENGTH: 598
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-943-762-69

Query Match      100.0%; Score 3135; DB 3; Length 598;
Best Local Similarity 100.0%; Pred. No. 2.4e-194;
Matches 598; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MCSRVPLLLPLLLLLALGPGVQCGPCGCGCQSQPQTVCCTARQGTTPRDVPPDPDTVGLYVF 60
DB      1 MCSRVPLLLPLLLLLALGPGVQCGPCGCGCQSQPQTVCCTARQGTTPRDVPPDPDTVGLYVF 60
QY      61 ENGITMLDASSFAGLPGLQLLDLSQNOIASRLPRLLLLDLSHNSLLALEPGLDITANVE 120
DB      61 ENGITMLDASSFAGLPGLQLLDLSQNOIASRLPRLLLLDLSHNSLLALEPGLDITANVE 120
QY      121 ALRLAGLGLQQLDEGLFSRLRNHDLVDNQLERVPPVIRGRLGRLTRLAGNTRIAQL 180
DB      121 ALRLAGLGLQQLDEGLFSRLRNHDLVDNQLERVPPVIRGRLGRLTRLAGNTRIAQL 180
QY      181 RPEDLAGLAALQELDVNSLSQALPGDLSGLFRLRLRLAAARNPFCVCLSWFGPWVRE 240
DB      181 RPEDLAGLAALQELDVNSLSQALPGDLSGLFRLRLRLAAARNPFCVCLSWFGPWVRE 240
QY      241 SHVTLASPEETRCHFFPKNAGRLLELDYADFGCPATTTTATVPTTRPVVREPTALSSSL 300
DB      241 SHVTLASPEETRCHFFPKNAGRLLELDYADFGCPATTTTATVPTTRPVVREPTALSSSL 300
QY      301 APTWLSPTAPATEAPSPPTAPPTVGPVQPDCCPSTCLNGGTCCHLGRHHLACLCPGEG 360
DB      301 APTWLSPTAPATEAPSPPTAPPTVGPVQPDCCPSTCLNGGTCCHLGRHHLACLCPGEG 360
QY      361 FTGLYCESQMGQGRPSPTPTVTPRPSRLTLGIEPVSPTSRLVGLQRLQSSVQLRSRLR 420
DB      361 FTGLYCESQMGQGRPSPTPTVTPRPSRLTLGIEPVSPTSRLVGLQRLQSSVQLRSRLR 420

; PRIOR APPLICATION NUMBER: PCT/US98/25108
; PRIOR FILING DATE: December 1, 1998
; PRIOR APPLICATION NUMBER: 09/216,021
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 09/218,517
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 09/254,311
; PRIOR FILING DATE: March 3, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: June 22, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: September 15, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28409
; PRIOR FILING DATE: No. US20020142958A1ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: No. US20020142958A1ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28301
; PRIOR FILING DATE: December 1, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: December 16, 1999
; PRIOR APPLICATION NUMBER: PCT/US00/03565
; PRIOR FILING DATE: February 11, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: February 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: March 2, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: March 30, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: May 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: July 28, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: December 1, 2000
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: February 28, 2001
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 69
; LENGTH: 598
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-943-762-69

; Sequence 69, Application US/09944654
; Patent No. US20020142959A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Baton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kijavich, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/944,654
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,335
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,278
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,425
; PRIOR FILING DATE: December 12, 1997
; PRIOR APPLICATION NUMBER: 60/069,696
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,694
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,702
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,870
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/069,873
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/068,017
; PRIOR FILING DATE: December 18, 1997
; PRIOR APPLICATION NUMBER: 60/070,440
; PRIOR FILING DATE: January 5, 1998
; PRIOR APPLICATION NUMBER: 60/074,086
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/074,092
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/075,945
; PRIOR FILING DATE: February 25, 1998
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	/	PRIOR APPLICATION NUMBER:	60/112,850	
	/	PRIOR FILING DATE:	December 16, 1998	
	/	PRIOR APPLICATION NUMBER:	60/113,296	
	/	PRIOR FILING DATE:	December 22, 1998	
	/	PRIOR APPLICATION NUMBER:	60/146,222	
	/	PRIOR FILING DATE:	July 28, 1999	
	/	PRIOR APPLICATION NUMBER:	PCT/US98/19330	
	/	PRIOR FILING DATE:	September 16, 1998	
	/	PRIOR APPLICATION NUMBER:	PCT/US98/25108	
	/	PRIOR FILING DATE:	December 1, 1998	
	/	PRIOR APPLICATION NUMBER:	09/216,021	
	/	PRIOR FILING DATE:	December 16, 1998	
	/	PRIOR APPLICATION NUMBER:	09/218,517	
	/	PRIOR FILING DATE:	December 22, 1998	
	/	PRIOR APPLICATION NUMBER:	09/254,311	
	/	PRIOR FILING DATE:	March 3, 1999	
	/	PRIOR APPLICATION NUMBER:	PCT/US99/12252	
	/	PRIOR FILING DATE:	June 22, 1999	
	/	PRIOR APPLICATION NUMBER:	PCT/US99/21090	
	/	PRIOR FILING DATE:	September 15, 1999	
	/	PRIOR APPLICATION NUMBER:	PCT/US99/28409	
	/	PRIOR FILING DATE:	No. US20020142959A	ember 30, 1999
	/	PRIOR APPLICATION NUMBER:	PCT/US99/28313	
	/	PRIOR FILING DATE:	No. US20020142959A	ember 30, 1999
	/	PRIOR APPLICATION NUMBER:	PCT/US99/28301	
	/	PRIOR FILING DATE:	December 1, 1999	
	/	PRIOR APPLICATION NUMBER:	PCT/US99/30095	
	/	PRIOR FILING DATE:	December 16, 1999	
	/	PRIOR APPLICATION NUMBER:	PCT/US00/03565	
	/	PRIOR FILING DATE:	February 11, 2000	
	/	PRIOR APPLICATION NUMBER:	PCT/US00/04414	
	/	PRIOR FILING DATE:	February 22, 2000	
	/	PRIOR APPLICATION NUMBER:	PCT/US00/05841	
	/	PRIOR FILING DATE:	March 2, 2000	
	/	PRIOR APPLICATION NUMBER:	PCT/US00/08439	
	/	PRIOR FILING DATE:	March 30, 2000	
	/	PRIOR APPLICATION NUMBER:	PCT/US00/14042	
	/	PRIOR FILING DATE:	May 22, 2000	
	/	PRIOR APPLICATION NUMBER:	PCT/US00/20710	
	/	PRIOR FILING DATE:	July 28, 2000	
	/	PRIOR APPLICATION NUMBER:	PCT/US00/32678	
	/	PRIOR FILING DATE:	December 1, 2000	
	/	PRIOR APPLICATION NUMBER:	PCT/US01/06520	
	/	PRIOR FILING DATE:	February 28, 2001	
	/	NUMBER OF SEQ ID NOS:	120	
	/	SEQ ID NO 69		
	/	LENGTH:	598	
	/	TYPE:	PRT	
	/	ORGANISM:	Homo Sapien	
	/	US-09-944-654-69		
		Query Match	100.0%; Score 3135; DB 3; Length 598;	
		Best Local Similarity	100.0%; Pred. No. 2.4e-194;	
		Matches 598; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
Qy	1	MCSRVPLLLPLLLLLALPGVQGCPGCGCCSQPQTVC	TARQGTTPRDPDPTVGLYVF	60
Dd	1	MCSRVPLLLPLLLLLALPGVQGCPGCGCCSQPQTVC	TARQGTTPREDVPDPTVGLYVF	60
Qy	61	ENGIETMLDASSFAGLPGLQLDLDSQNQIASRLPR	LILLDLSHNSLLALEPGILDITANVE	120
Dd	61	ENGIETMLDASSFAGLPGLQLDLDSQNQIASRLPR	LILLDLSHNSLLALEPGILDITANVE	120
Qy	121	ALRLIAGLGLOOLDEGLFSRLNLHDLVDSDNQLER	VPPVIRGLRGLTFLRLAGNTRIAQL	180
Dd	121	ALRLIAGLGLOOLDEGLFSRLNLHDLVDSDNQLER	VPPVIRGLRGLTFLRLAGNTRIAQL	180
Qy	181	RPEDLAGLAALQELDVSNLSIQALPGDSLGLFPRL	LILAAARNPFNCVCLSWFGPWVRE	240
Dd	181	RPEDLAGLAALQELDVSNLSIQALPGDSLGLFPRL	LILAAARNPFNCVCLSWFGPWVRE	240
Qy	241	SHVTLASPETRCHFFPKNAGRLLLELDYADFGCPA	TTTTATVPTTPPVREPTALSSSL	300

;; PRIOR APPLICATION NUMBER: 60/070,440
;; PRIOR FILING DATE: January 5, 1998
;; PRIOR APPLICATION NUMBER: 60/074,086
;; PRIOR FILING DATE: February 9, 1998
;; PRIOR APPLICATION NUMBER: 60/074,092
;; PRIOR FILING DATE: February 9, 1998
;; PRIOR APPLICATION NUMBER: 60/075,945
;; PRIOR FILING DATE: February 25, 1998
;; PRIOR APPLICATION NUMBER: 60/112,850
;; PRIOR FILING DATE: December 16, 1998
;; PRIOR APPLICATION NUMBER: 60/113,296
;; PRIOR FILING DATE: December 22, 1998
;; PRIOR APPLICATION NUMBER: 60/146,222
;; PRIOR FILING DATE: July 28, 1999
;; PRIOR APPLICATION NUMBER: PCT/US98/19330
;; PRIOR FILING DATE: September 16, 1998
;; PRIOR APPLICATION NUMBER: PCT/US98/25108
;; PRIOR FILING DATE: December 1, 1998
;; PRIOR APPLICATION NUMBER: 09/216,021
;; PRIOR FILING DATE: December 16, 1998
;; PRIOR APPLICATION NUMBER: 09/218,517
;; PRIOR FILING DATE: December 22, 1998
;; PRIOR APPLICATION NUMBER: 09/254,311
;; PRIOR FILING DATE: March 3, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/12252
;; PRIOR FILING DATE: June 22, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/21090
;; PRIOR FILING DATE: September 15, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/28409
;; PRIOR FILING DATE: December 16, 1999
;; PRIOR APPLICATION NUMBER: PCT/US00/03565
;; PRIOR FILING DATE: February 11, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/04414
;; PRIOR FILING DATE: February 22, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/05841
;; PRIOR FILING DATE: March 2, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/08439
;; PRIOR FILING DATE: March 30, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/14042
;; PRIOR FILING DATE: May 22, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/20710
;; PRIOR FILING DATE: July 28, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/32678
;; PRIOR FILING DATE: December 1, 2000
;; PRIOR APPLICATION NUMBER: PCT/US01/06520
;; PRIOR FILING DATE: February 28, 2001
;; NUMBER OF SEQ ID NOS: 120
;; SEQ ID NO 69
;; LENGTH: 598
;; TYPE: PRT
;; ORGANISM: Homo Sapien
US-09-943-851A-69

Query Match 100.0%; Score 3135; DB 3; Length 598;
Best Local Similarity 100.0%; Pred. No. 2.4e-194;
Matches 598; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MCSRVPLLLPLLLLALPGVQCSCQCSQPTVCTARQCTTVPRDVPDPTVGLYVF 60
Db 1 MCSRVPLLLPLLLLALPGVQCSCQCSQPTVCTARQCTTVPRDVPDPTVGLYVF 60
Qy 61 ENGTMLDASSFAGLPGQLLDLSQNOIASRLPRLLLDLSHNSLLALPFGILDTANVE 120
Db 61 ENGTMLDASSFAGLPGQLLDLSQNOIASRLPRLLLDLSHNSLLALPFGILDTANVE 120
Qy 121 ALRLAGLQQLDGLFSRLNLHDLVDVSNQLERVPPVIRGLRGLTRLRAGNTRIAQL 180

Db 121 ALRLAGLQQLDGLFSRLNLHDLVDVSNQLERVPPVIRGLRGLTRLRAGNTRIAQL 180
Qy 181 RPEDLAGLAALQELDVSNLSIQALPGDLISGLFPRRLRLAAARNPFCNCVCLSWFGPWVRE 240
Db 181 RPEDLAGLAALQELDVSNLSIQALPGDLISGLFPRRLRLAAARNPFCNCVCLSWFGPWVRE 240
Qy 241 SHVTLASPESTRCHFFPKNAGRLLELDYADFGCPATTTTATVPTTRPVVREPTALSSSL 300
Db 241 SHVTLASPESTRCHFFPKNAGRLLELDYADFGCPATTTTATVPTTRPVVREPTALSSSL 300
Qy 301 APTWLSPTAPATEAPSPSTAPPTVGPVPOQDCPPSTCLNGGTCGLGTRHHLACLCEG 360
Db 301 APTWLSPTAPATEAPSPSTAPPTVGPVPOQDCPPSTCLNGGTCGLGTRHHLACLCEG 360
Qy 361 FTGLYCSQMGQGRTRPSPTVTPRPSRLTLGIPEVSPSTSLRVGLORYLOGSSVOLRSUR 420
Db 361 FTGLYCSQMGQGRTRPSPTVTPRPSRLTLGIPEVSPSTSLRVGLORYLOGSSVOLRSUR 420
Qy 421 LTYRNLSPDKRLVTLRLPASLAETVTVTLRPNATYSVCVMPLGPRVPEGEACEAHT 480
Db 421 LTYRNLSPDKRLVTLRLPASLAETVTVTLRPNATYSVCVMPLGPRVPEGEACEAHT 480
Qy 481 PPAVSHNHAPVTVQAREGNLPLLIAPALAAVLLAALAAVGAAYCVRRRGRAMAAAAQDKGV 540
Db 481 PPAVSHNHAPVTVQAREGNLPLLIAPALAAVLLAALAAVGAAYCVRRRGRAMAAAAQDKGV 540
Qy 541 GPGAGPLEGKVKVLEPGPKATGGGALPGSGCEVPLMGFPGLQSLPHAKPYI 598
Db 541 GPGAGPLEGKVKVLEPGPKATGGGALPGSGCEVPLMGFPGLQSLPHAKPYI 598
RESULT 12
US-09-944-413-69
; Sequence 69, Application US/09944413
; Patent No. US20020156004A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gellitsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/944,413
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,335
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,278
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,425
; PRIOR FILING DATE: December 12, 1997
; PRIOR APPLICATION NUMBER: 60/069,696
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,694
; PRIOR FILING DATE: December 16, 1997

1 MCSRVPLLLPLLLLLALGPGVCGSCGCSQPOVTCTAROGTTVPRDVPDPTVGLYVF 60
PRIOR APPLICATION NUMBER: 60/069,702
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,870
PRIOR FILING DATE: December 17, 1997
PRIOR APPLICATION NUMBER: 60/069,873
PRIOR FILING DATE: December 17, 1997
PRIOR APPLICATION NUMBER: 60/068,017
PRIOR FILING DATE: December 18, 1997
PRIOR APPLICATION NUMBER: 60/070,440
PRIOR FILING DATE: January 5, 1998
PRIOR APPLICATION NUMBER: 60/074,086
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/074,092
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/075,945
PRIOR FILING DATE: February 25, 1998
PRIOR APPLICATION NUMBER: 60/112,850
PRIOR FILING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 60/113,296
PRIOR FILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 60/146,222
PRIOR FILING DATE: July 28, 1999
PRIOR APPLICATION NUMBER: PCT/US98/19330
PRIOR FILING DATE: September 16, 1998
PRIOR APPLICATION NUMBER: PCT/US98/25108
PRIOR FILING DATE: December 1, 1998
PRIOR APPLICATION NUMBER: 09/216,021
PRIOR FILING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 09/218,517
PRIOR FILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 09/254,311
PRIOR FILING DATE: March 3, 1999
PRIOR APPLICATION NUMBER: PCT/US99/12252
PRIOR FILING DATE: June 22, 1999
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: September 15, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28409
PRIOR FILING DATE: No. US20020156004A1ember 30, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: No. US20020156004A1ember 30, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28301
PRIOR FILING DATE: December 1, 1999
PRIOR APPLICATION NUMBER: PCT/US99/30095
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PRIOR APPLICATION NUMBER: PCT/US00/03565
PRIOR FILING DATE: February 11, 2000
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: February 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/05841
PRIOR FILING DATE: March 2, 2000
PRIOR APPLICATION NUMBER: PCT/US00/08439
PRIOR FILING DATE: March 30, 2000
PRIOR APPLICATION NUMBER: PCT/US00/14042
PRIOR FILING DATE: May 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/20710
PRIOR FILING DATE: July 28, 2000
PRIOR APPLICATION NUMBER: PCT/US00/32678
PRIOR FILING DATE: December 1, 2000
PRIOR APPLICATION NUMBER: PCT/US01/06520
PRIOR FILING DATE: February 28, 2001
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 69
LENGTH: 598
TYPE: PRT
ORGANISM: Homo Sapien
US-09-944-413-69
Query Match 100.0%; Score 3135; DB 3; Length 598;
Best Local Similarity 100.0%; Pred. No. 2.4e-194;
Matches 598; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 MCSRVPLLLPLLLLLALGPGVCGSCGCSQPOVTCTAROGTTVPRDVPDPTVGLYVF 60
|||||

Db 1 MCSRVPLLLPLLLLLALGPGVCGSCGCSQPOVTCTAROGTTVPRDVPDPTVGLYVF 60
QY 61 ENGITMLDASSFAGLPGQLLDLSQNIASRLPRLLLDLSHNSLLALEPGLDITANVE 120
Db 61 ENGITMLDASSFAGLPGQLLDLSQNIASRLPRLLLDLSHNSLLALEPGLDITANVE 120
QY 121 ALRLAGLGLQQLDEGLFSRLRNHLHDVSDNQLERPPVIRGLRGLTRLRAGNTRIAOL 180
Db 121 ALRLAGLGLQQLDEGLFSRLRNHLHDVSDNQLERPPVIRGLRGLTRLRAGNTRIAOL 180
QY 181 RPEDLAGLAALQELDVSNLSLOALPGDLSGLPRLRLAAARNPNCVCPPLSWFGPWRE 240
Db 181 RPEDLAGLAALQELDVSNLSLOALPGDLSGLPRLRLAAARNPNCVCPPLSWFGPWRE 240
QY 241 SHVTLASPEETRCRCHPPKXNAGRLLELDYADFGCPATTTTATVPTTRPVVREPTALSSSL 300
Db 241 SHVTLASPEETRCRCHPPKXNAGRLLELDYADFGCPATTTTATVPTTRPVVREPTALSSSL 300
QY 301 APTWLSPTAPATEAPSPSTAPPTVGPVPOPODCPPSCCLNGCTCHLGRHLACLCPG 360
Db 301 APTWLSPTAPATEAPSPSTAPPTVGPVPOPODCPPSCCLNGCTCHLGRHLACLCPG 360
QY 361 FTGLYCESQMGOGTRPSPTPTPRPSRLTLGIEPVSPSTSLRVGLQRYLQSSSVOLRSUR 420
Db 361 FTGLYCESQMGOGTRPSPTPTPRPSRLTLGIEPVSPSTSLRVGLQRYLQSSSVOLRSUR 420
QY 421 LTYRNLGPDRLVTLRLPASLAETVTQLRPNATYSVCVMPPLGPRVPEGEACGEAHT 480
Db 421 LTYRNLGPDRLVTLRLPASLAETVTQLRPNATYSVCVMPPLGPRVPEGEACGEAHT 480
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QY 541 GPGAGPLEGKVKVPLEPGPKATEGGGALPGSGSECEVPLMGFPGGLQSLPHAKPYI 598
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RESULT 13
US-09-944-403-69
Sequence 69, Application US/09944403
Patent No. US20020165143A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul
APPLICANT: Grimaldi, Christopher
APPLICANT: Gurney, Austin
APPLICANT: Hillan, Kenneth
APPLICANT: Kljavin, Ivar
APPLICANT: Napier, Mary
APPLICANT: Roy, Margaret
APPLICANT: Tumas, Daniel
APPLICANT: Wood, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P2548P1C1
CURRENT APPLICATION NUMBER: US/09/944, 403
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 09/866, 028
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/067,411
PRIOR FILING DATE: December 3, 1997
PRIOR APPLICATION NUMBER: 60/069,334
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,335
PRIOR FILING DATE: December 11, 1997

PRIOR APPLICATION NUMBER: 60/069,278
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,425
; PRIOR FILING DATE: December 12, 1997
; PRIOR APPLICATION NUMBER: 60/069,696
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,694
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,702
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,870
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/069,873
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/068,017
; PRIOR FILING DATE: December 18, 1997
; PRIOR APPLICATION NUMBER: 60/070,440
; PRIOR FILING DATE: January 5, 1998
; PRIOR APPLICATION NUMBER: 60/074,086
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/074,092
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/075,945
; PRIOR FILING DATE: February 25, 1998
; PRIOR APPLICATION NUMBER: 60/112,850
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 60/113,296
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 60/146,222
; PRIOR FILING DATE: July 28, 1999
; PRIOR APPLICATION NUMBER: PCT/US98/19330
; PRIOR FILING DATE: September 16, 1998
; PRIOR APPLICATION NUMBER: PCT/US98/25108
; PRIOR FILING DATE: December 1, 1998
; PRIOR APPLICATION NUMBER: 09/216,021
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 09/218,517
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 09/254,311
; PRIOR FILING DATE: March 3, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: June 22, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: September 15, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28409
; PRIOR FILING DATE: No. US20020165143A1ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: No. US20020165143A1ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28301
; PRIOR FILING DATE: December 1, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: December 16, 1999
; PRIOR APPLICATION NUMBER: PCT/US00/03565
; PRIOR FILING DATE: February 11, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: February 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: March 2, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: March 30, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: May 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: July 28, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: December 1, 2000
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: February 28, 2001
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 69
; LENGTH: 598
; TYPE: PRT
; ORGANISM: Homo Sapien

US-09-944-403-69

Query Match 100.0%; Score 3135; DB 3; Length 598;
Best Local Similarity 100.0%; Pred. No. 2.4e-194;
Matches 598; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 14

US-09-944-896-69
; Sequence 69, Application US/09944896
; Patent No. US20020168715A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/944,896
; CURRENT FILING DATE: 2001-08-31

;; PRIOR APPLICATION NUMBER: 09/866,028
;; PRIOR FILING DATE: 2001-05-25
;; PRIOR APPLICATION NUMBER: 60/069,334
;; PRIOR FILING DATE: December 11, 1997
;; PRIOR APPLICATION NUMBER: 60/069,335
;; PRIOR FILING DATE: December 11, 1997
;; PRIOR APPLICATION NUMBER: 60/069,278
;; PRIOR FILING DATE: December 11, 1997
;; PRIOR APPLICATION NUMBER: 60/069,425
;; PRIOR FILING DATE: December 12, 1997
;; PRIOR APPLICATION NUMBER: 60/069,696
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;; PRIOR APPLICATION NUMBER: 09/216,021
;; PRIOR FILING DATE: December 16, 1998
;; PRIOR APPLICATION NUMBER: 09/218,517
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;; PRIOR APPLICATION NUMBER: 09/254,311
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;; PRIOR APPLICATION NUMBER: PCT/US99/21090
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;; PRIOR APPLICATION NUMBER: PCT/US99/28409
;; PRIOR FILING DATE: No. US20020168715A1ember 30, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/28313
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;; PRIOR APPLICATION NUMBER: PCT/US99/28301
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;; PRIOR FILING DATE: February 11, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/04414
;; PRIOR FILING DATE: February 22, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/05841
;; PRIOR FILING DATE: March 2, 2000
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;; PRIOR FILING DATE: July 28, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/32678
;; PRIOR FILING DATE: December 1, 2000
;; PRIOR APPLICATION NUMBER: PCT/US01/06520

;; PRIOR FILING DATE: February 28, 2001
;; NUMBER OF SEQ ID NOS: 120
;; SEQ ID NO 69
;; LENGTH: 598
;; TYPE: PRT
;; ORGANISM: Homo Sapien
US-09-944-896-69

Query Match 100.0%; Score 3135; DB 3; Length 598;
Best Local Similarity 100.0%; Pred. No. 2.4e-194;
Matches 598; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MCSRVPLLLPILLIALLGPGVCGCGSCGCGCOPQTVCTAROGTTVPRDVPDDTVGLYVP 60

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DB 61 ENGITMLDASSFAGLPGLQLLDLSQNIASLRPLRLLLDLSHNSLLALEPGLDITANVE 120

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DB 121 ALRLAGLGLQQLDEGLFSLRLNHLHDVSDNQLERVPVIRGLRLTRLAGNTRIAQL 180

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DB 241 SHVTLASPEETRCHEPPKNAGRLLELDYADFGCCPATTATTTATVTRPVVREPTALSSSL 300

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QY 421 LTYRNLSGDPKRLVTLRLPASLAETVTLRNPATYSVCMPLGPGRVPEGEACGEAHT 480
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RESULT 15
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; Sequence 69, Application US/09944944
; Patent No. US20020173463A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kllavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel

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OM protein - protein search, using sw model

Run on: July 27, 2006, 12:07:03 ; Search time 33 Seconds
(without alignments)
1196.800 Million cell updates/sec

Title: US-10-677-669-69

Perfect score: 3135

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 232337 seqs, 56044171 residues

Total number of hits satisfying chosen parameters: 232337

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database : Published Applications_AA_New*

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- 2: /EMC_Celerra_SID33/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	322.5	10.3	811	6	US-10-505-928-32
6	322.5	10.3	811	6	US-10-505-928-87
7	316.5	10.1	713	7	US-11-030-653-26
8	313.5	10.0	656	7	US-11-030-653-38
9	312	10.0	592	6	US-10-486-020-19
10	312	10.0	592	6	US-11-030-653-14
11	309	9.9	649	6	US-10-196-749-384
12	309	9.9	649	7	US-11-101-316-132
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616	6	US-10-196-749-158	6.3	197.5	41
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1038	6	US-10-449-902-41369	5.5	172	63
1038	6	US-10-539-228-157	5.4	170	64
1036	6	US-10-539-228-160	5.4	169.5	65
577	6	US-10-449-902-50526	5.4	168	66
794	6	US-10-449-902-37455	5.3	167	67
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674	7	US-11-056-3558-69824	5.2	163.5	89
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826	7	US-11-056-3558-75177	5.2	163.5	93
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599	7	US-11-056-3558-91592	5.1	160	95
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Sequence 95347, A

99	160	5.1	744	7	US-11-056-355B-91590	Sequence 91590, A	172	147	4.7	2414	7	US-11-283-329-176	Sequence 176, App
100	160	5.1	744	7	US-11-056-355B-93346	Sequence 93346, A	173	146.5	4.7	925	7	US-11-056-355B-70331	Sequence 70331, A
101	159.5	5.1	494	7	US-11-056-355B-97011	Sequence 97011, A	174	146	4.7	293	6	US-10-953-348-22365	Sequence 22365, A
102	159	5.1	396	6	US-10-449-902-43379	Sequence 43379, A	175	146	4.7	748	6	US-10-953-348-3827	Sequence 3827, Ap
103	159	5.1	543	6	US-10-449-902-55599	Sequence 55599, A	176	146	4.7	785	6	US-10-953-349-3826	Sequence 3826, App
104	158.5	5.1	912	7	US-11-056-355B-87717	Sequence 87717, A	177	146	4.7	885	6	US-10-505-928-432	Sequence 432, App
105	158.5	5.1	993	7	US-11-056-355B-87716	Sequence 87716, A	178	146	4.7	785	7	US-11-251-465-20	Sequence 20, Appl
106	158.5	5.1	1070	7	US-11-056-355B-87715	Sequence 87715, A	179	146	4.7	978	6	US-10-953-349-9199	Sequence 9199, Ap
107	158	5.0	363	7	US-11-174-307B-4510	Sequence 4510, Ap	180	146	4.7	1173	6	US-10-953-349-9198	Sequence 9198, Ap
108	157.5	5.0	1032	6	US-10-496-749-552	Sequence 552, App	181	145.5	4.6	352	6	US-10-449-902-32358	Sequence 32358, A
109	157	5.0	1032	7	US-11-341-319-3	Sequence 3, Appli	182	145.5	4.6	352	6	US-10-449-902-32813	Sequence 32813, A
110	156.5	5.0	551	6	US-10-449-902-36375	Sequence 36375, A	183	145.5	4.6	352	6	US-10-449-902-44462	Sequence 44462, A
111	156.5	5.0	932	7	US-11-056-355B-87907	Sequence 87907, A	184	145.5	4.6	827	6	US-10-449-902-54991	Sequence 54991, A
112	156.5	5.0	932	7	US-11-056-355B-97149	Sequence 97149, A	185	145.5	4.6	1189	6	US-10-540-844-4	Sequence 4, Appli
113	156.5	5.0	965	7	US-11-056-355B-97148	Sequence 97148, A	186	145.5	4.6	1236	6	US-10-540-844-2	Sequence 2, Appli
114	156.5	5.0	980	7	US-11-056-355B-87906	Sequence 87906, A	187	145	4.6	292	7	US-11-056-355B-15849	Sequence 15849, A
115	156.5	5.0	980	7	US-11-056-355B-97147	Sequence 97147, A	188	145	4.6	338	7	US-11-105-233-144	Sequence 144, App
116	156.5	5.0	995	7	US-11-056-355B-87905	Sequence 87905, A	189	145	4.6	454	7	US-11-056-355B-56389	Sequence 56389, A
117	155.5	5.0	700	6	US-10-511-795-2	Sequence 2, Appli	190	145	4.6	518	7	US-11-056-355B-56388	Sequence 56388, A
118	155	4.9	411	6	US-10-953-349-33758	Sequence 33758, A	191	145	4.6	540	7	US-11-056-355B-56387	Sequence 56387, A
119	155	4.9	411	7	US-11-056-355B-7403	Sequence 7403, Ap	192	145	4.6	553	7	US-11-056-355B-15848	Sequence 15848, A
120	155	4.9	411	7	US-11-056-355B-19209	Sequence 19209, A	193	145	4.6	971	6	US-11-056-355B-52625	Sequence 52625, A
121	155	4.9	412	6	US-10-953-349-33757	Sequence 33757, A	194	145	4.6	1032	7	US-11-341-319-2	Sequence 2, Appli
122	155	4.9	412	7	US-11-056-355B-7402	Sequence 7402, Ap	195	144.5	4.6	692	6	US-10-196-749-560	Sequence 560, App
123	155	4.9	412	7	US-11-056-355B-19208	Sequence 19208, A	196	144.5	4.6	906	6	US-10-511-795-4	Sequence 4, Appli
124	155	4.9	581	6	US-10-449-902-55557	Sequence 55557, A	197	144	4.6	1072	6	US-10-449-902-53937	Sequence 53937, A
125	154.5	4.9	514	7	US-11-174-307B-4386	Sequence 4386, Ap	198	143.5	4.6	431	7	US-11-056-355B-106706	Sequence 106706, A
126	154.5	4.9	1192	7	US-11-056-355B-46297	Sequence 46297, A	199	143.5	4.6	431	7	US-11-056-355B-117945	Sequence 117945, A
127	154.5	4.9	2517	7	US-11-283-329-204	Sequence 204, App	200	143.5	4.6	450	7	US-11-056-355B-106705	Sequence 106705, A
128	154	4.9	461	6	US-10-953-349-24311	Sequence 24311, A	201	143.5	4.6	450	7	US-11-056-355B-117944	Sequence 117944, A
129	154	4.9	461	7	US-11-056-355B-52536	Sequence 52536, A	202	143.5	4.6	496	7	US-11-056-355B-106704	Sequence 106704, A
130	154	4.9	492	6	US-10-953-349-24310	Sequence 24310, A	203	143.5	4.6	603	7	US-11-056-355B-88145	Sequence 88145, A
131	154	4.9	492	7	US-11-056-355B-52535	Sequence 52535, A	204	143.5	4.6	605	7	US-11-056-355B-79474	Sequence 79474, A
132	154	4.9	1010	7	US-11-056-355B-78678	Sequence 78678, A	205	143.5	4.6	605	7	US-11-056-355B-88144	Sequence 88144, A
133	154	4.9	1090	7	US-11-056-355B-78677	Sequence 78677, A	206	143.5	4.6	611	7	US-11-056-355B-79473	Sequence 79473, A
134	153.5	4.9	775	7	US-11-056-355B-88930	Sequence 88930, A	207	143.5	4.6	613	7	US-11-056-355B-79472	Sequence 79472, A
135	153.5	4.9	775	7	US-11-056-355B-92686	Sequence 92686, A	208	143.5	4.6	935	6	US-10-449-902-46779	Sequence 46779, A
136	153.5	4.9	864	7	US-11-056-355B-79969	Sequence 79969, A	209	143.5	4.6	1335	6	US-10-449-902-56546	Sequence 56546, A
137	153.5	4.9	894	7	US-11-251-465-21	Sequence 21, Appl	210	143	4.6	827	6	US-10-449-902-41294	Sequence 41294, A
138	153.5	4.9	1032	7	US-11-341-319-1	Sequence 1, Appli	211	142.5	4.5	827	6	US-10-449-902-41294	Sequence 41294, A
139	153.5	4.9	1041	7	US-11-056-355B-96010	Sequence 96010, A	212	141.5	4.5	460	7	US-11-056-355B-46185	Sequence 46185, A
140	153.5	4.9	1121	6	US-10-449-902-52117	Sequence 52117, A	213	141.5	4.5	462	7	US-11-056-355B-46184	Sequence 46184, A
141	153.5	4.9	1121	6	US-10-449-902-53982	Sequence 53982, A	214	141.5	4.5	475	7	US-11-056-355B-46183	Sequence 46183, A
142	152	4.8	682	6	US-10-449-902-55729	Sequence 55729, A	215	141.5	4.5	1052	6	US-10-449-902-46489	Sequence 46489, A
143	152	4.8	682	6	US-10-449-902-55720	Sequence 55720, A	216	141.5	4.5	1084	6	US-10-449-902-52915	Sequence 52915, A
144	152	4.8	776	6	US-11-056-355B-69962	Sequence 69962, A	217	140.5	4.5	533	6	US-10-953-349-10988	Sequence 10988, A
145	151	4.8	470	6	US-10-449-902-43319	Sequence 43319, A	218	140.5	4.5	656	6	US-10-449-902-10987	Sequence 10987, A
146	150.5	4.8	1061	6	US-10-449-902-48173	Sequence 48173, A	219	140.5	4.5	757	7	US-11-226-554-134	Sequence 134, App
147	150.5	4.8	1109	7	US-11-330-403-3817	Sequence 3817, Ap	220	140.5	4.5	757	7	US-11-226-554-135	Sequence 135, App
148	150.5	4.8	1109	7	US-11-330-403-9397	Sequence 9397, Ap	221	140.5	4.5	757	7	US-11-248-718-134	Sequence 134, App
149	150	4.8	367	7	US-11-105-233-62	Sequence 62, Appl	222	140.5	4.5	757	7	US-11-248-718-135	Sequence 135, App
150	149.5	4.8	848	6	US-10-449-902-41026	Sequence 41026, A	223	140.5	4.5	757	7	US-11-248-718-135	Sequence 135, App
151	149	4.8	308	6	US-10-449-902-36640	Sequence 36640, A	224	140.5	4.5	953	7	US-11-056-355B-107904	Sequence 107904, A
152	149	4.8	419	6	US-10-449-902-38614	Sequence 38614, A	225	140.5	4.5	953	7	US-11-056-355B-119143	Sequence 119143, A
153	149	4.8	444	7	US-11-056-355B-106189	Sequence 106189, A	226	140.5	4.5	998	7	US-11-056-355B-46620	Sequence 46620, A
154	149	4.8	444	7	US-11-056-355B-117428	Sequence 117428, A	227	140.5	4.5	1009	7	US-11-056-355B-46619	Sequence 46619, A
155	149	4.8	471	7	US-11-056-355B-106188	Sequence 106188, A	228	140.5	4.5	1016	7	US-11-056-355B-46618	Sequence 46618, A
156	149	4.8	471	7	US-11-056-355B-117427	Sequence 117427, A	229	140	4.5	754	7	US-11-056-355B-69815	Sequence 69815, A
157	149	4.8	477	7	US-11-056-355B-106187	Sequence 106187, A	230	140	4.5	853	7	US-11-056-355B-81300	Sequence 81300, A
158	149	4.8	477	7	US-11-056-355B-117426	Sequence 117426, A	231	140	4.5	943	7	US-11-056-355B-81299	Sequence 81299, A
159	149	4.8	1504	6	US-10-505-928-662	Sequence 662, App	232	140	4.5	999	7	US-11-330-403-17817	Sequence 17817, A
160	148.5	4.7	511	6	US-10-449-902-44072	Sequence 44072, A	233	140	4.5	1039	7	US-11-056-355B-81298	Sequence 81298, A
161	147.5	4.7	386	7	US-11-056-355B-78532	Sequence 78532, A	234	140	4.5	2014	7	US-11-299-791-18	Sequence 18, Appl
162	147.5	4.7	398	7	US-11-056-355B-78531	Sequence 78531, A	235	139.5	4.4	439	7	US-11-056-355B-79833	Sequence 79833, A
163	147.5	4.7	445	7	US-11-056-355B-89859	Sequence 89859, A	236	139.5	4.4	451	7	US-11-056-355B-79832	Sequence 79832, A
164	147.5	4.7	445	7	US-11-056-355B-93615	Sequence 93615, A	237	139.5	4.4	453	6	US-10-953-349-22994	Sequence 22994, A
165	147.5	4.7	452	7	US-11-056-355B-78530	Sequence 78530, A	238	139.5	4.4	453	7	US-11-056-355B-59558	Sequence 59558, A
166	147.5	4.7	499	7	US-11-056-355B-89858	Sequence 89858, A	239	139.5	4.4	467	7	US-10-953-349-22993	Sequence 22993, A
167	147.5	4.7	499	7	US-11-056-355B-93614	Sequence 93614, A	240	139.5	4.4	467	7	US-11-056-355B-59557	Sequence 59557, A
168	147.5	4.7	521	7	US-11-056-355B-89857	Sequence 89857, A	241	139.5	4.4	470	6	US-10-953-349-22992	Sequence 22992, A
169	147.5	4.7	521	7	US-11-056-355B-93613	Sequence 93613, A	242	139.5	4.4	470	6	US-11-056-355B-59556	Sequence 59556, A
170	147.5	4.7	557	6	US-10-449-902-31160	Sequence 31160, A	243	139.5	4.4	506	7	US-11-056-355B-79831	Sequence 79831, A
171	147.5	4.7	964	6	US-10-449-902-47345	Sequence 47345, A	244	139	4.4	449	7	US-11-251-465-68	Sequence 68, Appl

245	139	4.4	5179	7	US-11-105-233-185	Sequence 185, App	318	128.5	4.1	697	6	US-10-953-349-328	Sequence 3828, Ap
246	138.5	4.4	660	6	US-10-449-902-36212	Sequence 36212, A	319	128.5	4.1	744	7	US-11-056-3558-95855	Sequence 95855, A
247	138.5	4.4	811	6	US-10-196-749-414	Sequence 414, App	320	128.5	4.1	925	7	US-11-293-697-3889	Sequence 3889, Ap
248	138	4.4	675	6	US-10-449-902-48447	Sequence 48447, A	321	128.5	4.1	962	6	US-10-449-902-52324	Sequence 52324, A
249	138	4.4	675	6	US-10-449-902-50618	Sequence 50618, A	322	128.5	4.1	985	7	US-11-056-3558-88230	Sequence 88230, A
250	137	4.4	207	7	US-11-174-3078-5004	Sequence 5004, Ap	323	128.5	4.1	985	7	US-11-056-3558-91986	Sequence 91986, A
251	137	4.4	412	7	US-11-056-3558-15925	Sequence 15925, A	324	128.5	4.1	1460	7	US-11-247-437-14	Sequence 14, Appl
252	137	4.4	973	6	US-10-449-902-45886	Sequence 45886, A	325	128	4.1	213	7	US-11-056-3558-1607	Sequence 1607, Ap
253	137	4.4	1059	6	US-10-449-902-56147	Sequence 56147, A	326	128	4.1	213	7	US-11-056-3558-8787	Sequence 8787, Ap
254	136.5	4.4	161	6	US-10-449-902-54204	Sequence 54204, A	327	128	4.1	280	7	US-11-056-3558-1606	Sequence 1606, Ap
255	136.5	4.4	535	6	US-10-449-902-41243	Sequence 41243, A	328	128	4.1	367	7	US-11-056-3558-8785	Sequence 8785, Ap
256	136	4.3	322	7	US-11-246-999-79	Sequence 79, Appl	329	128	4.1	998	7	US-11-330-403-13360	Sequence 13360, A
257	136	4.3	586	6	US-10-449-902-51689	Sequence 51689, A	330	128	4.1	1115	6	US-10-449-902-55146	Sequence 55146, A
258	135.5	4.3	406	6	US-10-953-349-31643	Sequence 31643, A	331	128	4.1	1145	7	US-11-330-403-7343	Sequence 7343, Ap
259	135.5	4.3	406	7	US-11-056-3558-68135	Sequence 68135, A	332	127.5	4.1	428	7	US-11-056-3558-2964	Sequence 2964, Ap
260	135.5	4.3	440	7	US-11-251-465-65	Sequence 65, Appl	333	127.5	4.1	544	7	US-11-056-3558-6962	Sequence 6962, Ap
261	135.5	4.3	464	7	US-11-056-3558-91633	Sequence 91633, A	334	127.5	4.1	628	7	US-11-056-3558-59963	Sequence 59963, A
262	135.5	4.3	464	7	US-11-056-3558-95389	Sequence 95389, A	335	127.5	4.1	749	7	US-11-293-697-4038	Sequence 4038, Ap
263	135.5	4.3	493	7	US-11-056-3558-91632	Sequence 91632, A	336	127.5	4.1	750	7	US-11-056-3558-46834	Sequence 46834, A
264	135.5	4.3	493	7	US-11-056-3558-95388	Sequence 95388, A	337	127.5	4.1	750	7	US-11-056-3558-91032	Sequence 91032, A
265	135.5	4.3	998	7	US-11-330-403-13357	Sequence 13357, A	338	127.5	4.1	750	7	US-11-056-3558-94788	Sequence 94788, A
266	135.5	4.3	1012	6	US-10-953-349-13624	Sequence 13624, A	339	127.5	4.1	768	7	US-11-056-3558-46833	Sequence 46833, A
267	135.5	4.3	1025	6	US-10-953-349-13623	Sequence 13623, A	340	127.5	4.1	768	7	US-11-056-3558-91031	Sequence 91031, A
268	134.5	4.3	812	7	US-11-056-3558-96011	Sequence 96011, A	341	127.5	4.1	768	7	US-11-056-3558-94787	Sequence 94787, A
269	134.5	4.3	847	7	US-11-056-3558-79588	Sequence 79588, A	342	127.5	4.1	860	7	US-11-056-3558-46832	Sequence 46832, A
270	134.5	4.3	2240	6	US-10-544-731-4	Sequence 4, Appl	343	127.5	4.1	860	7	US-11-056-3558-91030	Sequence 91030, A
271	134.5	4.3	2258	6	US-10-544-731-3	Sequence 3, Appl	344	127.5	4.1	860	7	US-11-056-3558-94786	Sequence 94786, A
272	134.5	4.3	2264	6	US-10-544-731-5	Sequence 5, Appl	345	127.5	4.1	905	7	US-11-056-3558-46299	Sequence 46299, A
273	134	4.3	476	7	US-11-056-3558-41606	Sequence 41606, A	346	127.5	4.1	948	7	US-11-056-3558-83031	Sequence 83031, A
274	134	4.3	502	7	US-11-174-3078-5262	Sequence 5262, Ap	347	127.5	4.1	1000	7	US-11-056-3558-46298	Sequence 46298, A
275	134	4.3	697	6	US-10-449-902-50662	Sequence 50662, A	348	127.5	4.1	1010	7	US-11-056-3558-83030	Sequence 83030, A
276	134	4.3	921	6	US-10-519-135-6	Sequence 6, Appl	349	127.5	4.1	1120	7	US-11-056-3558-83029	Sequence 83029, A
277	133.5	4.3	239	7	US-11-293-697-2474	Sequence 2474, Ap	350	127	4.1	773	7	US-11-056-3558-97107	Sequence 97107, A
278	133.5	4.3	239	7	US-11-293-697-2850	Sequence 2850, Ap	351	127	4.1	1073	6	US-10-713-648A-54	Sequence 54, Appl
279	133.5	4.3	288	6	US-10-449-902-40102	Sequence 40102, A	352	127	4.1	1595	6	US-10-486-020-18	Sequence 18, Appl
280	133.5	4.3	744	6	US-10-449-902-41606	Sequence 41606, A	353	127	4.1	1614	7	US-11-056-3558-98827	Sequence 98827, A
281	133	4.2	694	7	US-11-056-3558-72373	Sequence 72373, A	354	127	4.1	1614	7	US-11-056-3558-92583	Sequence 92583, A
282	133	4.2	932	6	US-10-519-135-8	Sequence 8, Appl	355	127	4.1	1660	7	US-11-056-3558-88826	Sequence 88826, A
283	133	4.2	4391	7	US-11-183-325-56	Sequence 56, Appl	356	127	4.1	1660	7	US-11-056-3558-92582	Sequence 92582, A
284	132.5	4.2	332	7	US-11-246-999-32	Sequence 32, Appl	357	127	4.1	1828	7	US-11-056-3558-88825	Sequence 88825, A
285	132.5	4.2	587	7	US-11-030-653-32	Sequence 32, Appl	358	127	4.1	1828	7	US-11-056-3558-88825	Sequence 88825, A
286	132.5	4.2	691	7	US-11-056-3558-79590	Sequence 79590, A	359	127	4.1	1842	7	US-11-056-3558-82005	Sequence 82005, A
287	132.5	4.2	717	7	US-11-056-3558-79589	Sequence 79589, A	360	127	4.1	1850	7	US-11-056-3558-82004	Sequence 82004, A
288	132	4.2	717	7	US-11-056-3558-71164	Sequence 71164, A	361	127	4.1	1895	7	US-11-056-3558-82003	Sequence 82003, A
289	132	4.2	891	6	US-10-449-902-53978	Sequence 53978, A	362	126.5	4.0	262	7	US-11-056-3558-50250	Sequence 50250, A
290	132	4.2	891	6	US-10-449-902-56281	Sequence 56281, A	363	126.5	4.0	638	6	US-10-196-749-110	Sequence 110, App
291	132	4.2	987	7	US-11-330-403-13361	Sequence 13361, A	364	126.5	4.0	638	6	US-10-449-902-56142	Sequence 56142, A
292	131	4.2	213	6	US-10-449-902-48867	Sequence 48867, A	365	126.5	4.0	685	7	US-11-175-714-2	Sequence 2, Appl
293	131	4.2	213	6	US-10-449-902-51210	Sequence 51210, A	366	126.5	4.0	685	7	US-11-175-714-28	Sequence 28, Appl
294	131	4.2	766	6	US-10-449-902-36778	Sequence 36778, A	367	126.5	4.0	685	7	US-11-175-714-32	Sequence 32, Appl
295	131	4.2	938	7	US-11-330-403-10157	Sequence 10157, A	368	126.5	4.0	685	7	US-11-175-714-34	Sequence 34, Appl
296	131	4.2	1074	6	US-10-449-902-52953	Sequence 52953, A	369	126.5	4.0	685	7	US-11-175-714-36	Sequence 36, Appl
297	130.5	4.2	177	7	US-11-056-3558-9410	Sequence 9410, Ap	370	126.5	4.0	685	7	US-11-175-714-38	Sequence 38, Appl
298	130.5	4.2	450	6	US-10-449-902-43069	Sequence 43069, A	371	126.5	4.0	685	7	US-11-178-724-20	Sequence 20, Appl
299	130.5	4.2	2003	7	US-11-264-243-8	Sequence 8, Appl	372	126.5	4.0	685	7	US-11-264-243-2	Sequence 2, Appl
300	130	4.1	296	7	US-11-056-3558-91655	Sequence 91655, A	373	126.5	4.0	685	7	US-11-071-796A-19	Sequence 19, Appl
301	130	4.1	296	7	US-11-056-3558-95411	Sequence 95411, A	374	126.5	4.0	717	6	US-10-449-902-53348	Sequence 53348, A
302	130	4.1	389	7	US-11-056-3558-91654	Sequence 91654, A	375	126.5	4.0	977	6	US-10-449-902-50081	Sequence 50081, A
303	130	4.1	389	7	US-11-056-3558-95410	Sequence 95410, A	376	126	4.0	670	7	US-11-056-3558-95856	Sequence 95856, A
304	130	4.1	693	7	US-11-293-697-3849	Sequence 3849, Ap	377	126	4.0	739	6	US-10-539-228-435	Sequence 425, App
305	130	4.1	915	6	US-10-523-014-4	Sequence 4, Appl	378	126	4.0	996	7	US-11-293-716-60	Sequence 60, Appl
306	129.5	4.1	806	7	US-11-056-3558-78679	Sequence 78679, A	379	126	4.0	1006	6	US-10-449-902-43074	Sequence 43074, A
307	129	4.1	652	6	US-10-953-349-5551	Sequence 5551, Ap	380	126	4.0	1786	6	US-10-519-328-2	Sequence 2, Appl
308	129	4.1	652	7	US-11-056-3558-30482	Sequence 30482, A	381	126	4.0	1821	6	US-10-505-928-451	Sequence 451, App
309	129	4.1	652	7	US-11-056-3558-34072	Sequence 34072, A	382	126	4.0	1821	6	US-10-519-328-1	Sequence 1, Appl
310	129	4.1	652	7	US-11-056-3558-97017	Sequence 97017, A	383	125.5	4.0	220	7	US-11-056-3558-50251	Sequence 50251, A
311	129	4.1	1040	7	US-11-056-3558-88229	Sequence 88229, A	384	125.5	4.0	258	6	US-10-196-749-284	Sequence 284, App
312	129	4.1	1040	7	US-11-056-3558-91985	Sequence 91985, A	385	125.5	4.0	508	6	US-10-449-902-30106	Sequence 30106, A
313	129	4.1	1126	7	US-11-293-697-3665	Sequence 3665, Ap	386	125.5	4.0	567	7	US-11-056-3558-38683	Sequence 38683, A
314	129	4.1	1210	7	US-11-056-3558-88228	Sequence 88228, A	387	125.5	4.0	577	7	US-11-056-3558-38682	Sequence 38682, A
315	129	4.1	1210	7	US-11-056-3558-91984	Sequence 91984, A	388	125.5	4.0	686	7	US-11-264-243-4	Sequence 4, Appl
316	129	4.1	2074	7	US-11-165-586-21	Sequence 21, Appl	389	125.5	4.0	944	7	US-11-056-3558-96336	Sequence 96336, A
317	128.5	4.1	671	6	US-10-449-902-52071	Sequence 52071, A	390	125.5	4.0	946	7	US-11-056-3558-96335	Sequence 96335, A

391	125.5	4.0	1003	7	US-11-056-355B-50497	Sequence 50497, A	464	122	3.9	1620	7	US-11-217-997-42	Sequence 42, Appl
392	125	4.0	293	6	US-10-953-349-31470	Sequence 31470, A	465	122	3.9	1653	7	US-11-217-997-40	Sequence 40, Appl
393	125	4.0	690	7	US-11-330-403-4347	Sequence 4347, Ap	466	122	3.9	2203	6	US-10-539-228-726	Sequence 726, App
394	125	4.0	706	6	US-10-449-902-44028	Sequence 44028, A	467	122	3.9	2511	7	US-11-051-725-12	Sequence 12, Appl
395	125	4.0	763	7	US-11-056-355B-107905	Sequence 107905,	468	122	3.9	2511	7	US-11-051-725-13	Sequence 13, Appl
396	125	4.0	763	7	US-11-056-355B-119144	Sequence 119144,	469	122	3.9	2523	7	US-11-051-725-11	Sequence 11, Appl
397	125	4.0	917	6	US-10-504-973-26	Sequence 26, Appl	470	121.5	3.9	294	7	US-11-056-355B-98134	Sequence 98134, A
398	125	4.0	2124	7	US-11-283-329-160	Sequence 160, App	471	121.5	3.9	294	7	US-11-056-355B-109373	Sequence 109373,
399	124.5	4.0	298	7	US-11-297-134-25	Sequence 25, Appl	472	121.5	3.9	296	7	US-11-056-355B-98133	Sequence 98133, A
400	124.5	4.0	546	6	US-10-196-749-412	Sequence 412, App	473	121.5	3.9	296	7	US-11-056-355B-109372	Sequence 109372,
401	124.5	4.0	884	6	US-10-449-902-53270	Sequence 53270, A	474	121.5	3.9	306	7	US-11-056-355B-84354	Sequence 84354, A
402	124.5	4.0	999	6	US-10-519-135-4	Sequence 4, Appli	475	121.5	3.9	314	7	US-11-056-355B-84353	Sequence 84353, A
403	124.5	4.0	1352	7	US-11-056-355B-44895	Sequence 44895, A	476	121.5	3.9	325	7	US-11-056-355B-40921	Sequence 40921, A
404	124.5	4.0	2556	7	US-11-264-243-6	Sequence 6, Appli	477	121.5	3.9	334	7	US-11-056-355B-91924	Sequence 91924, A
405	124	4.0	351	7	US-11-056-355B-65587	Sequence 65587, A	478	121.5	3.9	334	7	US-11-056-355B-85680	Sequence 85680, A
406	124	4.0	739	7	US-11-056-355B-79347	Sequence 79347, A	479	121.5	3.9	338	7	US-11-056-355B-88896	Sequence 88896, A
407	124	4.0	739	7	US-11-056-355B-84020	Sequence 84020, A	480	121.5	3.9	338	7	US-11-056-355B-92652	Sequence 92652, A
408	124	4.0	766	7	US-11-056-355B-79346	Sequence 79346, A	481	121.5	3.9	342	7	US-11-056-355B-40920	Sequence 40920, A
409	124	4.0	766	7	US-11-056-355B-84019	Sequence 84019, A	482	121.5	3.9	351	7	US-11-056-355B-91923	Sequence 91923, A
410	124	4.0	800	7	US-11-056-355B-84018	Sequence 84018, A	483	121.5	3.9	351	7	US-11-056-355B-95679	Sequence 95679, A
411	124	4.0	800	7	US-11-056-355B-91076	Sequence 91076, A	484	121.5	3.9	352	7	US-11-056-355B-40919	Sequence 40919, A
412	124	4.0	839	6	US-11-056-355B-94832	Sequence 94832, A	485	121.5	3.9	359	6	US-11-056-355B-34687	Sequence 34687, A
413	124	4.0	839	6	US-10-449-902-49998	Sequence 49998, A	486	121.5	3.9	367	7	US-10-449-902-34687	Sequence 34687, A
414	124	4.0	839	6	US-10-449-902-53600	Sequence 53600, A	487	121.5	3.9	367	7	US-11-056-355B-98132	Sequence 98132, A
415	124	4.0	891	7	US-11-056-355B-91075	Sequence 91075, A	488	121.5	3.9	395	7	US-11-056-355B-109371	Sequence 109371,
416	124	4.0	891	7	US-11-056-355B-94831	Sequence 94831, A	489	121.5	3.9	395	7	US-11-056-355B-47882	Sequence 47882, A
417	124	4.0	1011	7	US-11-056-355B-91074	Sequence 91074, A	490	121.5	3.9	395	7	US-11-056-355B-88895	Sequence 88895, A
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419	124	4.0	1035	6	US-10-449-902-55142	Sequence 55142, A	492	121.5	3.9	430	7	US-11-056-355B-92650	Sequence 92650, A
420	124	4.0	2617	7	US-11-051-725-14	Sequence 14, Appl	493	121.5	3.9	432	6	US-10-953-349-5788	Sequence 5788, Ap
421	123.5	3.9	334	6	US-10-449-902-34182	Sequence 34182, A	494	121.5	3.9	432	6	US-11-056-355B-27331	Sequence 27331, A
422	123.5	3.9	718	6	US-10-449-902-53222	Sequence 53222, A	495	121.5	3.9	436	7	US-11-056-355B-47880	Sequence 47880, A
423	123.5	3.9	898	7	US-11-056-355B-79052	Sequence 79052, A	496	121.5	3.9	436	6	US-11-056-355B-5787	Sequence 5787, Ap
424	123.5	3.9	1002	6	US-10-449-902-45681	Sequence 45681, A	497	121.5	3.9	436	7	US-11-056-355B-27330	Sequence 27330, A
425	123.5	3.9	1140	6	US-10-449-902-41227	Sequence 41227, A	498	121.5	3.9	686	7	US-11-175-714-25	Sequence 25, Appl
426	123.5	3.9	1198	7	US-11-217-997-14	Sequence 14, Appl	499	121.5	3.9	686	7	US-11-175-714-42	Sequence 42, Appl
427	123	3.9	411	6	US-10-953-349-16133	Sequence 16133, A	500	121.5	3.9	686	7	US-11-175-714-46	Sequence 46, Appl
428	123	3.9	441	7	US-11-174-307B-5246	Sequence 5246, Ap	501	121.5	3.9	760	7	US-11-056-355B-47907	Sequence 47907, A
429	123	3.9	458	6	US-10-953-349-16132	Sequence 16132, A	502	121.5	3.9	813	7	US-11-056-355B-37149	Sequence 37149, A
430	123	3.9	477	6	US-10-953-349-16131	Sequence 16131, A	503	121.5	3.9	813	7	US-11-056-355B-37204	Sequence 37204, A
431	123	3.9	618	7	US-11-078-724-19	Sequence 19, Appl	504	121.5	3.9	851	7	US-11-056-355B-37148	Sequence 37148, A
432	123	3.9	618	7	US-11-071-796A-18	Sequence 18, Appl	505	121.5	3.9	851	7	US-11-056-355B-37203	Sequence 37203, A
433	123	3.9	630	6	US-10-449-902-43648	Sequence 43648, A	511	121.5	3.9	863	7	US-11-289-102-215	Sequence 215, App
434	122.5	3.9	329	6	US-10-953-349-8629	Sequence 8629, Ap	512	121.5	3.9	863	7	US-11-289-102-264	Sequence 264, App
435	122.5	3.9	329	6	US-11-056-355B-42456	Sequence 42456, A	513	121.5	3.9	902	7	US-11-056-355B-37147	Sequence 37147, A
436	122.5	3.9	329	7	US-11-056-355B-106169	Sequence 106169,	514	121.5	3.9	902	7	US-11-056-355B-37202	Sequence 37202, A
437	122.5	3.9	329	7	US-11-056-355B-117408	Sequence 117408,	515	121.5	3.9	1332	6	US-10-449-902-41138	Sequence 41138, A
438	122.5	3.9	335	6	US-11-293-697-4002	Sequence 4002, Ap	516	121	3.9	294	7	US-11-051-725-71	Sequence 71, Appl
439	122.5	3.9	415	6	US-10-953-349-8628	Sequence 8628, Ap	517	121	3.9	294	7	US-11-051-725-72	Sequence 72, Appl
440	122.5	3.9	415	7	US-11-056-355B-42455	Sequence 42455, A	518	121	3.9	299	6	US-10-953-349-39478	Sequence 39478, A
441	122.5	3.9	415	7	US-11-056-355B-106168	Sequence 106168,	519	121	3.9	299	6	US-11-056-355B-13269	Sequence 13269, Ap
442	122.5	3.9	415	7	US-11-056-355B-117407	Sequence 117407,	520	121	3.9	522	6	US-10-449-902-44062	Sequence 44062, A
443	122.5	3.9	515	6	US-10-449-902-47898	Sequence 47898, A	521	121	3.9	522	6	US-10-449-902-41167	Sequence 41167, A
444	122.5	3.9	541	6	US-10-449-902-38744	Sequence 38744, A	522	121	3.9	2117	6	US-11-330-403-15081	Sequence 15081, A
445	122.5	3.9	702	6	US-11-056-355B-85266	Sequence 85266, A	523	120.5	3.8	647	7	US-11-056-355B-46418	Sequence 46418, A
446	122.5	3.9	848	6	US-10-539-228-371	Sequence 371, App	524	120.5	3.8	671	6	US-10-449-902-55560	Sequence 55560, A
447	122.5	3.9	884	6	US-10-449-902-56049	Sequence 56049,	525	120.5	3.8	671	6	US-10-449-902-55560	Sequence 55560, A
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449	122.5	3.9	1154	7	US-11-301-457-23	Sequence 23, Appl	527	120.5	3.8	695	7	US-11-056-355B-48176	Sequence 48176, A
450	122.5	3.9	22152	6	US-10-544-944-1	Sequence 35415, A	528	120.5	3.8	915	6	US-10-449-902-53511	Sequence 53511, A
451	122	3.9	434	6	US-10-449-902-35415	Sequence 35415, A	529	120.5	3.8	949	6	US-10-953-349-12074	Sequence 12074, A
452	122	3.9	434	6	US-10-449-902-36128	Sequence 36128, A	530	120.5	3.8	959	6	US-10-953-349-12073	Sequence 12073, A
453	122	3.9	495	7	US-11-174-307B-3112	Sequence 3112, Ap	531	120.5	3.8	966	6	US-10-519-135-10	Sequence 10, Appl
454	122	3.9	495	7	US-11-217-997-32	Sequence 32, Appl	532	120.5	3.8	976	6	US-11-056-355B-46416	Sequence 46416, A
455	122	3.9	715	7	US-11-056-355B-85259	Sequence 85259, A	533	120.5	3.8	976	7	US-11-056-355B-48175	Sequence 48175, A
456	122	3.9	718	7	US-11-056-355B-81584	Sequence 81584, A	534	120.5	3.8	976	7	US-10-953-349-12072	Sequence 12072, A
457	122	3.9	1398	7	US-11-217-997-4	Sequence 4, Appli	535	120.5	3.8	1003	7	US-11-056-355B-48695	Sequence 48695, A
458	122	3.9	1403	7	US-11-217-997-12	Sequence 12, Appl	536	120.5	3.8				
459	122	3.9	1404	7	US-11-217-997-2	Sequence 2, Appli							
460	122	3.9	1547	7	US-11-217-997-22	Sequence 22, Appl							
461	122	3.9	1577	7	US-11-217-997-16	Sequence 16, Appl							
462	122	3.9	1577	7	US-11-217-997-20	Sequence 20, Appl							
463	122	3.9	1594	7	US-11-217-997-18	Sequence 18, Appl							

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538	120	3.8	243	7	US-10-056-355B-15926	Sequence 15926, A	611	117	3.7	655	7	US-11-242-617-1	Sequence 1, Appl
539	120	3.8	292	7	US-11-051-725-58	Sequence 58, Appl	612	117	3.7	681	6	US-10-953-349-10919	Sequence 10919, A
540	120	3.8	294	7	US-11-051-725-60	Sequence 60, Appl	613	117	3.7	681	7	US-11-056-355B-45477	Sequence 45477, A
541	120	3.8	294	7	US-11-051-725-80	Sequence 80, Appl	614	117	3.7	681	7	US-11-056-355B-49007	Sequence 49007, A
542	120	3.8	294	7	US-11-051-725-82	Sequence 82, Appl	615	117	3.7	698	6	US-10-449-902-53993	Sequence 53993, A
543	120	3.8	294	7	US-11-051-725-88	Sequence 88, Appl	616	117	3.7	727	6	US-10-449-902-38675	Sequence 38675, A
544	120	3.8	294	7	US-11-051-725-98	Sequence 98, Appl	617	117	3.7	988	7	US-11-056-355B-72321	Sequence 72321, A
545	120	3.8	332	6	US-10-449-902-32733	Sequence 32733, A	618	117	3.7	1238	7	US-11-178-724-22	Sequence 22, Appl
546	120	3.8	332	6	US-10-449-902-47788	Sequence 54788, A	619	117	3.7	1238	7	US-11-071-796A-21	Sequence 21, Appl
547	120	3.8	373	6	US-10-953-349-31149	Sequence 31149, A	620	117	3.7	1463	7	US-11-288-992-48	Sequence 48, Appl
548	120	3.8	546	7	US-11-056-355B-19161	Sequence 19161, A	621	117	3.7	2082	7	US-11-330-403-9531	Sequence 9531, Ap
549	120	3.8	560	6	US-10-449-902-53097	Sequence 53097, A	622	116.5	3.7	184	7	US-11-056-355B-30244	Sequence 30244, A
550	120	3.8	1047	6	US-10-449-902-53278	Sequence 53278, A	623	116.5	3.7	184	7	US-11-056-355B-33834	Sequence 33834, A
551	119.5	3.8	383	6	US-10-449-902-43496	Sequence 43496, A	624	116.5	3.7	710	6	US-10-449-902-53008	Sequence 53008, A
552	119.5	3.8	941	7	US-11-056-355B-72901	Sequence 72901, A	625	116.5	3.7	736	7	US-11-056-355B-117906	Sequence 117906, A
553	119.5	3.8	1031	6	US-10-449-902-52986	Sequence 52986, A	626	116.5	3.7	736	7	US-11-056-355B-119145	Sequence 119145, A
554	119.5	3.8	1104	7	US-11-056-355B-106433	Sequence 106433, A	627	116.5	3.7	942	7	US-11-056-355B-44897	Sequence 44897, A
555	119.5	3.8	1104	7	US-11-056-355B-117672	Sequence 117672, A	628	116.5	3.7	1081	7	US-11-056-355B-44896	Sequence 44896, A
556	119.5	3.8	1106	7	US-11-056-355B-106432	Sequence 106432, A	629	116	3.7	321	6	US-10-540-845-5	Sequence 5, Appl
557	119.5	3.8	1106	7	US-11-056-355B-117671	Sequence 117671, A	630	116	3.7	363	6	US-10-540-845-17	Sequence 17, Appl
558	119.5	3.8	1128	7	US-11-056-355B-106431	Sequence 106431, A	631	116	3.7	377	6	US-10-953-349-9913	Sequence 9913, Ap
559	119.5	3.8	1128	7	US-11-056-355B-117670	Sequence 117670, A	632	116	3.7	383	6	US-10-540-845-16	Sequence 16, Appl
560	119	3.8	272	6	US-10-953-349-3121	Sequence 3121, A	633	116	3.7	389	6	US-10-540-845-18	Sequence 18, Appl
561	119	3.8	406	6	US-10-449-902-42711	Sequence 42711, A	634	116	3.7	418	6	US-10-953-349-9912	Sequence 9912, Ap
562	119	3.8	554	6	US-10-449-902-46816	Sequence 46816, A	635	116	3.7	474	6	US-10-953-349-9911	Sequence 9911, Ap
563	119	3.8	598	6	US-10-953-349-8508	Sequence 8508, Ap	636	116	3.7	673	6	US-10-449-902-54153	Sequence 54153, A
564	119	3.8	598	7	US-11-056-355B-39871	Sequence 39871, A	637	116	3.7	680	6	US-10-449-902-47513	Sequence 47513, A
565	119	3.8	599	6	US-10-953-349-8507	Sequence 8507, Ap	638	116	3.7	1014	6	US-10-449-902-52994	Sequence 52994, A
566	119	3.8	599	7	US-11-056-355B-39870	Sequence 39870, A	639	116	3.7	1953	7	US-11-264-243-15	Sequence 16, Appl
567	119	3.8	627	7	US-11-056-355B-91407	Sequence 91407, A	640	116	3.7	2556	7	US-11-071-796A-22	Sequence 22, Appl
568	119	3.8	629	6	US-10-449-902-50256	Sequence 50256, A	641	116	3.7	3934	7	US-11-163-586-20	Sequence 20, Appl
569	119	3.8	695	6	US-10-449-902-48334	Sequence 48334, A	642	115.5	3.7	374	6	US-10-953-349-33957	Sequence 33957, A
570	119	3.8	737	7	US-11-056-355B-47908	Sequence 47908, A	643	115.5	3.7	375	7	US-11-056-355B-3621	Sequence 3621, Ap
571	119	3.8	750	7	US-11-056-355B-86396	Sequence 86396, A	644	115.5	3.7	396	7	US-11-056-355B-83842	Sequence 83842, A
572	119	3.8	751	7	US-11-056-355B-86395	Sequence 86395, A	645	115.5	3.7	822	7	US-11-056-355B-96337	Sequence 96337, A
573	119	3.8	751	7	US-11-296-444-47	Sequence 47, Appl	646	115.5	3.7	849	7	US-11-056-355B-79057	Sequence 79057, A
574	119	3.8	752	7	US-11-056-355B-91409	Sequence 91409, A	647	115.5	3.7	856	7	US-10-449-902-41385	Sequence 41385, A
575	119	3.8	752	7	US-11-056-355B-95165	Sequence 95165, A	648	115.5	3.7	911	7	US-11-226-554-89	Sequence 89, Appl
576	119	3.8	765	7	US-11-056-355B-91408	Sequence 91408, A	649	115.5	3.7	911	7	US-11-248-718-89	Sequence 89, Appl
577	119	3.8	765	7	US-11-056-355B-95164	Sequence 95164, A	650	115.5	3.7	970	7	US-11-056-355B-79056	Sequence 79056, A
578	119	3.8	809	7	US-11-056-355B-91407	Sequence 91407, A	651	115.5	3.7	1450	7	US-11-217-997-6	Sequence 6, Appl
579	119	3.8	809	6	US-10-505-928-150	Sequence 95163, A	652	115	3.7	227	6	US-10-953-349-3122	Sequence 3122, A
580	119	3.8	5738	6	US-10-505-928-150	Sequence 150, App	653	115	3.7	337	7	US-11-174-307B-4220	Sequence 4220, Ap
581	118.5	3.8	248	6	US-10-953-349-20505	Sequence 20505, A	654	115	3.7	492	6	US-10-953-349-29544	Sequence 29544, A
582	118.5	3.8	373	7	US-11-056-355B-62373	Sequence 62373, A	655	115	3.7	492	6	US-11-056-355B-65692	Sequence 65692, A
583	118.5	3.8	890	7	US-11-056-355B-91072	Sequence 91072, A	656	115	3.7	679	7	US-11-056-355B-89082	Sequence 89082, A
584	118.5	3.8	890	7	US-11-056-355B-94828	Sequence 94828, A	657	115	3.7	679	7	US-11-056-355B-92838	Sequence 92838, A
585	118.5	3.8	895	7	US-11-056-355B-72905	Sequence 72905, A	658	115	3.7	680	7	US-11-056-355B-50712	Sequence 50712, A
586	118.5	3.8	998	7	US-11-056-355B-91071	Sequence 91071, A	659	115	3.7	740	6	US-10-449-902-53111	Sequence 53111, A
587	118.5	3.8	998	7	US-11-056-355B-94827	Sequence 94827, A	660	115	3.7	756	7	US-11-056-355B-89081	Sequence 89081, A
588	118.5	3.8	1010	7	US-11-056-355B-91070	Sequence 91070, A	661	115	3.7	756	7	US-11-056-355B-92837	Sequence 92837, A
589	118.5	3.8	1010	7	US-11-056-355B-94826	Sequence 94826, A	662	115	3.7	757	7	US-11-056-355B-50711	Sequence 50711, A
590	118.5	3.8	2245	7	US-11-248-956-3	Sequence 3, Appl	663	115	3.7	1375	6	US-10-553-436-181	Sequence 181, App
591	118	3.8	262	6	US-10-953-349-27149	Sequence 27149, A	664	114.5	3.7	297	6	US-10-953-349-31196	Sequence 31196, A
592	118	3.8	262	7	US-11-056-355B-63081	Sequence 63081, A	665	114.5	3.7	297	7	US-11-056-355B-66249	Sequence 66249, A
593	118	3.8	438	7	US-11-056-355B-7182	Sequence 7182, Ap	666	114.5	3.7	310	6	US-10-449-902-45786	Sequence 45786, A
594	118	3.8	493	7	US-11-056-355B-65494	Sequence 65494, A	667	114.5	3.7	330	7	US-11-056-355B-41942	Sequence 41942, A
595	118	3.8	1000	7	US-11-056-355B-46949	Sequence 46949, A	668	114.5	3.7	341	7	US-11-056-355B-72398	Sequence 72398, A
596	118	3.8	1031	7	US-11-056-355B-46948	Sequence 46948, A	669	114.5	3.7	368	7	US-11-056-355B-72397	Sequence 72397, A
597	118	3.8	1031	6	US-10-449-902-55424	Sequence 55424, A	670	114.5	3.7	373	7	US-11-056-355B-41941	Sequence 41941, A
598	118	3.8	1034	7	US-11-056-355B-46947	Sequence 46947, A	671	114.5	3.7	411	6	US-10-953-349-31856	Sequence 31856, A
599	118	3.8	1060	6	US-10-449-902-41453	Sequence 41453, A	672	114.5	3.7	411	7	US-11-056-355B-66649	Sequence 66649, A
600	118	3.8	2471	7	US-11-071-796A-23	Sequence 23, Appl	673	114.5	3.7	412	6	US-10-953-349-31855	Sequence 31855, A
601	117.5	3.7	369	6	US-10-449-902-50707	Sequence 50707, A	674	114.5	3.7	412	7	US-11-056-355B-66648	Sequence 66648, A
602	117.5	3.7	413	7	US-11-056-355B-4735	Sequence 4735, Ap	675	114.5	3.7	435	6	US-10-449-902-42063	Sequence 42063, A
603	117.5	3.7	550	7	US-11-056-355B-75616	Sequence 75616, A	676	114.5	3.7	451	6	US-10-953-349-31854	Sequence 31854, A
604	117.5	3.7	550	7	US-11-056-355B-96078	Sequence 96078, A	677	114.5	3.7	451	7	US-11-056-355B-66647	Sequence 66647, A
605	117.5	3.7	559	7	US-11-056-355B-87370	Sequence 87370, A	678	114.5	3.7	492	7	US-11-056-355B-10398	Sequence 10398, A
606	117.5	3.7	573	7	US-11-056-355B-75615	Sequence 75615, A	679	114.5	3.7	607	7	US-11-330-403-1414	Sequence 1414, Ap
607	117.5	3.7	582	7	US-11-056-355B-87369	Sequence 87369, A	680	114.5	3.7	688	7	US-11-330-403-5573	Sequence 5573, Ap
608	117.5	3.7	795	6	US-10-449-902-34693	Sequence 34693, A	681	114.5	3.7	910	7	US-11-056-355B-79291	Sequence 79291, A
609	117.5	3.7	870	6	US-10-539-228-358	Sequence 358, App	682	114.5	3.7	970	7	US-11-056-355B-79290	Sequence 79290, A

683	114.5	3.7	1046	7	US-11-056-355B-79289	Sequence 79289, A	756	112.5	3.6	142	7	US-11-056-355B-30245	Sequence 30245, A
684	114.5	3.7	1139	6	US-10-449-902-52733	Sequence 52733, A	757	112.5	3.6	142	7	US-11-056-355B-33835	Sequence 33835, A
685	114.5	3.7	1218	7	US-11-071-796A-20	Sequence 20, Appl	758	112.5	3.6	331	6	US-10-449-902-32293	Sequence 32293, A
686	114.5	3.7	1218	7	US-11-071-796A-20	Sequence 20, Appl	759	112.5	3.6	359	7	US-11-056-355B-83843	Sequence 83843, A
687	114.5	3.7	1360	7	US-11-330-403-40141	Sequence 4001, Ap	760	112.5	3.6	380	6	US-10-449-902-31350	Sequence 31350, A
688	114	3.6	177	6	US-10-953-349-34144	Sequence 34144, A	761	112.5	3.6	405	6	US-10-449-902-36521	Sequence 36521, A
689	114	3.6	184	7	US-11-293-697-2749	Sequence 2749, Ap	762	112.5	3.6	405	6	US-10-449-902-54849	Sequence 54849, A
690	114	3.6	190	6	US-10-953-349-34143	Sequence 34143, A	763	112.5	3.6	426	6	US-10-953-349-5421	Sequence 5421, Ap
691	114	3.6	195	6	US-10-953-349-35816	Sequence 35816, A	764	112.5	3.6	459	6	US-10-449-902-53360	Sequence 53360, A
692	114	3.6	251	7	US-11-056-355B-4501	Sequence 4501, Ap	765	112.5	3.6	531	6	US-10-953-349-5420	Sequence 5420, Ap
693	114	3.6	275	6	US-10-953-349-1558	Sequence 1558, Ap	766	112.5	3.6	562	7	US-11-056-355B-7605	Sequence 7605, Ap
694	114	3.6	275	7	US-11-056-355B-21327	Sequence 21327, A	767	112.5	3.6	564	7	US-11-056-355B-7604	Sequence 7604, Ap
695	114	3.6	275	7	US-11-056-355B-25213	Sequence 25213, A	768	112.5	3.6	574	6	US-10-953-349-12942	Sequence 12942, A
696	114	3.6	275	7	US-11-056-355B-38933	Sequence 38933, A	769	112.5	3.6	574	6	US-10-449-902-40978	Sequence 40978, A
697	114	3.6	275	7	US-11-056-355B-101263	Sequence 101263, A	770	112.5	3.6	630	6	US-10-449-902-40978	Sequence 40978, A
698	114	3.6	275	7	US-11-056-355B-112502	Sequence 112502, A	771	112.5	3.6	636	6	US-10-539-228-4428	Sequence 428, App
699	114	3.6	322	7	US-11-056-355B-72399	Sequence 72399, A	772	112.5	3.6	637	6	US-10-953-349-12941	Sequence 12941, A
700	114	3.6	372	6	US-10-953-349-1557	Sequence 1557, Ap	773	112.5	3.6	638	6	US-11-293-697-3198	Sequence 3198, Ap
701	114	3.6	372	7	US-11-056-355B-21326	Sequence 21326, A	774	112.5	3.6	720	6	US-10-953-349-12940	Sequence 12940, A
702	114	3.6	372	7	US-11-056-355B-28212	Sequence 28212, A	775	112.5	3.6	754	6	US-10-539-228-432	Sequence 432, App
703	114	3.6	372	7	US-11-056-355B-38932	Sequence 38932, A	776	112.5	3.6	772	6	US-10-953-349-9200	Sequence 9200, Ap
704	114	3.6	372	7	US-11-056-355B-101262	Sequence 101262, A	777	112.5	3.6	772	7	US-11-056-355B-75114	Sequence 75114, A
705	114	3.6	372	7	US-11-056-355B-112501	Sequence 112501, A	778	112	3.6	772	7	US-11-056-355B-96477	Sequence 96477, A
706	114	3.6	381	6	US-10-953-349-1556	Sequence 1556, Ap	779	112	3.6	216	7	US-11-056-355B-15927	Sequence 15927, A
707	114	3.6	381	7	US-11-056-355B-21325	Sequence 21325, A	780	112	3.6	240	6	US-10-953-349-18175	Sequence 18175, A
708	114	3.6	381	7	US-11-056-355B-28211	Sequence 28211, A	781	112	3.6	240	6	US-11-056-355B-59359	Sequence 59359, A
709	114	3.6	381	7	US-11-056-355B-38931	Sequence 38931, A	782	112	3.6	246	6	US-10-953-349-18174	Sequence 18174, A
710	114	3.6	381	7	US-11-056-355B-101261	Sequence 101261, A	783	112	3.6	246	6	US-11-056-355B-59358	Sequence 59358, A
711	114	3.6	381	7	US-11-056-355B-112500	Sequence 112500, A	784	112	3.6	275	7	US-11-056-355B-22076	Sequence 22076, A
712	114	3.6	413	6	US-10-511-937-2428	Sequence 2428, Ap	785	112	3.6	293	6	US-11-056-355B-22075	Sequence 22075, A
713	114	3.6	620	7	US-11-293-697-3458	Sequence 3458, Ap	786	112	3.6	318	7	US-10-953-349-27976	Sequence 27976, A
714	114	3.6	620	7	US-10-449-902-53399	Sequence 5399, Ap	787	112	3.6	334	6	US-11-056-355B-69074	Sequence 69074, A
715	114	3.6	691	6	US-10-449-902-45030	Sequence 45030, A	788	112	3.6	334	7	US-10-953-349-27975	Sequence 27975, A
716	113.5	3.6	159	6	US-10-953-349-34145	Sequence 34145, A	789	112	3.6	355	6	US-11-056-355B-69072	Sequence 69072, A
717	113.5	3.6	179	6	US-10-953-349-27151	Sequence 27151, A	790	112	3.6	355	6	US-10-953-349-27974	Sequence 27974, A
718	113.5	3.6	179	6	US-11-056-355B-63083	Sequence 63083, A	791	112	3.6	382	6	US-10-953-349-16918	Sequence 16918, A
719	113.5	3.6	218	6	US-10-953-349-27150	Sequence 27150, A	792	112	3.6	542	6	US-10-449-902-42550	Sequence 42550, A
720	113.5	3.6	218	7	US-11-056-355B-63082	Sequence 63082, A	793	112	3.6	641	6	US-10-449-902-47052	Sequence 47052, A
721	113.5	3.6	289	7	US-11-056-355B-63092	Sequence 63092, A	794	112	3.6	731	7	US-11-056-355B-80297	Sequence 80297, A
722	113.5	3.6	300	7	US-11-056-355B-62375	Sequence 62375, A	795	112	3.6	785	6	US-10-537-228A-6029	Sequence 63, Appl
723	113.5	3.6	309	7	US-11-056-355B-62374	Sequence 62374, A	796	112	3.6	864	7	US-11-178-724-27	Sequence 27, Appl
724	113.5	3.6	395	6	US-10-449-902-41536	Sequence 41536, A	797	112	3.6	1014	7	US-11-056-355B-72514	Sequence 72514, A
725	113.5	3.6	534	7	US-11-056-355B-88146	Sequence 88146, A	798	112	3.6	1015	7	US-11-056-355B-72513	Sequence 72513, A
726	113.5	3.6	601	7	US-11-293-697-4589	Sequence 4589, Ap	799	112	3.6	1019	7	US-11-056-355B-72512	Sequence 72512, A
727	113.5	3.6	635	7	US-11-056-355B-17644	Sequence 17644, A	800	112	3.6	1066	6	US-10-449-902-43289	Sequence 43289, A
728	113.5	3.6	638	7	US-11-174-307B-3660	Sequence 3660, Ap	801	111.5	3.6	1066	6	US-10-449-902-43289	Sequence 43289, A
729	113.5	3.6	907	7	US-11-056-355B-107030	Sequence 107030, A	802	111.5	3.6	315	6	US-10-953-349-28294	Sequence 28294, A
730	113.5	3.6	1008	7	US-11-056-355B-118269	Sequence 118269, A	803	111.5	3.6	452	6	US-11-056-355B-62479	Sequence 62479, A
731	113.5	3.6	1008	7	US-11-288-992-11	Sequence 11, Appl	804	111.5	3.6	460	6	US-10-953-349-8194	Sequence 8194, Ap
732	113.5	3.6	1021	6	US-10-449-902-48223	Sequence 48223, A	805	111.5	3.6	498	7	US-10-953-349-8193	Sequence 8193, Ap
733	113.5	3.6	1034	7	US-11-288-992-47	Sequence 47, Appl	806	111.5	3.6	593	6	US-11-056-355B-19162	Sequence 19162, A
734	113.5	3.6	1113	7	US-11-056-355B-77057	Sequence 77057, A	807	111.5	3.6	647	7	US-11-056-355B-18712	Sequence 18712, A
735	113	3.6	193	6	US-10-953-349-36904	Sequence 36904, A	808	111.5	3.6	656	6	US-10-517-420-50	Sequence 50, Appl
736	113	3.6	262	6	US-10-953-349-16177	Sequence 16177, A	809	111.5	3.6	662	6	US-10-449-902-40037	Sequence 40037, A
737	113	3.6	274	6	US-10-953-349-16176	Sequence 16176, A	810	111.5	3.6	672	6	US-10-449-902-55623	Sequence 55623, A
738	113	3.6	275	6	US-10-953-349-1384	Sequence 1384, Ap	811	111.5	3.6	678	6	US-10-517-420-52	Sequence 52, Appl
739	113	3.6	276	7	US-11-056-355B-3034	Sequence 3034, Ap	812	111.5	3.6	832	7	US-11-056-355B-107032	Sequence 107032, A
740	113	3.6	359	7	US-11-154-977-29	Sequence 29, Appl	813	111.5	3.6	832	7	US-11-056-355B-118271	Sequence 118271, A
741	113	3.6	371	6	US-10-953-349-1353	Sequence 1353, Ap	814	111.5	3.6	858	7	US-11-056-355B-107031	Sequence 107031, A
742	113	3.6	382	7	US-11-056-355B-34852	Sequence 34852, A	815	111.5	3.6	858	7	US-11-056-355B-118270	Sequence 118270, A
743	113	3.6	391	7	US-11-056-355B-34851	Sequence 34851, A	816	111.5	3.6	958	6	US-10-449-902-53356	Sequence 53356, A
744	113	3.6	394	6	US-10-953-349-1352	Sequence 1352, Ap	817	111.5	3.6	1030	7	US-11-056-355B-107275	Sequence 107275, A
745	113	3.6	647	6	US-10-449-902-56469	Sequence 56469, A	818	111.5	3.6	1030	7	US-11-056-355B-118514	Sequence 118514, A
746	113	3.6	864	6	US-10-449-902-41028	Sequence 41028, A	819	111.5	3.6	1073	6	US-10-449-902-41088	Sequence 41088, A
747	113	3.6	899	7	US-11-056-355B-95940	Sequence 95940, A	820	111.5	3.6	1073	7	US-11-056-355B-107274	Sequence 107274, A
748	113	3.6	928	7	US-11-056-355B-95939	Sequence 95939, A	821	111.5	3.6	1073	7	US-11-056-355B-118513	Sequence 118513, A
749	113	3.6	999	7	US-11-056-355B-90832	Sequence 90832, A	822	111	3.5	214	6	US-10-449-902-31897	Sequence 31897, A
750	113	3.6	999	7	US-11-056-355B-94588	Sequence 94588, A	823	111	3.5	274	7	US-11-056-355B-5773	Sequence 5773, Ap
751	113	3.6	1002	7	US-11-056-355B-50734	Sequence 50734, A	824	111	3.5	478	7	US-11-056-355B-84488	Sequence 84488, A
752	113	3.6	1018	7	US-11-056-355B-90831	Sequence 90831, A	825	111	3.5	482	7	US-11-056-355B-84487	Sequence 84487, A
753	113	3.6	1018	7	US-11-056-355B-94587	Sequence 94587, A	826	111	3.5	495	7	US-11-293-697-4277	Sequence 4277, Ap
754	113	3.6	1025	7	US-11-056-355B-90830	Sequence 90830, A	827	111	3.5	617	7	US-11-056-355B-70041	Sequence 70041, A
755	113	3.6	1025	7	US-11-056-355B-94586	Sequence 94586, A	828	111	3.5	706	7	US-11-056-355B-48697	Sequence 48697, A

829	111	3.5	706	7	US-11-056-355B-50499	Sequence 50499, A	902	109.5	3.5	517	7	US-11-174-307B-4664	Sequence 4664, Ap
830	111	3.5	712	7	US-11-056-355B-48696	Sequence 48696, A	903	109.5	3.5	645	6	US-10-449-902-37568	Sequence 37568, A
831	111	3.5	712	7	US-11-056-355B-50498	Sequence 50498, A	904	109.5	3.5	690	7	US-11-330-403-4570	Sequence 4570, Ap
832	111	3.5	771	7	US-11-056-355B-72906	Sequence 72906, A	905	109.5	3.5	839	7	US-11-326-389-14	Sequence 14, Appl
833	110.5	3.5	269	7	US-11-056-355B-2619	Sequence 2619, Ap	906	109.5	3.5	1418	7	US-11-217-997-38	Sequence 38, Appl
834	110.5	3.5	312	6	US-10-953-349-31493	Sequence 31493, A	907	109.5	3.5	1866	6	US-10-511-937-2368	Sequence 2368, Ap
835	110.5	3.5	312	6	US-11-056-355B-68325	Sequence 68325, A	908	109	3.5	182	7	US-11-056-355B-8304	Sequence 8304, Ap
836	110.5	3.5	319	7	US-11-056-355B-20183	Sequence 20183, A	909	109	3.5	259	7	US-11-293-697-4741	Sequence 4741, Ap
837	110.5	3.5	346	7	US-11-036-257-33	Sequence 33, Appl	910	109	3.5	329	6	US-10-953-349-23958	Sequence 23958, A
838	110.5	3.5	376	6	US-10-953-349-34877	Sequence 34877, A	911	109	3.5	329	6	US-11-056-355B-58321	Sequence 58321, A
839	110.5	3.5	376	7	US-11-056-355B-3057	Sequence 3057, Ap	912	109	3.5	416	6	US-10-505-928-276	Sequence 276, App
840	110.5	3.5	376	7	US-11-056-355B-20271	Sequence 20271, A	913	109	3.5	443	7	US-10-505-928-276	Sequence 276, App
841	110.5	3.5	379	6	US-10-953-349-34876	Sequence 34876, A	914	109	3.5	475	7	US-11-056-355B-7046	Sequence 7046, A
842	110.5	3.5	379	7	US-11-056-355B-3056	Sequence 3056, Ap	915	109	3.5	498	6	US-11-056-355B-7046	Sequence 7046, A
843	110.5	3.5	379	7	US-11-056-355B-20270	Sequence 20270, A	916	109	3.5	595	6	US-10-953-349-7418	Sequence 7418, Ap
844	110.5	3.5	394	6	US-10-449-902-33848	Sequence 33848, A	917	109	3.5	595	6	US-10-953-349-7418	Sequence 7418, Ap
845	110.5	3.5	394	6	US-10-449-902-36841	Sequence 36841, A	918	109	3.5	864	6	US-10-953-349-9928	Sequence 9928, Ap
846	110.5	3.5	394	6	US-10-449-902-40453	Sequence 40453, A	919	109	3.5	866	6	US-10-953-349-9927	Sequence 9927, Ap
847	110.5	3.5	394	6	US-10-449-902-46114	Sequence 46114, A	920	109	3.5	951	6	US-10-953-349-9926	Sequence 9926, Ap
848	110.5	3.5	411	7	US-11-036-257-89	Sequence 89, Appl	921	109	3.5	1278	6	US-10-486-020-8	Sequence 8, Appl
849	110.5	3.5	418	6	US-10-953-349-34875	Sequence 34875, A	922	109	3.5	1358	6	US-10-528-542-23	Sequence 23, Appl
850	110.5	3.5	418	7	US-11-056-355B-3055	Sequence 3055, Ap	923	108.5	3.5	160	7	US-11-056-355B-8305	Sequence 8305, Ap
851	110.5	3.5	418	7	US-11-056-355B-20269	Sequence 20269, A	924	108.5	3.5	315	6	US-10-449-902-35365	Sequence 35365, A
852	110.5	3.5	577	7	US-11-293-697-3929	Sequence 3929, Ap	925	108.5	3.5	393	6	US-10-449-902-35570	Sequence 35570, A
853	110.5	3.5	606	7	US-11-056-355B-69816	Sequence 69816, A	926	108.5	3.5	402	7	US-11-056-355B-40984	Sequence 40984, A
854	110.5	3.5	622	6	US-10-449-902-55221	Sequence 55221, A	927	108.5	3.5	445	7	US-11-293-697-4319	Sequence 4319, Ap
855	110.5	3.5	630	6	US-10-449-902-42293	Sequence 42293, A	928	108.5	3.5	445	7	US-11-056-355B-19163	Sequence 19163, A
856	110.5	3.5	643	6	US-10-505-928-249	Sequence 249, App	929	108.5	3.5	940	6	US-10-449-902-56749	Sequence 56749, A
857	110.5	3.5	684	7	US-11-056-355B-14442	Sequence 14442, A	930	108.5	3.5	1125	7	US-10-449-902-41416	Sequence 41416, A
858	110.5	3.5	714	7	US-11-056-355B-80298	Sequence 80298, A	931	108.5	3.5	1255	7	US-11-252-276-152	Sequence 152, App
859	110.5	3.5	809	7	US-11-056-355B-72899	Sequence 72899, A	932	108.5	3.5	1610	7	US-11-252-276-22	Sequence 22, Appl
860	110.5	3.5	930	7	US-11-056-355B-72897	Sequence 72897, A	933	108	3.4	256	6	US-10-449-902-37046	Sequence 37046, A
861	110.5	3.5	1006	7	US-11-056-355B-41332	Sequence 41332, A	934	108	3.4	316	6	US-10-449-902-37138	Sequence 37138, A
862	110.5	3.5	1243	6	US-10-449-902-41332	Sequence 41332, A	935	108	3.4	403	6	US-10-449-902-36074	Sequence 36074, A
863	110	3.5	216	6	US-10-449-902-39091	Sequence 39091, A	936	108	3.4	428	7	US-11-056-355B-3391	Sequence 3391, Ap
864	110	3.5	275	7	US-11-056-355B-40593	Sequence 40593, A	937	108	3.4	476	6	US-10-449-902-47026	Sequence 47026, A
865	110	3.5	275	7	US-11-056-355B-104448	Sequence 104448, A	938	108	3.4	599	6	US-10-547-207-15	Sequence 15, Appl
866	110	3.5	275	7	US-11-056-355B-115687	Sequence 115687, A	939	108	3.4	638	7	US-11-330-403-15603	Sequence 15603, A
867	110	3.5	374	7	US-11-056-355B-38684	Sequence 38684, A	940	108	3.4	671	6	US-10-449-902-54834	Sequence 54834, A
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869	110	3.5	440	6	US-10-449-902-40711	Sequence 40711, A	942	108	3.4	776	6	US-10-449-902-41391	Sequence 41391, A
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871	110	3.5	467	7	US-11-246-999-34	Sequence 34, Appl	944	108	3.4	1730	7	US-11-270-040-6	Sequence 6, Appl
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873	110	3.5	550	7	US-11-297-315-30	Sequence 30, Appl	946	107.5	3.4	306	6	US-10-953-349-3730	Sequence 3730, A
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879	110	3.5	708	7	US-11-056-355B-94335	Sequence 94335, A	952	107.5	3.4	447	6	US-10-449-902-54102	Sequence 54102, A
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883	110	3.5	1030	6	US-10-449-902-41538	Sequence 41538, A	956	107.5	3.4	713	6	US-10-449-902-41723	Sequence 41723, A
884	110	3.5	1123	6	US-10-953-349-4749	Sequence 4749, Ap	957	107.5	3.4	723	7	US-11-178-724-18	Sequence 18, Appl
885	110	3.5	1551	6	US-10-449-902-41326	Sequence 41326, A	958	107.5	3.4	723	7	US-11-071-796A-17	Sequence 17, Appl
886	109.5	3.5	148	6	US-10-449-902-48536	Sequence 48536, A	959	107.5	3.4	765	7	US-11-292-634-2	Sequence 2, Appl
887	109.5	3.5	191	7	US-11-056-355B-84744	Sequence 84744, A	960	107.5	3.4	900	7	US-11-056-355B-90828	Sequence 90828, A
888	109.5	3.5	288	6	US-10-953-349-22296	Sequence 22296, A	961	107.5	3.4	900	7	US-11-056-355B-94584	Sequence 94584, A
889	109.5	3.5	288	7	US-11-056-355B-62481	Sequence 62481, A	962	107.5	3.4	949	7	US-11-056-355B-49856	Sequence 49856, A
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897	109.5	3.5	383	6	US-10-540-845-10	Sequence 10, Appl	970	107	3.4	255	6	US-10-449-902-56595	Sequence 56595, A
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981	106.5	3.4	229	6	US-10-449-902-39832	Sequence 39832, A	1054	104.5	3.3	276	7	US-11-056-355B-6311	Sequence 6311, Ap
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987	106.5	3.4	912	6	US-10-449-902-43619	Sequence 43619, A	1060	104.5	3.3	1479	7	US-11-056-355B-82452	Sequence 82452, A
988	106	3.4	128	7	US-11-056-355B-10528	Sequence 10528, A	1061	104.5	3.3	1544	7	US-11-056-355B-82451	Sequence 82451, A
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991	106	3.4	312	6	US-10-449-902-34826	Sequence 34826, A	1064	104	3.3	306	7	US-11-241-106-7	Sequence 395, App
992	106	3.4	418	6	US-10-449-902-39915	Sequence 39915, A	1065	104	3.3	320	7	US-11-056-355B-8066	Sequence 8066, Ap
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995	106	3.4	653	7	US-11-242-617-2	Sequence 2, Appli	1068	104	3.3	384	6	US-10-953-349-27432	Sequence 27432, A
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			181	6	US-10-449-902-44231	Sequence 44231, A							

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1122	103.5	3.3	1601	7	US-11-056-355B-86185	Sequence 86185, A	1195	102	3.3	218	7	US-11-056-355B-97887	Sequence 97887, A
1123	103.5	3.3	1994	6	US-10-544-731-2	Sequence 2, Appli	1196	102	3.3	218	7	US-11-056-355B-109126	Sequence 109126, A
1124	103	3.3	241	6	US-10-449-902-32572	Sequence 32572, A	1197	102	3.3	235	6	US-10-449-902-32497	Sequence 32497, A
1125	103	3.3	258	7	US-11-056-355B-6313	Sequence 6313, Ap	1198	102	3.3	235	6	US-10-449-902-32594	Sequence 32594, A
1126	103	3.3	263	7	US-11-056-355B-6312	Sequence 6312, Ap	1199	102	3.3	269	7	US-11-056-355B-97886	Sequence 97886, A
1127	103	3.3	335	6	US-10-449-902-29697	Sequence 29697, A	1200	102	3.3	269	7	US-11-056-355B-109125	Sequence 109125, A
1128	103	3.3	355	6	US-10-449-902-43969	Sequence 43969, A	1201	102	3.3	301	7	US-11-056-355B-4386	Sequence 4386, Ap
1129	103	3.3	355	7	US-11-330-403-4829	Sequence 4829, Ap	1202	102	3.3	319	7	US-11-056-355B-5230	Sequence 5230, Ap
1130	103	3.3	355	7	US-11-330-403-13098	Sequence 13098, A	1203	102	3.3	335	7	US-11-056-355B-62801	Sequence 62801, A
1131	103	3.3	410	7	US-11-056-355B-3392	Sequence 3392, Ap	1204	102	3.3	497	7	US-11-056-355B-84651	Sequence 84651, A
1132	103	3.3	496	7	US-11-056-355B-46181	Sequence 46181, A	1205	102	3.3	477	7	US-11-056-355B-84650	Sequence 84650, A
1133	103	3.3	496	7	US-11-056-355B-48884	Sequence 48884, A	1206	102	3.3	500	7	US-11-293-697-4365	Sequence 4255, Ap
1134	103	3.3	554	7	US-11-242-111-20	Sequence 20, Appli	1207	102	3.3	508	7	US-11-293-697-3028	Sequence 3028, Ap
1135	103	3.3	605	6	US-10-953-349-32398	Sequence 32398, A	1208	102	3.3	534	7	US-11-056-355B-84649	Sequence 84649, A
1136	103	3.3	610	7	US-11-056-355B-30798	Sequence 30798, A	1209	102	3.3	656	7	US-11-293-697-4326	Sequence 4326, Ap
1137	103	3.3	610	7	US-11-056-355B-34388	Sequence 34388, A	1210	102	3.3	705	7	US-11-056-355B-50736	Sequence 50736, A
1138	103	3.3	610	7	US-11-056-355B-45696	Sequence 45696, A	1211	102	3.3	721	7	US-11-056-355B-50735	Sequence 50735, A
1139	103	3.3	611	7	US-11-056-355B-46180	Sequence 46180, A	1212	102	3.3	721	7	US-11-175-714-4	Sequence 4, Appli
1140	103	3.3	611	7	US-11-056-355B-48883	Sequence 48883, A	1213	102	3.3	729	7	US-11-175-714-8	Sequence 8, Appli
1141	103	3.3	615	7	US-11-056-355B-30797	Sequence 30797, A	1214	102	3.3	798	7	US-11-292-634-6	Sequence 6, Appli
1142	103	3.3	615	7	US-11-056-355B-34387	Sequence 34387, A	1215	102	3.3	1007	6	US-10-519-342-4	Sequence 4, Appli
1143	103	3.3	615	7	US-11-056-355B-45695	Sequence 45695, A	1216	102	3.3	1024	6	US-10-449-902-46823	Sequence 46823, A
1144	103	3.3	677	7	US-11-056-355B-46179	Sequence 46179, A	1217	102	3.3	1247	7	US-11-330-403-18943	Sequence 18943, A
1145	103	3.3	677	7	US-11-056-355B-48882	Sequence 48882, A	1218	102	3.3	3696	7	US-11-330-363-4	Sequence 4, Appli
1146	103	3.3	695	6	US-10-539-228-376	Sequence 376, App	1219	101.5	3.2	155	6	US-10-953-349-15526	Sequence 15526, A
1147	103	3.3	881	6	US-10-539-228-374	Sequence 374, App	1220	101.5	3.2	164	6	US-10-953-349-22367	Sequence 22367, A
1148	103	3.3	928	6	US-10-449-902-41341	Sequence 41341, A	1221	101.5	3.2	173	6	US-10-953-349-15525	Sequence 15525, A
1149	103	3.3	935	6	US-10-449-902-44414	Sequence 44414, A	1222	101.5	3.2	180	6	US-10-953-349-22366	Sequence 22366, A
1150	103	3.3	935	6	US-10-449-902-53206	Sequence 53206, A	1223	101.5	3.2	218	6	US-10-449-902-32811	Sequence 32811, A
1151	103	3.3	1127	7	US-11-056-355B-46398	Sequence 46398, A	1224	101.5	3.2	218	6	US-10-449-902-47744	Sequence 47744, A
1152	103	3.3	1191	7	US-11-056-355B-46397	Sequence 46397, A	1225	101.5	3.2	244	7	US-11-105-233-138	Sequence 198, App
1153	103	3.3	1201	7	US-11-056-355B-46396	Sequence 46396, A	1226	101.5	3.2	340	7	US-11-259-133-54	Sequence 54, Appli
1154	103	3.3	1217	7	US-11-105-233-186	Sequence 186, App	1227	101.5	3.2	433	6	US-10-449-902-50765	Sequence 50765, A
1155	102.5	3.3	198	6	US-10-953-349-18154	Sequence 18154, A	1228	101.5	3.2	577	6	US-10-449-902-52690	Sequence 52690, A
1156	102.5	3.3	222	7	US-10-953-349-27868	Sequence 27868, A	1229	101.5	3.2	667	7	US-11-330-403-10227	Sequence 10227, A
1157	102.5	3.3	222	7	US-11-056-355B-65337	Sequence 65337, A	1230	101.5	3.2	692	7	US-11-330-403-9024	Sequence 9024, Ap
1158	102.5	3.3	298	6	US-10-953-349-2724	Sequence 2724, Ap	1231	101.5	3.2	719	6	US-10-449-902-43712	Sequence 43712, A
1159	102.5	3.3	298	7	US-11-056-355B-42502	Sequence 42502, A	1232	101.5	3.2	719	6	US-10-449-902-56264	Sequence 56264, A
1160	102.5	3.3	312	7	US-11-056-355B-72580	Sequence 72580, A	1233	101.5	3.2	805	6	US-10-449-902-44460	Sequence 44460, A
1161	102.5	3.3	328	7	US-11-056-355B-80802	Sequence 80802, A	1234	101.5	3.2	858	6	US-10-449-902-43272	Sequence 43272, A
1162	102.5	3.3	330	6	US-10-953-349-2723	Sequence 2723, Ap	1235	101.5	3.2	966	6	US-10-449-902-41240	Sequence 41240, A
1163	102.5	3.3	330	7	US-11-056-355B-42501	Sequence 42501, A	1236	101.5	3.2	1005	6	US-10-449-902-41117	Sequence 41117, A
1164	102.5	3.3	330	7	US-11-056-355B-72579	Sequence 72579, A	1237	101	3.2	219	7	US-11-056-355B-1126	Sequence 1126, Ap
1170	102.5	3.3	409	7	US-11-056-355B-68164	Sequence 68164, A	1238	101	3.2	244	6	US-10-953-349-2725	Sequence 2725, Ap
1166	102.5	3.3	461	7	US-11-056-355B-68162	Sequence 68162, A	1239	101	3.2	244	7	US-11-056-355B-42503	Sequence 42503, A
1167	102.5	3.3	575	7	US-11-287-157A-254	Sequence 254, App	1240	101	3.2	244	7	US-11-056-355B-72581	Sequence 72581, A
1168	102.5	3.3	637	7	US-11-289-102-335	Sequence 335, App	1241	101	3.2	279	6	US-10-449-902-39085	Sequence 39085, A
1169	102.5	3.3	637	7	US-11-056-355B-89084	Sequence 89084, A	1242	101	3.2	291	7	US-11-056-355B-16400	Sequence 16400, A
1171	102.5	3.3	656	7	US-11-056-355B-92840	Sequence 92840, A	1243	101	3.2	343	7	US-11-056-355B-58826	Sequence 58826, A
1171	102.5	3.3	674	7	US-11-056-355B-69475	Sequence 69475, A	1244	101	3.2	386	7	US-11-330-403-15574	Sequence 15574, A
1172	102.5	3.3	751	7	US-11-056-355B-88640	Sequence 88640, A	1245	101	3.2	413	7	US-11-056-355B-58825	Sequence 58825, A
1173	102.5	3.3	751	7	US-11-056-355B-88644	Sequence 88644, A	1246	101	3.2	413	7	US-11-056-355B-58824	Sequence 58824, A
1174	102.5	3.3	751	7	US-11-056-355B-92396	Sequence 92396, A	1247	101	3.2	442	7	US-11-056-355B-58824	Sequence 58824, A
1175	102.5	3.3	751	7	US-11-056-355B-92400	Sequence 92400, A	1248	101	3.2	443	6	US-10-511-937-2464	Sequence 2464, Ap
1176	102.5	3.3	774	7	US-11-056-355B-90281	Sequence 90281, A	1249	101	3.2	443	7	US-11-289-102-300	Sequence 300, App
1177	102.5	3.3	774	7	US-11-056-355B-90280	Sequence 90280, A	1250	101	3.2	443	7	US-11-289-102-354	Sequence 354, App
1178	102.5	3.3	811	7	US-11-056-355B-90280	Sequence 90280, A	1251	101	3.2	443	7	US-11-289-102-379	Sequence 379, App
1179	102.5	3.3	811	7	US-11-056-355B-94036	Sequence 94036, A	1252	101	3.2	448	6	US-10-519-135-20	Sequence 20, Appli
1180	102.5	3.3	907	7	US-11-056-355B-90279	Sequence 90279, A	1253	101	3.2	461	7	US-11-293-697-3238	Sequence 3238, Ap
1181	102.5	3.3	907	7	US-11-056-355B-94035	Sequence 94035, A	1254	101	3.2	712	7	US-11-105-233-182	Sequence 182, Ap
1182	102.5	3.3	911	7	US-11-056-355B-106453	Sequence 106453, A	1255	101	3.2	804	6	US-10-449-902-55004	Sequence 55004, A
1183	102.5	3.3	911	7	US-11-056-355B-117692	Sequence 117692, A	1256	101	3.2	929	6	US-10-449-902-56392	Sequence 56392, A
1184	102.5	3.3	939	6	US-10-449-902-44431	Sequence 44431, A	1257	101	3.2	1267	7	US-11-056-355B-71361	Sequence 71361, A
1185	102.5	3.3	942	7	US-11-056-355B-106452	Sequence 106452, A	1258	101	3.2	1274	7	US-11-056-355B-71360	Sequence 71360, A
1186	102.5	3.3	942	7	US-11-056-355B-117691	Sequence 117691, A	1259	101	3.2	1298	6	US-10-449-902-41177	Sequence 41177, A
1187	102.5	3.3	976	7	US-11-259-133-2	Sequence 2, Appli	1260	101	3.2	1480	7	US-11-056-355B-71359	Sequence 71359, A
1188	102.5	3.3	1047	7	US-11-293-697-3852	Sequence 3852, Ap	1261	100.5	3.2	3176	6	US-11-105-233-135	Sequence 135, App
1189	102.5	3.3	1047	7	US-11-288-992-12	Sequence 12, Appli	1262	100.5	3.2	187	6	US-10-449-902-39255	Sequence 39255, A
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1191	102	3.3	210	6	US-10-953-349-23295	Sequence 23295, A	1264	100.5	3.2	256	6	US-10-953-349-35427	Sequence 35427, A
1192	102	3.3	210	7	US-11-056-355B-56947	Sequence 56947, A	1265	100.5	3.2	256	7	US-11-056-355B-19103	Sequence 19103, A
1193	102	3.3	218	7	US-11-056-355B-21774	Sequence 21774, A	1266	100.5	3.2	274	7	US-11-056-355B-90495	Sequence 90495, A
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1268	100.5	3.2	335	6	US-10-953-349-23256	Sequence 25256, A	1341	99	3.2	374	6	US-10-449-902-35013	Sequence 35013, A
1269	100.5	3.2	338	6	US-10-449-902-36986	Sequence 36986, A	1342	99	3.2	427	7	US-10-449-902-50174	Sequence 50174, A
1270	100.5	3.2	338	6	US-10-449-902-37100	Sequence 37100, A	1343	99	3.2	326	6	US-11-293-697-2833	Sequence 2833, Ap
1271	100.5	3.2	391	6	US-10-449-902-40132	Sequence 40132, A	1344	99	3.2	536	7	US-11-330-403-7245	Sequence 7245, Ap
1272	100.5	3.2	402	7	US-11-056-355B-13690	Sequence 13690, A	1345	99	3.2	575	6	US-10-953-349-13351	Sequence 13351, A
1273	100.5	3.2	440	6	US-10-449-902-52131	Sequence 52131, A	1346	99	3.2	631	7	US-11-056-355B-25434	Sequence 25434, A
1274	100.5	3.2	441	7	US-11-330-403-7841	Sequence 7841, Ap	1347	99	3.2	632	7	US-11-056-355B-25433	Sequence 25433, A
1275	100.5	3.2	464	6	US-10-953-349-32673	Sequence 32673, A	1348	99	3.2	638	7	US-11-056-355B-25432	Sequence 25432, A
1276	100.5	3.2	464	6	US-11-056-355B-68075	Sequence 68075, A	1349	99	3.2	649	7	US-11-056-355B-97414	Sequence 97414, A
1277	100.5	3.2	610	6	US-10-449-902-55889	Sequence 52889, A	1350	99	3.2	649	7	US-11-056-355B-97414	Sequence 97414, A
1278	100.5	3.2	616	7	US-11-056-355B-58993	Sequence 58993, A	1351	99	3.2	686	7	US-11-330-403-11868	Sequence 11868, A
1279	100.5	3.2	640	6	US-10-449-902-56478	Sequence 56478, A	1352	99	3.2	751	7	US-11-056-355B-72902	Sequence 72902, A
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1281	100.5	3.2	737	7	US-11-296-092-15	Sequence 15, Appl	1354	99	3.2	756	7	US-11-056-355B-95169	Sequence 95169, A
1282	100.5	3.2	737	7	US-11-296-155-15	Sequence 15, Appl	1355	99	3.2	769	7	US-11-056-355B-91412	Sequence 91412, A
1283	100.5	3.2	826	7	US-11-056-355B-106454	Sequence 106454, A	1356	99	3.2	769	7	US-11-056-355B-95168	Sequence 95168, A
1284	100.5	3.2	826	7	US-11-056-355B-117693	Sequence 117693, A	1357	99	3.2	775	7	US-11-293-697-4433	Sequence 4433, Ap
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1287	100.5	3.2	1310	6	US-10-449-902-41328	Sequence 41328, A	1360	99	3.2	822	6	US-10-449-902-50261	Sequence 50261, A
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1289	100	3.2	167	7	US-11-056-355B-52630	Sequence 52630, A	1362	99	3.2	1202	7	US-11-056-355B-75882	Sequence 75882, A
1290	100	3.2	183	6	US-10-449-902-49984	Sequence 49984, A	1363	99	3.2	1257	7	US-11-056-355B-75881	Sequence 75881, A
1291	100	3.2	279	7	US-11-056-355B-30231	Sequence 30231, A	1364	99	3.2	1276	7	US-11-330-403-12662	Sequence 12662, A
1292	100	3.2	279	7	US-11-056-355B-33821	Sequence 33821, A	1365	99	3.2	1295	7	US-11-056-355B-75880	Sequence 75880, A
1293	100	3.2	308	7	US-11-056-355B-30230	Sequence 30230, A	1366	99	3.2	1296	7	US-11-056-355B-69735	Sequence 69735, A
1294	100	3.2	308	7	US-11-056-355B-33820	Sequence 33820, A	1367	99	3.2	1389	7	US-11-056-355B-69734	Sequence 69734, A
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1296	100	3.2	452	6	US-10-953-349-19321	Sequence 19321, A	1369	98.5	3.1	161	7	US-11-056-355B-13957	Sequence 13957, A
1297	100	3.2	456	6	US-10-953-349-17970	Sequence 17970, A	1370	98.5	3.1	179	7	US-11-056-355B-69212	Sequence 69212, A
1298	100	3.2	456	6	US-10-953-349-19320	Sequence 19320, A	1371	98.5	3.1	216	7	US-11-056-355B-69065	Sequence 69065, A
1299	100	3.2	482	6	US-10-953-349-19319	Sequence 19319, A	1372	98.5	3.1	273	7	US-11-056-355B-10131	Sequence 10131, A
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1301	100	3.2	510	6	US-10-449-902-51764	Sequence 51764, A	1374	98.5	3.1	280	7	US-11-056-355B-7373	Sequence 7373, Ap
1302	100	3.2	537	6	US-10-953-349-17968	Sequence 17968, A	1375	98.5	3.1	286	7	US-11-056-355B-10320	Sequence 10320, A
1303	100	3.2	583	6	US-10-953-349-13350	Sequence 13350, A	1376	98.5	3.1	315	7	US-11-056-355B-10319	Sequence 10319, A
1304	100	3.2	584	6	US-10-449-902-40017	Sequence 40017, A	1377	98.5	3.1	328	7	US-11-056-355B-39844	Sequence 39844, A
1305	100	3.2	590	7	US-11-293-697-3236	Sequence 3236, Ap	1378	98.5	3.1	328	7	US-11-056-355B-98694	Sequence 98694, A
1306	100	3.2	628	7	US-11-056-355B-96152	Sequence 96152, A	1379	98.5	3.1	328	7	US-11-056-355B-109933	Sequence 109933, A
1307	100	3.2	768	7	US-11-056-355B-96151	Sequence 96151, A	1380	98.5	3.1	335	6	US-10-953-349-37485	Sequence 37485, A
1308	100	3.2	849	6	US-10-449-902-41290	Sequence 41290, A	1381	98.5	3.1	335	7	US-11-056-355B-82728	Sequence 82728, A
1309	100	3.2	881	7	US-11-056-355B-96150	Sequence 96150, A	1382	98.5	3.1	341	6	US-10-196-749-224	Sequence 224, App
1310	100	3.2	945	6	US-10-449-902-45439	Sequence 45439, A	1383	98.5	3.1	345	7	US-11-056-355B-39843	Sequence 39843, A
1311	100	3.2	1148	7	US-11-247-437-6	Sequence 6, Appl1	1384	98.5	3.1	467	7	US-11-293-697-3606	Sequence 3606, Ap
1312	100	3.2	1189	6	US-10-449-902-41223	Sequence 41223, A	1385	98.5	3.1	469	6	US-10-519-342-6	Sequence 6, Appl1
1313	99.5	3.2	154	6	US-10-953-349-26759	Sequence 26759, A	1386	98.5	3.1	484	6	US-10-953-349-37307	Sequence 37307, A
1314	99.5	3.2	154	7	US-11-174-307B-4062	Sequence 4062, Ap	1387	98.5	3.1	486	6	US-10-953-349-37306	Sequence 37306, A
1315	99.5	3.2	157	6	US-10-953-349-34092	Sequence 34092, A	1388	98.5	3.1	497	7	US-11-293-697-4244	Sequence 4244, Ap
1316	99.5	3.2	177	6	US-10-953-349-32339	Sequence 32339, A	1389	98.5	3.1	513	6	US-10-953-349-37305	Sequence 37305, A
1317	99.5	3.2	177	6	US-11-056-355B-63146	Sequence 63146, A	1390	98.5	3.1	530	7	US-11-293-697-4331	Sequence 4331, Ap
1318	99.5	3.2	193	6	US-10-449-902-44938	Sequence 44938, A	1391	98.5	3.1	633	7	US-11-330-403-3010	Sequence 3010, Ap
1319	99.5	3.2	202	6	US-10-953-349-39055	Sequence 39055, A	1392	98.5	3.1	706	6	US-10-449-902-53173	Sequence 53173, A
1320	99.5	3.2	221	6	US-10-953-349-34090	Sequence 34090, A	1393	98.5	3.1	914	6	US-10-449-902-41306	Sequence 41306, A
1321	99.5	3.2	223	6	US-10-953-349-16319	Sequence 16319, A	1394	98.5	3.1	1809	6	US-10-559-415-190	Sequence 190, App
1322	99.5	3.2	259	7	US-11-217-997-34	Sequence 34, Appl	1395	98.5	3.1	1919	6	US-10-559-415-253	Sequence 2, Appl1
1323	99.5	3.2	334	7	US-11-293-697-4241	Sequence 4241, Ap	1396	98.5	3.1	2087	7	US-11-287-157A-253	Sequence 253, App
1324	99.5	3.2	355	6	US-10-449-973-33	Sequence 33, Appl	1397	98	3.1	182	7	US-11-056-355B-82136	Sequence 82136, A
1325	99.5	3.2	366	6	US-10-504-902-36205	Sequence 36205, A	1398	98	3.1	184	7	US-11-238-281-26	Sequence 26, Appl
1326	99.5	3.2	417	7	US-11-293-697-4262	Sequence 4262, Ap	1399	98	3.1	191	7	US-11-291-690A-36	Sequence 36, Appl
1327	99.5	3.2	434	7	US-11-293-697-4078	Sequence 4078, Ap	1400	98	3.1	184	7	US-11-056-355B-82135	Sequence 82135, A
1328	99.5	3.2	494	7	US-11-293-697-4275	Sequence 4275, Ap	1401	98	3.1	193	7	US-11-293-697-3630	Sequence 3630, Ap
1329	99.5	3.2	495	7	US-11-293-697-4114	Sequence 4114, Ap	1402	98	3.1	306	7	US-11-056-355B-19566	Sequence 19566, A
1330	99.5	3.2	496	7	US-11-293-697-4058	Sequence 4058, Ap	1403	98	3.1	336	6	US-10-449-902-53307	Sequence 53307, A
1331	99.5	3.2	500	7	US-11-293-697-4684	Sequence 4684, Ap	1404	98	3.1	339	7	US-11-056-355B-2245	Sequence 2245, Ap
1332	99.5	3.2	502	7	US-11-293-697-4245	Sequence 4245, Ap	1405	98	3.1	341	7	US-11-056-355B-2244	Sequence 2244, Ap
1333	99.5	3.2	607	6	US-10-449-902-44025	Sequence 44025, A	1406	98	3.1	353	7	US-11-056-355B-7759	Sequence 7759, Ap
1334	99.5	3.2	607	6	US-10-449-902-55011	Sequence 55011, A	1407	98	3.1	375	7	US-11-056-355B-45521	Sequence 45521, A
1335	99.5	3.2	621	7	US-11-056-355B-14443	Sequence 14443, A	1408	98	3.1	419	7	US-11-056-355B-45520	Sequence 45520, A
1336	99.5	3.2	646	7	US-11-056-355B-80746	Sequence 80746, A	1409	98	3.1	538	7	US-11-246-999-138	Sequence 138, App
1337	99.5	3.2	665	7	US-11-330-403-8510	Sequence 8510, Ap	1410	98	3.1	627	6	US-10-953-349-32295	Sequence 32295, A
1338	99.5	3.2	688	7	US-11-056-355B-79054	Sequence 79054, A	1411	98	3.1	627	7	US-11-174-307B-3824	Sequence 3824, Ap
1339	99.5	3.2	757	7	US-11-292-634-4	Sequence 4, Appl1	1412	98	3.1	713	7	US-11-175-714-5	Sequence 5, Appl1

1413	98	3.1	860	7	US-11-292-431-3	Sequence 3, Appli
1414	98	3.1	1006	7	US-10-511-937-2425	Sequence 2425, Ap
1415	98	3.1	1006	7	US-11-259-133-32	Sequence 32, Appl
1416	98	3.1	1873	6	US-10-829-000-2	Sequence 2, Appli
1417	97.5	3.1	173	6	US-10-953-349-37388	Sequence 37388, A
1418	97.5	3.1	287	6	US-10-953-349-25731	Sequence 25731, A
1419	97.5	3.1	305	6	US-10-953-349-25730	Sequence 25730, A
1420	97.5	3.1	351	6	US-11-056-3558-8948	Sequence 8948, Ap
1421	97.5	3.1	444	6	US-11-330-403-7430	Sequence 7430, Ap
1422	97.5	3.1	454	6	US-10-953-349-33323	Sequence 33323, A
1423	97.5	3.1	454	6	US-11-056-3558-18325	Sequence 18325, A
1424	97.5	3.1	501	6	US-10-449-902-45991	Sequence 45991, A
1425	97.5	3.1	557	6	US-10-953-349-13352	Sequence 13352, A
1426	97.5	3.1	563	7	US-11-330-403-10774	Sequence 10774, A
1427	97.5	3.1	570	7	US-11-056-3558-66120	Sequence 66120, A
1428	97.5	3.1	574	6	US-10-536-440-6	Sequence 6, Appli
1429	97.5	3.1	624	6	US-10-449-902-55923	Sequence 55923, A
1430	97.5	3.1	627	7	US-11-358-419-47	Sequence 47, Appl
1431	97.5	3.1	710	7	US-11-056-3558-90644	Sequence 90644, A
1432	97.5	3.1	710	7	US-11-056-3558-94400	Sequence 94400, A
1433	97.5	3.1	717	7	US-11-175-714-9	Sequence 9, Appli
1434	97.5	3.1	849	6	US-10-953-349-1432	Sequence 1432, Ap
1435	97.5	3.1	1003	6	US-10-953-349-1431	Sequence 1431, Ap
1436	97.5	3.1	1025	6	US-10-449-902-42266	Sequence 42266, A
1437	97.5	3.1	1392	6	US-10-953-349-1430	Sequence 1430, Ap
1438	97.5	3.1	1935	6	US-10-480-962-6	Sequence 6, Appli
1439	97	3.1	155	6	US-10-953-349-35213	Sequence 35213, A
1440	97	3.1	183	7	US-11-036-257-21	Sequence 21, Appl
1441	97	3.1	187	6	US-10-953-349-8848	Sequence 8848, Ap
1442	97	3.1	187	7	US-11-056-3558-38541	Sequence 38541, A
1443	97	3.1	187	7	US-11-056-3558-50067	Sequence 50067, A
1444	97	3.1	188	7	US-11-056-3558-17056	Sequence 17056, A
1445	97	3.1	266	6	US-10-449-902-51283	Sequence 51283, A
1446	97	3.1	286	7	US-11-056-3558-80695	Sequence 80695, A
1447	97	3.1	319	6	US-10-953-349-36568	Sequence 36568, A
1448	97	3.1	354	6	US-10-953-613C-1011	Sequence 1011, Ap
1449	97	3.1	354	7	US-11-091-234A-31	Sequence 31, Appl
1450	97	3.1	385	7	US-11-056-3558-80694	Sequence 80694, A
1451	97	3.1	385	7	US-11-056-3558-89467	Sequence 89467, A
1452	97	3.1	385	7	US-11-056-3558-93223	Sequence 93223, A
1453	97	3.1	386	7	US-11-056-3558-16279	Sequence 16279, A
1454	97	3.1	394	6	US-10-953-349-20645	Sequence 20645, A
1455	97	3.1	395	6	US-10-516-032-4	Sequence 4, Appli
1456	97	3.1	395	7	US-11-056-3558-80693	Sequence 80693, A
1457	97	3.1	395	7	US-11-056-3558-89466	Sequence 89466, A
1458	97	3.1	395	7	US-11-056-3558-93222	Sequence 93222, A
1459	97	3.1	396	7	US-11-056-3558-89465	Sequence 89465, A
1460	97	3.1	396	7	US-11-056-3558-93221	Sequence 93221, A
1461	97	3.1	397	7	US-11-056-3558-89464	Sequence 89464, A
1462	97	3.1	397	7	US-11-056-3558-93220	Sequence 93220, A
1463	97	3.1	403	7	US-11-274-634-22	Sequence 22, Appl
1464	97	3.1				

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Query Match      100.0%; Score 3135; DB 7; Length 598;
Best Local Similarity 100.0%; Pred. No. 1.5e-186;
Matches 598; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCSRVPLLLPLLLLALGPGVQCPCSGCQCQSQPQTVCFTARQGTTPRDPVPPDVTGLYVF 60
DB 1 MCSRVPLLLPLLLLALGPGVQCPCSGCQCQSQPQTVCFTARQGTTPRDPVPPDVTGLYVF 60
QY 61 ENGITMDASSFAGLPGQLQLDLSQNIASRLPRLLLDLSHNSLLALEPGILDANVE 120
DB 61 ENGITMDASSFAGLPGQLQLDLSQNIASRLPRLLLDLSHNSLLALEPGILDANVE 120
QY 121 ALRAGLGLQQLDEGLFSRLNLDLDVSDNQLERVPPVIRGLRGLTRLAGNTRIAQL 180
DB 121 ALRAGLGLQQLDEGLFSRLNLDLDVSDNQLERVPPVIRGLRGLTRLAGNTRIAQL 180
QY 181 RPEDLAGLAALQELDVSNLSLOALPGDLSGLFPRLRLAAARNPNCVPLSWFGPWVRE 240
DB 181 RPEDLAGLAALQELDVSNLSLOALPGDLSGLFPRLRLAAARNPNCVPLSWFGPWVRE 240
QY 241 SHVTLASPEETRCHFPKKNAGRLLELDYADFGCPATTTTATVPTTRPVVREPTALSSSL 300
DB 241 SHVTLASPEETRCHFPKKNAGRLLELDYADFGCPATTTTATVPTTRPVVREPTALSSSL 300
QY 301 APTWLSPTAPATEAPSPPTAPPTVGPVQPCPCPSTCLNGTCHLGRHHLACLCPG 360
DB 301 APTWLSPTAPATEAPSPPTAPPTVGPVQPCPCPSTCLNGTCHLGRHHLACLCPG 360
QY 361 FTGLYCESOMGQGTRESPTVTPRPRSLTLGTEPVSPSLRVGLORYLOGSSVQLRSRLR 420
DB 361 FTGLYCESOMGQGTRESPTVTPRPRSLTLGTEPVSPSLRVGLORYLOGSSVQLRSRLR 420
QY 421 LTYRNLSGDPDKRLVTLRLPASLAETVTLQLRPNATYSVCVMPPLGPGRVPEGEACGAHT 480
DB 421 LTYRNLSGDPDKRLVTLRLPASLAETVTLQLRPNATYSVCVMPPLGPGRVPEGEACGAHT 480
QY 481 PPAVHNSHAPVTOAREGNLPLLIAPALAAVLLAALAAVGAAYCVRGRGMAAAQDKGV 540
DB 481 PPAVHNSHAPVTOAREGNLPLLIAPALAAVLLAALAAVGAAYCVRGRGMAAAQDKGV 540
QY 541 GPGAGPLELGGVKVPLEPGPKATEGGGEALPSGSECEVPLMGPGGLQSLPHAKPYI 598
DB 541 GPGAGPLELGGVKVPLEPGPKATEGGGEALPSGSECEVPLMGPGGLQSLPHAKPYI 598

RESULT 2
US-11-296-155-69
; Sequence 69, Application US/11296155
; Publication No. US20060127983A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Geritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/11/296,155
; CURRENT FILING DATE: 2005-12-06
; PRIOR APPLICATION NUMBER: US/09/866,028
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Query Match      100.0%; Score 3135; DB 7; Length 598;
Best Local Similarity 100.0%; Pred. No. 1.5e-186;
Matches 598; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCSRVPLLLPLLLLALGPGVQCPCSGCQCQSQPQTVCFTARQGTTPRDPVPPDVTGLYVF 60
DB 1 MCSRVPLLLPLLLLALGPGVQCPCSGCQCQSQPQTVCFTARQGTTPRDPVPPDVTGLYVF 60
QY 61 ENGITMDASSFAGLPGQLQLDLSQNIASRLPRLLLDLSHNSLLALEPGILDANVE 120
DB 61 ENGITMDASSFAGLPGQLQLDLSQNIASRLPRLLLDLSHNSLLALEPGILDANVE 120
QY 121 ALRAGLGLQQLDEGLFSRLNLDLDVSDNQLERVPPVIRGLRGLTRLAGNTRIAQL 180
DB 121 ALRAGLGLQQLDEGLFSRLNLDLDVSDNQLERVPPVIRGLRGLTRLAGNTRIAQL 180
QY 181 RPEDLAGLAALQELDVSNLSLOALPGDLSGLFPRLRLAAARNPNCVPLSWFGPWVRE 240
DB 181 RPEDLAGLAALQELDVSNLSLOALPGDLSGLFPRLRLAAARNPNCVPLSWFGPWVRE 240
QY 241 SHVTLASPEETRCHFPKKNAGRLLELDYADFGCPATTTTATVPTTRPVVREPTALSSSL 300
DB 241 SHVTLASPEETRCHFPKKNAGRLLELDYADFGCPATTTTATVPTTRPVVREPTALSSSL 300
QY 301 APTWLSPTAPATEAPSPPTAPPTVGPVQPCPCPSTCLNGTCHLGRHHLACLCPG 360
DB 301 APTWLSPTAPATEAPSPPTAPPTVGPVQPCPCPSTCLNGTCHLGRHHLACLCPG 360
QY 361 FTGLYCESOMGQGTRESPTVTPRPRSLTLGTEPVSPSLRVGLORYLOGSSVQLRSRLR 420
DB 361 FTGLYCESOMGQGTRESPTVTPRPRSLTLGTEPVSPSLRVGLORYLOGSSVQLRSRLR 420
QY 421 LTYRNLSGDPDKRLVTLRLPASLAETVTLQLRPNATYSVCVMPPLGPGRVPEGEACGAHT 480
DB 421 LTYRNLSGDPDKRLVTLRLPASLAETVTLQLRPNATYSVCVMPPLGPGRVPEGEACGAHT 480
QY 481 PPAVHNSHAPVTOAREGNLPLLIAPALAAVLLAALAAVGAAYCVRGRGMAAAQDKGV 540
DB 481 PPAVHNSHAPVTOAREGNLPLLIAPALAAVLLAALAAVGAAYCVRGRGMAAAQDKGV 540
QY 541 GPGAGPLELGGVKVPLEPGPKATEGGGEALPSGSECEVPLMGPGGLQSLPHAKPYI 598
DB 541 GPGAGPLELGGVKVPLEPGPKATEGGGEALPSGSECEVPLMGPGGLQSLPHAKPYI 598

RESULT 3
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Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 120

SEQ ID NO 69

TYPE: PRT

ORGANISM: Homo Sapien

US-11-296-155-69

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US-11-101-316-16
; Sequence 16, Application US/11101316
; Publication No. US20060099657A1
; GENERAL INFORMATION:
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: ANTIBODIES TO A POLYPEPTIDE ENCODED BY A NUCLEIC ACID
; TITLE OF INVENTION: UNDEREXPRESSED IN MELANOMA
; FILE REFERENCE: P3230R1C17C1
; CURRENT APPLICATION NUMBER: US/11/101,316
; CURRENT FILING DATE: 2005-04-06
; PRIOR APPLICATION NUMBER: 10/063526
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: 10/006867
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: 09/380137
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: 1999-06-02
; PRIOR APPLICATION NUMBER: 60/087759
; PRIOR FILING DATE: 1998-06-02
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 16
; LENGTH: 673
; TYPE: PRT
; ORGANISM: Homo Sapien
US-11-101-316-16

Query Match      98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 2.6e-183;
Matches 597; Conservative 0; Mismatches 1; Indels 75; Gaps 1;

QY      1 MCSRVPLLLPLLLALGPGVCGPCGCGCQSQPQTVECTARQGTTPRDPVPPDTVGLYVF 60
DB      1 MCSRVPLLLPLLLALGPGVCGPCGCGCQSQPQTVECTARQGTTPRDPVPPDTVGLYVF 60
QY      61 ENGITMLDASSFAGLQGLDLSQNIAS-----LRLPRLLLDLSHNS 105
DB      61 ENGITMLDAGSFAGLQGLDLSQNIASLPSGVFQPLANLSNLDLTANRLHEITNETF 120
QY      91 -----LRLPRLLLDLSHNS 180
DB      121 RGLRRLRLYLGKNRIRHTQPGAFDTLDRLLLEKLQDNELRALPRLRLPRLLLLDLSHNS 180
QY      106 LLALEPGILDTANVEALRLAGLQGLDLSQNIASLPSGVFQPLANLSNLDLTANRLHEITNETF 120
DB      181 LLALEPGILDTANVEALRLAGLQGLDLSQNIASLPSGVFQPLANLSNLDLTANRLHEITNETF 120
QY      166 LTRLRAGNTRIAQLRPEDLAGLAALQELDVSNLSQALPGDLSGLFPRLRLLLAAARNPF 225
DB      241 LTRLRAGNTRIAQLRPEDLAGLAALQELDVSNLSQALPGDLSGLFPRLRLLLAAARNPF 300
QY      226 NCVCPLSWFGPWVRESHVTLASPEETRCHFPKPNAGRLLELDYADFGCPATTTATVPT 285
DB      301 NCVCPLSWFGPWVRESHVTLASPEETRCHFPKPNAGRLLELDYADFGCPATTTATVPT 360
QY      286 TRPVREPTALSSSLAPTMTLSPATAPATEAPSPSTAPPTVGPVQDQCPSPCLNGGTC 345
DB      361 TRPVREPTALSSSLAPTMTLSPATAPATEAPSPSTAPPTVGPVQDQCPSPCLNGGTC 420
QY      346 HLGTRHHLACLCEGTGLYCESQMGQTRPSTPTVTPRPRSLTLGIEPVSTSLRVGL 405
DB      421 HLGTRHHLACLCEGTGLYCESQMGQTRPSTPTVTPRPRSLTLGIEPVSTSLRVGL 480
QY      406 QRYLGSSVQLRSLRITYNLSPDKRLVTLRLPASIAEYTVTLQRLPNATYSYCVNPLGP 465
DB      481 QRYLGSSVQLRSLRITYNLSPDKRLVTLRLPASIAEYTVTLQRLPNATYSYCVNPLGP 540

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Db 361 TRPVVREPTALSSSLAPTWLSPTAPATEAPSPSTAPPTVPQPODCCPSPSTCLNGGTC 420
Qy 346 HLGTRHHLACLCEGTGLCYCESQMGCTRPSTPTVTPRPSRLTLGIEPVSPTSRLVGL 405
Db 421 HLGTRHHLACLCEGTGLCYCESQMGCTRPSTPTVTPRPSRLTLGIEPVSPTSRLVGL 480
Qy 406 QRYLOGSSVOLRSRLTYRNLGPDKRLVTLRLPASIAEYVTTQLRPNATYSVCVMPLGP 465
Db 481 QRYLOGSSVOLRSRLTYRNLGPDKRLVTLRLPASIAEYVTTQLRPNATYSVCVMPLGP 540
Qy 466 GRYPEGEACGEAHTPPAVHSNHPVTOAREGNLPLLIAPALAAVLLAALAAVGAAYCYVR 525
Db 541 GRYPEGEACGEAHTPPAVHSNHPVTOAREGNLPLLIAPALAAVLLAALAAVGAAYCYVR 600
Qy 526 RGRAMAAAAQKQVGPAGPGLLEGVVPLEPGPKATEGGGALPSGSECEVPLMGFFG 585
Db 601 RGRAMAAAAQKQVGPAGPGLLEGVVPLEPGPKATEGGGALPSGSECEVPLMGFFG 660
Qy 586 PGLQSPHAKPYI 598
Db 661 PGLQSPHAKPYI 673

RESULT 5
US-10-505-928-32
; Sequence 32, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: Patentin 3.2
; SEQ ID NO 32
; LENGTH: 811
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-505-928-32

Query Match 10.3%; Score 322.5; DB 6; Length 811;
Best Local Similarity 22.0%; Pred. No. 1.4e-12;
Matches 184; Conservative 62; Mismatches 272; Indels 317; Gaps 28;

Qy 7 LLLPLLLLALGPGVQG-CPSGCQCQOPQTVFCTARQGTTPR-----DVPPDTVGLVYFE 61
Db 9 LLLVCGCLALPPLAEPVPCERCDQHPQLLCTNGLRVVPKTSLLPSPHDVITYSLGG 68
Qy 62 NGITMLDASSFAGLPGQLDLDSQNIASL-----RLPRLLLDLSHNSLLALEPGILD 115
Db 69 NFITNITAFDHLRGLQRLDLQVNIQIRSLHPKTFEKLRLLELYLGNLLQALAPGTLA 128
Qy 116 T----- 116
Db 129 PLRKLIRLYANGNEISRLSRGSFEGLESVKLRDGNALGALPDVAFAPGNLLYLHLES 188
Qy 117 -----ANVEALRLAGLGLQQLDEGL-----FSRLRNLDLSDVSNQLERV--- 156
Db 189 NRIRFLGKNFAQGLKRLFNLSANELQPSLRHAATFAPLRSLSSLLSLSANSLOHLGPRI 248
Qy 157 -----PPVIRGLRGLTRLRAGN----- 174

US-10-505-928-87
; Sequence 87, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: Patentin 3.2
; SEQ ID NO 87
; LENGTH: 811
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-505-928-87

Query Match 10.3%; Score 322.5; DB 6; Length 811;
Best Local Similarity 22.0%; Pred. No. 1.4e-12;
Matches 184; Conservative 62; Mismatches 272; Indels 317; Gaps 28;

Qy 7 LLLPLLLLALGPGVQG-CPSGCQCQOPQTVFCTARQGTTPR-----DVPPDTVGLVYFE 61
Db 9 LLLVCGCLALPPLAEPVPCERCDQHPQLLCTNGLRVVPKTSLLPSPHDVITYSLGG 68
Qy 62 NGITMLDASSFAGLPGQLDLDSQNIASL-----RLPRLLLDLSHNSLLALEPGILD 115
Db 69 NFITNITAFDHLRGLQRLDLQVNIQIRSLHPKTFEKLRLLELYLGNLLQALAPGTLA 128
Qy 116 T----- 116
Db 129 PLRKLIRLYANGNEISRLSRGSFEGLESVKLRDGNALGALPDVAFAPGNLLYLHLES 188
Qy 117 -----ANVEALRLAGLGLQQLDEGL-----FSRLRNLDLSDVSNQLERV--- 156
Db 189 NRIRFLGKNFAQGLKRLFNLSANELQPSLRHAATFAPLRSLSSLLSLSANSLOHLGPRI 248
Qy 157 -----PPVIRGLRGLTRLRAGN----- 174

US-10-505-928-87
; Sequence 87, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: Patentin 3.2
; SEQ ID NO 87
; LENGTH: 811
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-505-928-87

Query Match 10.3%; Score 322.5; DB 6; Length 811;
Best Local Similarity 22.0%; Pred. No. 1.4e-12;
Matches 184; Conservative 62; Mismatches 272; Indels 317; Gaps 28;

Qy 7 LLLPLLLLALGPGVQG-CPSGCQCQOPQTVFCTARQGTTPR-----DVPPDTVGLVYFE 61
Db 9 LLLVCGCLALPPLAEPVPCERCDQHPQLLCTNGLRVVPKTSLLPSPHDVITYSLGG 68
Qy 62 NGITMLDASSFAGLPGQLDLDSQNIASL-----RLPRLLLDLSHNSLLALEPGILD 115
Db 69 NFITNITAFDHLRGLQRLDLQVNIQIRSLHPKTFEKLRLLELYLGNLLQALAPGTLA 128
Qy 116 T----- 116
Db 129 PLRKLIRLYANGNEISRLSRGSFEGLESVKLRDGNALGALPDVAFAPGNLLYLHLES 188
Qy 117 -----ANVEALRLAGLGLQQLDEGL-----FSRLRNLDLSDVSNQLERV--- 156
Db 189 NRIRFLGKNFAQGLKRLFNLSANELQPSLRHAATFAPLRSLSSLLSLSANSLOHLGPRI 248
Qy 157 -----PPVIRGLRGLTRLRAGN----- 174
```

Db 249 FOHLPRGLLSLRGNQLTHLAPFAWGLEALRELBELRLEGNRLSQLPTALLEPLHSLEALDL 308
QY 175 --TRIAQLRPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLRLIAAARNPFCVCPIL- 231
Db 309 SGNELSAHPATFGHLGRLESLRNNALSAGDIFAASPALYRLDLDGNGWTCDCRLR 368
QY 232 ---SWFGPMVRESHYTLASPEETRCHFPKPNAGRLLLELDYAD- ---FGCPATTTAT 282
Db 369 GLKRWGMDHWSOORLLTVF- ---VQCRHPPALRGY- ---LDYLDQOOLONGSCADSPSAS 422
QY 283 VPTTRPVVREPTALSSSLAP- ---TW- --- 304
Db 423 LTADRERQPLTAAGBEMTPPAGLABELPPQLQOQGRFLAGVADGGAARELVGNRSAL 482
QY 305 -LSPTAPATEASPSSTAPPTVGPVPODPCPPSTCLNGTCHLGRHHLACLCPGFTG 363
Db 483 RLSRRGPGIQQPSVA- ---AAGPAQSLD- --- 510
QY 364 LVCESQMGOTRPSPTVTPRPSRLTLGIEPVS- ---PTSRLRVGLQRY- --- 408
Db 511 LHKFORGRTRADPALAEPPTASPGSAPSAGDPWQARATKRLGTEHQRRAADSDGA 570
QY 409 - ---LQSSVQLRSRLTYRN- ---LSGPDKRLVTLR- --- 437
Db 571 GLPPLVSDPCDFNKFILCNLTVEAGDASVRAVREHRSRPLCGARFRLLFDRFGQ 630
QY 438 - ---LPASIAEYTVTLRPNATYSVCVMPLGGRVPEGEAEAGHAHTPPAVHSNHA 489
Db 631 PKFHRFVLPSSDSATLRELGRDTPYLVCVEGLGRV- ---C- ---PVAPRDHC 678
QY 490 P- ---VTQAREGN- ---LPLLIAPALAAVLLAALAAVGAAYCYVRRGMAAAQAQDKQ 539
Db 679 AGLVTLPEAGSRGGVDYQLLTALLTVNALLVLLAALAAWASRWLRKLRAR- --- 730
QY 540 VQPGAGPLELE- ---GVKPLE- ---PGKATEGGGEA-LPSGSEC- ---EVLPMGEPP 584
Db 731 --KGAPVHVHRMYSTRRLSRMGTVSADFSFGQSHRPTTVCALEADLIEFP 783
RESULT 7
US-11-030-653-26
; Sequence 26, Application US/11030653
; Publication No. US20060147945A1
; GENERAL INFORMATION:
; APPLICANT: Edmonds, Brian
; APPLICANT: Micanovic, Radmila
; APPLICANT: Ou, Weijia
; APPLICANT: Su, Eric
; APPLICANT: Tschang, Sheng-Hung
; APPLICANT: Wang, He
; TITLE OF INVENTION: Novel secreted proteins and their uses
; FILE REFERENCE: X-14001
; CURRENT APPLICATION NUMBER: US/11/030,653
; CURRENT FILING DATE: 2005-01-06
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 713
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-030-653-26

Query Match 10.1%; Score 316.5; DB 7; Length 713;
Best Local Similarity 23.1%; Pred. No. 3e-12;
Matches 166; Conservative 76; Mismatches 251; Indels 225; Gaps 28;

QY 19 PGVQCGSPGCGCS-QPQTVFCTARQTTVPDRVDPDTVGLYVFENGITWLDASSFAGLPG 77
Db 52 PPATSCPACSCSNQASRVICTRRDLAEVPASIPVNTRYLNQENGIOVIRDTDFKHLR 111
QY 78 LQLLDLSONQIASLR- ---LPRLLLDLSHNSLLALEPGILDAN- --- 118
Db 112 LEILQLSKNLVRKIEVGAFNGFLPSLNTLELFDNRLTTVPTQAFEYLSKLRELWLNRP 171

QY 119 -----VEALRIAGLG-----LQQLDEGLFSRLRLNHLDDVDNQLERVPVIRGLRG 165
Db 172 SIPSVAFNVRPSPRLRLDLGELKRLVISEAAFEGLVNLRYNLGMCLNKDINLNTALVR- 230
QY 166 LTRPLAGNTRTAQLRPEDLAGLA- ---ALQELDVSNLSL 201
Db 231 LEELELSGN-RULLIRPGSFQGLTSLRKLWLMHQAQVATERNAFDLDLSLEELNLSHNL 289
QY 202 QALPGDLSGLFRLRLAAARNPFCVPLSGFPGVWRESHVTLASPEET- ---RCHFP 257
Db 290 MSLPHDLTTPHLRLERVLHNPNWNCNCDVLWSWLKET- ---VPSNTTCCARCHA 344
QY 258 KNAGRLLELDYADGCGPATTTTATPTTRPVVREPTALSSSLAPTWLSPT-APATEAPS 316
Db 345 GLKGRYIGELDQSHFTCYA- ---PVIVEP- ---PTDLNVTGEMAAELKC 385
QY 317 PSTAPPVGPVPOQDCPPSTCLNGGT- ---CHLGRHHLACLCPGFTGLY-CES 368
Db 386 RTGTSMTSNWL- ---TPNGTLMTHGSRVVRISVLHDGTLNFTNVTVO- ---TGQVTCMV 438
QY 369 QMGQOTRPSPTVTPRPSRLTLGIEPVSPTS- ---LRVGLQRYLQGS 412
Db 439 TNSAGNTTA- ---SATLNVSAVDPAAGGTGSGGGPGSGGGVGGGYTYFT 488
QY 413 SVOLRSRLTYRNLSGDPKRLVTLRLPASLABYTVTLRPNATYSVCVMPLGP- --- 465
Db 489 TVTVETLETO- ---PGEEA- ---LQPRGTEK- ---EPPGTTDGVWG 523
QY 466 -GRVPEGEAEAGHAHTPPAVHSNH- ---APVTOAREGNL- ---PLLIAPAL 507
Db 524 GGRGDAAGPSSSTTAPAPRSSRPTKAFVPIITDVNTENALKDLDVNMKTKIILGCFV 583
QY 508 AAVLLAALAAVGAAYCYVRRGR- ---AMAAAQDKG 538
Db 584 AITFWAAVMLV-AFYKLRKQHLKHGHPTRTEIINVEDELPAASAVSVAASG 642
QY 539 QVPGAGPLELEV- ---KVPLEPGPKATEGGGAALPSGSECEVPLM 581
Db 643 GVG-GDSHLALPALERDHLNHHYVAAAFKAHYSSNPGSGCGGKPPCLNSIHEPLL 699
RESULT 8
US-11-030-653-38
; Sequence 38, Application US/11030653
; Publication No. US20060147945A1
; GENERAL INFORMATION:
; APPLICANT: Edmonds, Brian
; APPLICANT: Micanovic, Radmila
; APPLICANT: Ou, Weijia
; APPLICANT: Su, Eric
; APPLICANT: Tschang, Sheng-Hung
; APPLICANT: Wang, He
; TITLE OF INVENTION: Novel secreted proteins and their uses
; FILE REFERENCE: X-14001
; CURRENT APPLICATION NUMBER: US/11/030,653
; CURRENT FILING DATE: 2005-01-06
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 38
; LENGTH: 656
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-030-653-38

Query Match 10.0%; Score 313.5; DB 7; Length 656;
Best Local Similarity 23.6%; Pred. No. 4.2e-12;
Matches 158; Conservative 79; Mismatches 239; Indels 193; Gaps 27;

QY 19 PGVQCGSPGCGCS-QPQTVFCTARQTTVPDRVDPDTVGLYVFENGITWLDASSFAGLPG 77
Db 52 PPATSCPACSCSNQASRVICTRRDLAEVPASIPVNTRYLNQENGIOVIRDTDFKHLR 111

QY 188 -----LAALQELDVNSLSQALPGDLSGLFPRRLRLAARNPF 225
 DB 248 NURKLYLQDNHINRVPPNFAFSLRQLYRLDMSNNLSNLPQGFDDLDNITQILIRNPNW 307
 QY 226 NCVCPLSWFPGWVRSHVTLASPEETRCHFPKNAKGRLLLELDYADFGCPATTTATVPT 285
 DB 308 YCCCKMKWRDMLQSLPVKV-NVRGLMCQAPKVRGMAIKDLNAELFDCCKSGIVSTIQI 366
 QY 286 TRPVVREPTALSSSLAPT---WLSPTAPATEAPSPSTAPPTVGPVPOQDCPPSTCLNG 342
 DB 367 T-----TAIPNTVYPAQOWPAPVTKOPDIKNPKLT----- 397
 QY 343 GTCHLGRHHLACLPCEGTGLYCESQMGQTPPTVTPRPPRSILTLGIEBPVSPSTLR 402
 DB 398 -----KQQTGSPS-----RKTTITTVKSVTSDTIH 424
 QY 403 VGLQRYLGSSVOLRSILRLTYRNLSP-DKRLVTLRLPASLAETVTLQRLPNATYSCVM 461
 DB 425 ISWKLALPMTALRLSWLKLGHSPAFGSITETIVT-----GERSEYLVTALEPDSPYKVCMV 480
 QY 462 PLGGRVPEGEE--ACGEAHTPPAVHSHAPVT-----QARE-----GNLPL--LIAPALA 508
 DB 481 PMETSNLYLDFETPVCIETETAPLRMYN--PTTLNREQEKEPKYKNPPLAIIIGGAVA 538
 QY 509 AVLLAALAAVGAAYCVRGRGMAA-AAQDKGQ 539
 DB 539 LVTIALLALV-CWYVHRNGLSFRNCAYSKGR 569

RESULT 12

US-11-101-316-132
 ; Sequence 132, Application US/11101316
 ; Publication No. US20060099657A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, Christopher J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: ANTIBODIES TO A POLYPEPTIDE ENCODED BY A NUCLEIC ACID
 ; FILE REFERENCE: P230R1C17C1
 ; CURRENT APPLICATION NUMBER: US/11/101,316
 ; CURRENT FILING DATE: 2005-04-06
 ; PRIOR APPLICATION NUMBER: 10/063526
 ; PRIOR FILING DATE: 2002-05-03
 ; PRIOR APPLICATION NUMBER: 10/006867
 ; PRIOR FILING DATE: 2001-12-06
 ; PRIOR APPLICATION NUMBER: PCT/US00/23328
 ; PRIOR FILING DATE: 2000-08-24
 ; PRIOR APPLICATION NUMBER: 09/380137
 ; PRIOR FILING DATE: 1999-08-25
 ; PRIOR APPLICATION NUMBER: PCT/US99/12252
 ; PRIOR FILING DATE: 1999-06-02
 ; PRIOR APPLICATION NUMBER: 60/087759
 ; PRIOR FILING DATE: 1998-06-02
 ; NUMBER OF SEQ ID NOS: 170
 ; SEQ ID NO 132
 ; LENGTH: 649
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 US-11-101-316-132

Query Match 9.9%; Score 309; DB 7; Length 649;
 Best Local Similarity 22.3%; Pred. No. 7.8e-12;
 Matches 141; Conservative 93; Mismatches 214; Indels 184; Gaps 25;
 QY 13 LLLALGP---GVQCPCSGCQSQPQVCTARQGTTPVDRVDPDTVGLYVFENGITMLDA 69
 DB 17 LFLQVAPLSVMAKSCPSVCRC-DAGFTYCNDRFLTSTGIPEDATTLYLQNNQI----- 70
 QY 70 SSFAGLPG-----LQLLDLSQNIQASL-----RLPR 95

DB 71 -NNAGIPSDKNLLKVERIYLVHNSLDEFPPTNLPKVVKELHQENNIRTTIVDSLSKIPY 129
 QY 96 LLLLDLSHNSL--LALPGILDANVEALRALAGLGLQQLDEGLFSLRLNLHLDLDVSDNQL 153
 DB 130 LEEELHDDNSVSAVIEGAFRDSNY--LRLFLSRNHLSTIPWGLPRTIEELRLDDNRI 187
 QY 154 ERV-PPVIRGLRGLRRLRAGN-----TRIAQLR-----PEDLAG- 187
 DB 188 STISSPSLQGLTSLRKLRLVLDGNLNNHGLGDKVFNVLNLTLSLVRNLSLTAAPVNLPGT 247
 QY 188 -----LAALQELDVNSLSQALPGDLSGLFPRRLRLAARNPF 225
 DB 248 NURKLYLQDNHINRVPPNFAFSLRQLYRLDMSNNLSNLPQGFDDLDNITQILIRNPNW 307
 QY 226 NCVCPLSWFPGWVRSHVTLASPEETRCHFPKNAKGRLLLELDYADFGCPATTTATVPT 285
 DB 308 YCCCKMKWRDMLQSLPVKV-NVRGLMCQAPKVRGMAIKDLNAELFDCCKSGIVSTIQI 366
 QY 286 TRPVVREPTALSSSLAPT---WLSPTAPATEAPSPSTAPPTVGPVPOQDCPPSTCLNG 342
 DB 367 T-----TAIPNTVYPAQOWPAPVTKOPDIKNPKLT----- 397
 QY 343 GTCHLGRHHLACLPCEGTGLYCESQMGQTPPTVTPRPPRSILTLGIEBPVSPSTLR 402
 DB 398 -----KQQTGSPS-----RKTTITTVKSVTSDTIH 424
 QY 403 VGLQRYLGSSVOLRSILRLTYRNLSP-DKRLVTLRLPASLAETVTLQRLPNATYSCVM 461
 DB 425 ISWKLALPMTALRLSWLKLGHSPAFGSITETIVT-----GERSEYLVTALEPDSPYKVCMV 480
 QY 462 PLGGRVPEGEE--ACGEAHTPPAVHSHAPVT-----QARE-----GNLPL--LIAPALA 508
 DB 481 PMETSNLYLDFETPVCIETETAPLRMYN--PTTLNREQEKEPKYKNPPLAIIIGGAVA 538
 QY 509 AVLLAALAAVGAAYCVRGRGMAA-AAQDKGQ 539
 DB 539 LVTIALLALV-CWYVHRNGLSFRNCAYSKGR 569

RESULT 13

US-11-376-673-132
 ; Sequence 132, Application US/11376673
 ; Publication No. US20060160186A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: A NUCLEIC ACID UNDEREXPRESSED IN STOMACH TUMOR AND
 ; FILE REFERENCE: P3230R1C165C
 ; CURRENT APPLICATION NUMBER: US/11/376,673
 ; CURRENT FILING DATE: 2006-03-14
 ; PRIOR APPLICATION NUMBER: 10/063742
 ; PRIOR FILING DATE: 2002-05-09
 ; PRIOR APPLICATION NUMBER: 10/006867
 ; PRIOR FILING DATE: 2001-12-06
 ; PRIOR APPLICATION NUMBER: PCT/US00/23328
 ; PRIOR FILING DATE: 2000-08-24
 ; PRIOR APPLICATION NUMBER: 60/170262
 ; PRIOR FILING DATE: 1999-12-09
 ; NUMBER OF SEQ ID NOS: 170
 ; SEQ ID NO 132
 ; LENGTH: 649
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 US-11-376-673-132

Query Match 9.9%; Score 309; DB 7; Length 649;
 Best Local Similarity 22.3%; Pred. No. 7.8e-12;
 Matches 141; Conservative 93; Mismatches 214; Indels 184; Gaps 25;

QY 13 LLLALGP---GVQCPSCQCSQPQVFTCTARQGTTPRDPVDPDTVGLYVFPENGITMLDA 69
DB 17 LFLQVAPLSVMAKSCPSVCRCDAGFIYCNDRLFTSIPGTIPEDATTLQNNQI----- 70
QY 70 SSFAGLPG-----LQLDLSONQIASL-----RLPR 95
DB 71 -NNAGIPSLDKNLLKVERIYLYHNSLDEFTNLPKVVKELHQENNIRIITYDLSKIPY 129
QY 96 LLLLDLSHNSL--LALPGLTANVEALRLAGLGLQQLDEGLFSLRLNHLDLSDNQL 153
DB 130 LSELHDDNSVSAVSTIEGAFRDSNY--LRLFLSRNHLSTIPWGLPRTIEELRDDNRI 187
QY 154 ERV-PPVIEGLAGLTLRLAGN-----TRIAQLR-----PEDLAG- 187
DB 188 STISSPSLQGLTSLKRLVLDGNLLNHHGLDKVFFNLVNLTELSLVRNLSLTAAPVNLPGT 247
QY 188 -----LALQELDVSNLSLQALPGDLGSLGFLPRLRLLAARNPF 225
DB 248 NLRLKLYLDNHINRVPPNFAFYLRLYLRLDMNNLSNLPQGFDDLDNITQLILRNPNW 307
QY 226 NVCPLSWFGPWVRESHVTLASPEETRCHFPKPKNAGRLLLELDYADFGCPATTTTATVPT 285
DB 308 YGCKMKWVRDWLQSLPVKV-NVRGLMCOAPEKVRGMAIKDLNAELFDCCKDSGIIVSTIQI 366
QY 286 TPVVRPRETALSSSLAPT---WLSPTAPATEAPSPSTAPPTVGPVPOQDCPPSTCLNG 342
DB 367 T-----TAIPNTVTPAQOMPAPVTKQPDKNPKLT----- 397
QY 343 GTCHLGRHHLACLCPGEGTGLYCESQMGQTRPSPTVTPRPRSLTLGIEPVSPTSUR 402
DB 398 -----KQQTGSPS-----RKTIITVKSVTSDTIH 424
QY 403 VGLORYLOGSSVQLRSLRITYRLNLGSP-DKRLVTLRLPASLAETVTLQRLPNATYSVCVM 461
DB 425 ISWKALPMTALRLSLWLGHPAFGSIETIVT---GERSEYLVTALEPSPYKVCNV 480
QY 462 PLGGRVPEGBE--ACGEAHTPPAVHSNHPVT-----QARE-----GNLPL--LIAPALA 508
DB 481 PMETSNLYLDFETPCVETETAPLRMYN--PTTTLNREGEKEPYKNPNLPLAAIIGGAVA 538
QY 509 AVLLAALAAVGAAYCVRRGRAMAA-AAQDKGO 539
DB 539 LVTIALALV-CWYVHRNGSLFSRNCAYSKGR 569

RESULT 14

US-11-293-697-3826
; Sequence 3826, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3826
; LENGTH: 745
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-293-697-3826

Query Match 9.0%; Score 282.5; DB 7; Length 745;

Best Local Similarity 22.7%; Pred. No. 3.9e-10;
Matches 171; Conservative 58; Mismatches 254; Indels 271; Gaps 29;

QY 8 LLPLLLALLGPGVQO-CPSGCQCSQP---QTVFCTARQGTTPRDPVDPDTVGLYVFPENG 63
DB 4 LRALMLVWAL-LGVAGSCPCEACVDKYAHQADCAKRELVPEVPEGLPANVTTLISANK 62

QY 64 ITMLDASSFAGLPGQLQLDLSONQIASLRLPRLLLLDLSHNSLLALEPGILDTANVEALR 123
DB 63 ITVLRRGAFADV-----TQVTSW-----LAHNEVRTVEPGAL----- 95
QY 124 LAGLGLQQLDEGLFSLRLNHLHDVSDNQLRVP-PVIRGLRGLTLRLRLAGNTRIAQLRP 182
DB 96 -----AVLSQLKN-----LDLSHNFISFFPWSDLNLSALQLLKNHN-RLGSLPR 140
QY 183 EDLAGLALQELDVSNLSLQAL-PGDLGSLGPLRLRLLAARNPFNCVCLSPFGPWVRES 241
DB 141 DALGALPDLRLSRIRINNRLRTLAPGTFOAL-SALSHLQLYHNPFFHCCGGLVWLQAWAAS 199
QY 242 HVTLASPETRCHFPKPKNAGRLLLELDYADFCPATTTTATVPTTRP----- 288
DB 200 RVSLPEPDSIACAPALQGVFVYRLPALPCAPPSVHLSAEPPLBAPGTPPLRAGLAFVLH 259
QY 289 -----VVREPTALSS----- 300
DB 260 CIADGHPTRLOWIQTGGTVVLEPPVLSGEDDGVGAEEGEGDGLLTOTQATPTP 319
QY 301 APTWLSPTAP----- 319
DB 320 APAPWAPPATPRFLALANGSLVPLLSAKEAGVYTCRAHNELGANSTSIKRVAAATGPPK 379
QY 320 TAPPTVGPVPOQDCPP-----STCLNGGTCHLGRHHLACLCPG-----FTGLYCESQMG 371
DB 380 HAPGAGG---EPDGAQPTSERKSTAKGRNSVLPK-----PEGIKGOGLKAVSILG 429
QY 372 QGTRPSPTVPTPR----- 393
DB 430 E-TETEPEEDTSEGEAEADQIILADPAEORCGNGDPDSRVSNHAFNQSAELKPHVFLGV 488
QY 394 -----EPVSPSTSLRVGLORYLOGSSVQ---LRSRLTYRLNLGSPDKRLVTLRLPA 440
DB 489 IALDVAEREARVQLTFLAARMGPGGAGGAPRPGRRPLRLLYLCPAGGAAVQWSRVEE 548
QY 441 SLAETVTLQRLPNATYSVCVMPLGPRVPEGEACGEAHTPPAVHSNHPVTQAREGNLP 500
DB 549 GVNAYWFRGLRGTNYSVCLALAG-----EAC-----HVQVVFSTKKELP 588
QY 501 LLIIAPALAAVLLAALAAV---GAAVCVRRG-----RAMAAAAADK---GGVGG 543
DB 589 SLIVIVAVSVFLVLVLTATVPLLGAACHLLAKHGPYRLLRPQAPDPMEKRIADFDPR 648
QY 544 AGPLELEGVKVPLEPGPKATEGGGEALPSPGSECE 577
DB 649 ASYLESE-----KSYPAGGEA--GGBEPE 670

RESULT 15

US-10-196-749-290
; Sequence 290, Application US/10196749
; Publication No. US20060094864A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C340
; CURRENT APPLICATION NUMBER: US/10/196,749
; CURRENT FILING DATE: 2002-07-16
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263

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; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; PRIOR Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 290
; LENGTH: 1523
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-196-749-290

Query Match      8.2%; Score 258; DB 6; Length 1523;
Best Local Similarity 25.7%; Pred. No. 2.7e-08;
Matches 94; Conservative 39; Mismatches 115; Indels 118; Gaps 15;

Qy      24  CPSCGCSQPTVFCYCTARQTTVPDRVPPDTVGLYVFENGITWLDASSFAGLPGLQLLDL 83
Db      725  CPEQCTCME--TVVRCNKGRLALPGMPKDVTELYLEGHNLTA----- 767

Qy      84  SQNQIASLRPLRLDLLSHNSLLALEPGILDANVEALFAGLGLQQLDEGLFSRLRL 143
Db      768  -PRELSALR--HLTLIDLNN-----ISMLTNYTFSNMSHL 801

Qy      144  HDLDVSDNQLRVP-PVIRGLGLRLRLAGNTRIAQLRPEDLAGLAALQELDVSNLSLQ 202
Db      802  STLILSYNRLRCIPVHAFNGLSRLVLTGHN-----DISSVPEGSFNDLTSL-- 850

Qy      203  ALPGDLGLFRLRLUAAARNPNCVCLSWFGPWPVRESHVTLASPEETRCFPKPNAGR 262
Db      851  -----HLALGNPLHDCSLRWLSEWKAGY---KEPGIARCSSPEPNADR 893

Qy      263  LLELDYADFGCPATTTTATVTPRPVVRPTALSSSLAPTILSPTAPATEAPSP--ST 320
Db      894  LLL-----TTPTHRFQCKGPVDINI-----VAKCNACLSSPCCKN 928

Qy      321  APPTVGVPV-----QPDC--PPSTCL-----NGGTCILGTRHH--LACLCPGEGF 361
Db      929  GTCTQDFVELYRCACPYSGKDCQTVINTCIQNPQOHGGTCHLSDSHKGDFSCCPGLG 988

Qy      362  TGLYCE 367
Db      989  EGRCE 994
```

Search completed: July 27, 2006, 12:10:26
Job time : 44 secs

GenCore version 5.1.9

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OM protein - protein search, using sw model

Run on: July 27, 2006, 12:03:02 ; Search time 42 Seconds
(without alignments)
1369.943 Million cell updates/sec

Title: US-10-677-669-69

Perfect score: 3135

Sequence: 1 MCSRVPLLLPLLLALLGPG.....PLMGPPGQLSPLHAKPYI 598

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database :

PIR 80:**

1: Piri:**

2: Piri2:**

3: Piri3:**

4: Piri4:**

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	322	10.3	605	2 JCS239	insulin-like growth
2	302	9.6	605	2 A41915	insulin-like growth
3	282	9.0	626	1 NBHUIA	platelet glycoprot
4	281.5	9.0	603	2 JCI282	insulin-like growth
5	278.5	8.9	603	2 JCI282	insulin-like growth
6	278	8.9	1531	2 T42218	slit-1 protein hom
7	264.5	8.4	420	2 A53531	oncofetal trophobl
8	261	8.3	1523	2 T13953	MEGF5 protein - ra
9	255.5	8.1	1469	2 B36665	slit protein 2 pre
10	255.5	8.1	1480	2 A36665	slit protein 1 pre
11	251	8.0	622	2 JC7973	synleurin - human
12	243.5	7.8	312	1 NBHUA2	leucine-rich alpha
13	240	7.7	560	2 A60164	platelet membrane
14	237	7.6	707	2 JC7763	neutonal leucine-r
15	231	7.4	1025	2 T42626	secreted leucine-r
16	222.5	7.1	536	2 A34901	lysine carboxypept
17	214.5	6.8	1535	2 S46224	peroxidase - frui
18	212.5	6.8	361	2 A53860	chondroadherin pre
19	210.5	6.7	4302	2 A38971	polycystic kidney
20	209	6.7	1091	2 A58532	glial cell membran
21	208.5	6.7	382	2 T39068	proline-arginine-
22	200	6.4	653	2 T23194	hypothetical prote
23	199	6.3	1328	2 T23007	hypothetical prote
24	194.5	6.2	789	2 T28714	hypothetical prote
25	194.5	6.2	1355	2 T28715	hypothetical prote
26	193.5	6.2	421	2 T46266	hypothetical prote
27	193.5	6.2	721	2 E70766	hypothetical prote
28	192.5	6.1	575	2 T29972	hypothetical prote
29	189	6.0	369	2 S20811	proteoglycan I - m

30	189	6.0	369	2	S32793	biglycan precursor
31	189	6.0	839	2	T04859	extensin homolog F
32	188.5	6.0	440	2	A47530	oligodendrocyte-my
33	186	5.9	440	2	A39613	oligodendrocyte-my
34	184	5.9	368	1	BGHUN	biglycan precursor
35	183	5.8	662	2	S42799	garp precursor - h
36	182	5.8	369	2	S32559	biglycan precursor
37	181.5	5.8	357	2	S24317	decorin precursor
38	177.5	5.7	2493	2	A55481	adenylate cyclase
39	176.5	5.6	1495	2	T31434	denin-180 - rat
40	175	5.6	343	2	A41748	lumican precursor
41	173	5.5	925	2	JC2033	G protein-coupled
42	172.5	5.5	359	1	NSHUC8	decorin precursor
43	172	5.5	1134	2	T04587	hypothetical prote
44	170.5	5.4	2145	2	T04747	adenylate cyclase
45	170	5.4	907	2	JE0176	orphan G protein-c
46	169.5	5.4	760	2	T06291	extensin homolog T
47	169	5.4	354	2	A55454	decorin precursor
48	169	5.4	839	2	F75518	hypothetical prote
49	168.5	5.4	907	2	JG0193	G protein-coupled
50	167	5.3	800	2	S37387	internalin A precu
51	167	5.3	1112	2	T10504	disease resistance
52	166.5	5.3	549	2	T41744	hypothetical prote
53	166.5	5.3	800	2	AB1129	internalin A limpo
54	165.5	5.3	360	2	S06280	decorin precursor
55	165.5	5.3	526	2	C84552	hypothetical prote
56	165.5	5.3	1256	2	S60461	gene flightless-I
57	165.5	5.3	1268	2	A49674	flightless-I homol
58	165	5.3	994	2	H96510	probable disease r
59	163.5	5.2	786	2	T01456	extensin homolog F
60	162	5.2	249	2	T4791	hypothetical prote
61	161	5.1	559	2	T42998	Ras-binding protei
62	161	5.1	682	2	A49121	cell-surface molec
63	161	5.1	682	2	A43318	connectin precuso
64	160.5	5.1	2910	2	T42214	otogelin - mouse
65	160	5.1	744	2	E86253	hypothetical prote
66	159.5	5.1	1112	2	T00952	hypothetical prote
67	159	5.1	572	2	T30947	protein AC7.2 [imp
68	159	5.1	613	2	A88684	hypothetical prote
69	159	5.1	702	2	T21148	hypothetical prote
70	159	5.1	1119	2	AD1822	leucine-rich-repea
71	158.5	5.1	738	2	T19938	hypothetical prote
72	158	5.0	1066	2	T15864	hypothetical prote
73	158	5.0	3570	2	T45025	mucin MUC5B, trach
74	156.5	5.0	360	2	I47020	decorin - rabbit
75	156.5	5.0	980	2	H84632	probable receptor-
76	156	5.0	354	2	S29145	decorin precursor
77	156	5.0	594	2	T23841	hypothetical prote
78	155.5	5.0	903	2	T00705	N-chimerin homolog
79	155.5	5.0	1334	2	T50568	probable multi-dom
80	155	4.9	961	2	T23395	hypothetical prote
81	154.5	4.9	1013	2	T10659	probable serine/th
82	154.5	4.9	1143	2	T10636	hypothetical prote
83	154.5	4.9	1192	2	T48499	receptor-like prot
84	154.5	4.9	1495	2	S60255	transcription co-r
85	153.5	4.9	864	2	T08575	protein kinase hom
86	153.5	4.9	894	1	A41527	protein-tyrosine k
87	153	4.9	699	2	C43674	US4 protein - huma
88	152	4.8	786	2	T08664	Toll protein-like
89	151.5	4.8	695	1	JN0898	follicotropin recept
90	151	4.8	540	2	T12704	leucine-rich prote
91	151	4.8	1389	2	T13852	gene wheeler prote
92	150.5	4.8	695	1	QRHUF	follicotropin recept
93	150.5	4.8	1109	2	T18536	receptor-like prot
94	150	4.8	1134	1	A29944	chaoptin precursor
95	149.5	4.8	224	2	T32185	hypothetical prote
96	149.5	4.8	696	2	JC7361	follicotropin recept
97	149	4.8	1025	1	A57676	protein kinase Xa2
98	149	4.8	1143	2	B84431	probable receptor
99	149	4.8	2357	2	A59249	class VII unconven
100	148.5	4.7	375	2	S05390	fibromodulin precu
101	148.5	4.7	610	2	T23836	hypothetical prote
102	148.5	4.7	680	2	T19939	hypothetical prote

103	148.5	4.7	890	2	C96654	hypothetical prote	176	136	4.3	4957	2	T03455	ALR protein - huma
104	148.5	4.7	964	2	T49038	hypothetical prote	177	135.5	4.3	427	2	JC4915	ags protein precu
105	148.5	4.7	1115	2	S40241	G protein-coupled	178	135.5	4.3	499	2	DB3333	hypothetical prote
106	148	4.7	338	2	S52284	lumicon, secretory	179	135.5	4.3	1124	2	B84742	probable receptor-
107	148	4.7	1188	2	S49915	extensin-like prot	180	135.5	4.3	5262	2	T03454	ALR protein - huma
108	147.5	4.7	316	2	A41781	proteoglycan-Ib -	181	135	4.3	601	2	S56144	SH3 domain binding
109	147.5	4.7	1385	2	T13887	tlr protein - frui	182	134.5	4.3	613	2	T15489	hypothetical prote
110	147	4.7	1964	2	T29059	notch4 - mouse	183	134.5	4.3	847	2	F96531	hypothetical prote
111	147	4.7	2414	2	A54277	transcription adap	184	134.5	4.3	1039	2	T22117	hypothetical prote
112	146.5	4.7	382	2	T04260	hypothetical prote	185	134	4.3	530	2	A45690	transactivator EBN
113	146.5	4.7	925	2	C84538	probable LRR recep	186	134	4.3	656	2	B47096	hyliB homolog - Str
114	146.5	4.7	1408	2	S16148	gene serrate prote	187	134	4.3	886	2	T40734	probable adenylate
115	146	4.7	369	2	G83434	translocation prot	188	133.5	4.3	277	2	S25770	RSP-1 protein - mo
116	145.5	4.6	380	2	S71876	fibromodulin - chi	189	133.5	4.3	384	2	A41710	promastigote surfa
117	145.5	4.6	886	2	S29605	MHC class III hist	190	133	4.3	1068	2	H96769	hypothetical prote
118	145.5	4.6	2142	2	B35098	hypothetical prote	191	133	4.2	576	2	T36729	probable serine/thr
119	145	4.6	458	2	T19941	hypothetical prote	192	133	4.2	852	2	I51259	tyrosine kinase C
120	145	4.6	679	2	T20713	folitropin recept	193	133	4.2	932	2	T48489	receptor-like prot
121	145	4.6	694	2	JC2237	adenylate cyclase	194	133	4.2	1257	2	A88536	protein B0523.5 [i
122	145	4.6	1839	1	OYBYK	hypothetical prote	195	132.5	4.2	4391	2	A38096	perlecan precursor
123	144.5	4.6	486	2	B86460	nascent polypeptid	196	132.5	4.2	463	1	A36479	milk fat globule m
124	144.5	4.6	2187	2	T30826	BPLF1 protein - hu	197	132.5	4.2	2035	2	A40718	host cell factor C
125	144.5	4.6	3149	1	Q0888	follicle stimulat	198	132	4.2	3164	1	WMBEH6	UL36 protein - hum
126	144	4.6	695	2	I45896	probable disease r	199	131.5	4.2	346	2	T46916	hypothetical prote
127	144	4.6	1019	2	C96519	mucin 2 precursor,	200	131.5	4.2	890	2	T00800	disease resistance
128	144	4.6	3020	2	A43932	promastigote surfa	201	131.5	4.2	1097	2	A29943	Toll protein precu
129	143.5	4.6	243	2	B41710	hypothetical prote	202	131	4.2	612	2	T10727	protein kinase Xa2
130	143.5	4.6	476	2	T27051	hypothetical prote	203	131	4.2	767	2	B84594	probable LRR recep
131	143.5	4.6	496	2	C96832	hypothetical prote	204	131	4.2	905	2	T00475	probable disease r
132	143.5	4.6	605	2	T50817	protein serine/thr	205	131	4.2	915	2	T09575	smoothelin - human
133	143.5	4.6	683	2	T24486	hypothetical prote	206	131	4.2	1095	2	G96746	hypothetical prote
134	142.5	4.5	1870	2	S37671	MHC class III hist	207	131	4.2	1196	2	T09356	brassinosteroid-in
135	142.5	4.5	1872	2	S36152	MHC class III hist	208	131	4.2	448	2	T27395	hypothetical prote
136	142	4.5	661	2	I56258	RP105 - mouse	209	130.5	4.2	268	2	T19697	hypothetical prote
137	142	4.5	983	2	G84524	probable disease r	210	130	4.1	389	2	H86266	hypothetical prote
138	141.5	4.5	462	2	D84858	hypothetical prote	211	130	4.1	395	2	H75457	hypothetical prote
139	141.5	4.5	836	2	T46070	hypothetical prote	212	130	4.1	768	2	T17462	disease resistance
140	141.5	4.5	1029	2	T05050	protein kinase hom	213	130	4.1	800	2	H84740	proline rich prote
141	141.5	4.5	1051	2	T13174	gp150 protein - fr	214	130	4.1	315	2	T06806	hypothetical prote
142	141	4.5	630	2	AC1129	Internalin B [impo	215	129.5	4.1	780	2	T00366	Notch homolog Motc
143	141	4.5	717	2	T33295	fibromodulin precu	216	129.5	4.1	861	2	A48825	brevican precursor
144	140.5	4.5	376	2	S55275	rsu-1 homolog - hu	217	129.5	4.1	912	2	A54423	protein-tyrosine k
145	140	4.5	277	2	I60122	chitinase [EC 3.2.	218	129.5	4.1	942	2	S21251	procr2 - chicken
146	140	4.5	474	2	S65763	probable LRR recep	219	129.5	4.1	1173	2	I50620	basal transcriptio
147	140	4.5	754	2	A85043	protein kinase hom	220	129.5	4.1	1469	2	T09219	promastigote surfa
148	140	4.5	1029	2	T00712	hypothetical prote	221	129.5	4.1	371	2	S20075	probable disease r
149	139.5	4.4	333	2	T34555	hypothetical prote	222	129	4.1	835	2	T05259	hypothetical prote
150	139.5	4.4	527	2	A75399	probable csp prote	223	129	4.1	910	2	B96770	receptor protein k
151	139.5	4.4	539	2	G70520	MEGF1 protein - ra	224	129	4.1	1027	2	B85089	probable Protein k
152	139.5	4.4	4351	2	T00252	insect-stage-speci	225	129	4.1	1064	2	B86465	hypothetical prote
153	139	4.4	581	2	A45551	hypothetical prote	226	129	4.1	1232	2	T05322	probable receptor-
154	139	4.4	603	2	T24315	hypothetical prote	227	129	4.1	1329	2	C84527	hypothetical prote
155	139	4.4	720	2	T02361	hypothetical prote	228	129	4.1	1342	2	A64828	hypothetical prote
156	139	4.4	1088	2	B86312	FltA6.9 protein -	229	129	4.1	1342	2	E85614	cell division prot
157	139	4.4	2240	2	T37057	FltA6.9 protein -	230	129	4.1	1342	2	G90750	cell division prot
158	138.5	4.4	342	2	A46743	lumican precursor	231	129	4.1	1359	1	AGRT	agrin - rat
159	138.5	4.4	990	2	T14756	hypothetical prote	232	129	4.1	2321	2	S78549	notch3 protein - h
160	138.5	4.4	1650	2	S53457	dominant autoantig	233	128.5	4.1	487	2	S42442	nuclear protein EB
161	138	4.4	630	2	C39990	hypothetical prote	234	128.5	4.1	677	2	H86208	protein F2205.26 l
162	138	4.4	858	2	T00258	hypothetical prote	235	128.5	4.1	727	2	C84534	hypothetical prote
163	138	4.4	1952	2	T48814	hypothetical prote	236	128.5	4.1	744	2	C84527	probable receptor-
164	137.5	4.4	1151	2	T18535	high molecular mas	237	128.5	4.1	825	2	T29634	hypothetical prote
165	137.5	4.4	4660	2	T42737	gp330 protein prec	238	128.5	4.1	1113	2	T00271	hypothetical prote
166	137	4.4	562	2	T34319	hypothetical prote	239	128.5	4.1	3968	2	A44265	trithorax homolog
167	137	4.4	695	2	JC1493	folitropin recept	240	128	4.1	597	2	S72468	probable transcrip
168	137	4.4	788	2	AG0786	secreted effector	241	128	4.1	967	2	T48210	hypothetical prote
169	137	4.4	907	1	Q08E21	membrane antigen 9	242	128	4.1	1428	2	T08852	lustrin A - Califo
170	137	4.4	4544	1	S02392	alpha-2-macroglobu	243	128	4.1	1914	2	T42535	tenascin Y precurs
171	137	4.4	4545	1	S25111	alpha-2-macroglobu	244	127.5	4.1	1750	2	D86245	hypothetical prote
172	136	4.3	322	2	S72271	proteoglycan Ib pr	245	127.5	4.1	1120	2	B86479	hypothetical prote
173	136	4.3	626	2	A80123	probable antigenic	246	127.5	4.1	1784	2	C96615	hypothetical prote
174	136	4.3	692	2	A34548	folitropin recept	247	127	4.1	327	2	S20074	promastigote surfa
175	136	4.3	1008	2	D84434	Probable receptor-	248	127	4.1	773	2	T00502	probable receptor-

249	127	4.1	775	1	EDB11	immediate-early pr	322	121.5	3.9	432	2	E96712	unknown protein, 6
250	127	4.1	800	2	G84740	hypothetical prote	323	121.5	3.9	519	2	T07026	ethylene receptor
251	127	4.1	1366	2	T35985	probable large Pro	324	121.5	3.9	635	2	T07794	ethylene receptor
252	127	4.1	1895	2	T06609	disease resistance	325	121.5	3.9	686	2	JC7569	Delta-4 protein -
253	127	4.1	1955	1	AGCH	agrin precursor -	326	121.5	3.9	760	2	F86387	probable Pto kinase
254	126.5	4.0	268	2	T45616	hypothetical prote	327	121.5	3.9	902	2	T00588	hypothetical prote
255	126.5	4.0	685	2	JC7570	Delta-4 protein -	328	121.5	3.9	1251	2	A57293	latent transmembr
256	126.5	4.0	694	2	JC4301	folitropin recept	329	121.5	3.9	1409	2	T37188	presynaptic activi
257	126.5	4.0	862	2	T46289	hypothetical prote	330	121.5	3.9	2265	1	FNBO	fibronectin - bovi
258	126.5	4.0	999	1	S27756	receptor-like prot	331	121.5	3.9	2297	2	T34918	polyketide synthas
259	126.5	4.0	1091	2	S33596	protein-tyrosine k	332	121.5	3.9	2318	2	A53306	notch 3 protein -
260	126.5	4.0	1777	2	T34369	hypothetical prote	333	121.5	3.9	3530	2	A59266	nonconventional myo
261	126	4.0	500	2	S49302	AWJL218 protein -	334	121	3.9	306	2	T52340	cell wall-plasma m
262	126	4.0	865	2	A47282	calcium-binding pr	335	121	3.9	480	2	T00971	probable disease r
263	126	4.0	873	2	A47283	calphotin - fruit	336	121	3.9	485	2	A33647	sulfated surface g
264	126	4.0	996	2	F86410	protein F3M18.12 [337	121	3.9	733	2	A45301	microtubule-associ
265	126	4.0	1152	2	T31911	hypothetical prote	338	121	3.9	1203	2	A49175	Notch B protein -
266	126	4.0	1820	2	A55494	latent transmembr	339	121	3.9	1520	2	T00273	hypothetical prote
267	125.5	4.0	283	2	T13383	hydroxyproline-ric	340	121	3.9	2531	2	S18188	notch protein homo
268	125.5	4.0	548	2	AH1107	internalin H limpo	341	120.5	3.8	299	2	A35272	osteoinductive fac
269	125.5	4.0	635	2	F75477	hypothetical prote	342	120.5	3.8	753	2	JQ0532	OP protein - Kenne
270	125.5	4.0	764	2	A40077	thytotropin recept	343	120.5	3.8	821	2	AB1126	internalin, peptid
271	125.5	4.0	1003	2	T05898	hypothetical prote	344	120.5	3.8	855	2	T17460	disease resistance
272	125	4.0	350	2	S22456	hydroxyproline-ric	345	120.5	3.8	976	2	B84659	probable receptor-
273	125	4.0	476	2	A36478	surface glycoprote	346	120.5	3.8	976	2	T05897	protein kinase hom
274	125	4.0	783	2	T45899	receptor protein k	347	120.5	3.8	981	2	T50851	receptor protein k
275	125	4.0	818	2	F96586	hypothetical prote	348	120.5	3.8	987	2	T50850	receptor protein k
276	125	4.0	991	2	T52400	receptor-like prot	349	120.5	3.8	1118	2	A48292	mucin, tracheobron
277	125	4.0	1504	2	T49896	glycine/proline-ri	350	120.5	3.8	1152	2	A33183	microtubule-associ
278	125	4.0	2026	1	OVBY	adenylate cyclase	351	120.5	3.8	1722	2	E99753	protein FilC7.4 [i
279	124.5	4.0	298	2	B35272	osteoinductive fac	352	120.5	3.8	1778	2	A81116	internalin protein
280	124.5	4.0	756	2	T27642	hypothetical prote	353	120.5	3.8	3566	1	A40701	tenascin-X precurs
281	124.5	4.0	849	2	G97303	hypothetical prote	354	120	3.8	361	2	AH1469	internalin protein
282	124.5	4.0	910	2	G84648	probable disease r	355	120	3.8	376	2	S15558	probable cell wall
283	124.5	4.0	977	2	G86745	hypothetical prote	356	120	3.8	458	2	T31631	hypothetical prote
284	124.5	4.0	1223	2	E88451	protein K10D2.1 [i	357	120	3.8	892	2	T09071	SH3 domains-contai
285	124.5	4.0	2176	2	T13806	toucan gene protei	358	120	3.8	962	2	T04124	receptor-like prot
286	124	4.0	496	2	D75261	conserved hypothet	359	120	3.8	1126	2	T20801	hypothetical prote
287	124	4.0	543	2	S35047	mucin JUL7 - human	360	120	3.8	1224	2	T40765	webi protein homol
288	124	4.0	574	2	T43556	Wiskott-Aldrich sy	361	119.5	3.8	267	2	S08314	cell wall glycopro
289	124	4.0	605	2	AG0123	probable antigenic	362	119.5	3.8	479	1	A31753	transcription fact
290	124	4.0	729	2	E70803	hypothetical prote	363	119.5	3.8	660	2	T45569	receptor protein k
291	124	4.0	766	2	B85440	receptor kinase-li	364	119.5	3.8	1048	1	XPBEA9	large structural p
292	124	4.0	978	2	E96787	protein T4012.5 [i	365	119.5	3.8	1079	2	C96772	probable receptor
293	124	4.0	1011	2	T45718	receptor-kinase li	366	119.5	3.8	1166	2	F96598	protein F20N2.4 [i
294	124	4.0	1472	2	B54774	ATP binding casses	367	119.5	3.8	1400	2	B70963	hypothetical prote
295	124	4.0	4135	2	T42629	tenascin-X - bovin	368	119.5	3.8	1596	2	A35927	190K DNA-binding p
296	123.5	3.9	380	2	T01281	probable leucine-r	369	119.5	3.8	1643	2	T14274	versican precursor
297	123.5	3.9	492	2	F86263	hypothetical prote	370	119	3.8	164	2	I33641	mucin SAC - human
298	123.5	3.9	656	2	AE1479	probable cell surf	371	119	3.8	352	2	S49299	AWJL172 protein -
299	123.5	3.9	690	2	T41296	probable alcohol d	372	119	3.8	424	2	S27783	hypothetical prote
300	123	3.9	528	2	T15198	hypothetical prote	373	119	3.8	550	2	C75557	hypothetical prote
301	123	3.9	574	2	T38819	wiskott-aldrich sy	374	119	3.8	651	2	T42644	hypothetical prote
302	123	3.9	888	2	S23065	ufo protein - mous	375	119	3.8	660	1	QBEB3	BHLF1 protein - hu
303	123	3.9	1072	2	A37127	microtubule-associ	376	119	3.8	808	2	T23129	hypothetical prote
304	123	3.9	2591	2	T30288	pristinamycin I sy	377	119	3.8	864	2	D84740	hypothetical prote
305	122.5	3.9	303	2	S28264	hydroxyproline-xic	378	119	3.8	1006	2	T42731	atrophin-1 relate
306	122.5	3.9	415	2	T13435	hypothetical prote	379	119	3.8	1045	2	T41119	internalin- relate
307	122.5	3.9	592	2	D70863	hypothetical prote	380	118.5	3.8	222	2	H96711	hypothetical prote
308	122.5	3.9	699	2	T05225	extensin homolog F	381	118.5	3.8	400	1	A39822	leukosialin precu
309	122.5	3.9	809	2	B84634	probable receptor-	382	118.5	3.8	677	2	E70722	hypothetical prote
310	122.5	3.9	845	2	T12537	hypothetical prote	383	118.5	3.8	751	2	AC2098	hypothetical prote
311	122.5	3.9	1016	2	T30553	disease resistance	384	118.5	3.8	869	2	A71400	probable disease r
312	122.5	3.9	2944	2	A54849	collagen alpha 1(V	385	118.5	3.8	883	2	S57653	brevican precursor
313	122	3.9	298	2	JC4130	osteoglycin precu	386	118.5	3.8	988	2	T45717	receptor-kinase li
314	122	3.9	326	2	T24722	hypothetical prote	387	118.5	3.8	1173	2	T25893	hypothetical prote
315	122	3.9	596	2	AE1515	internalin like pr	388	118.5	3.8	1356	2	A45445	janusin precursor,
316	122	3.9	623	2	T19876	hypothetical prote	389	118.5	3.8	1607	2	T02837	long chain fatty a
317	122	3.9	672	2	B84782	probable receptor-	390	118	3.8	294	2	A37232	mucin, tracheal (A
318	122	3.9	715	2	G86239	protein F20B24.6 [391	118	3.8	599	2	T10798	perlecan-S - Vo
319	122	3.9	719	2	T47727	hypothetical prote	392	118	3.8	667	2	S74254	homeotic protein s
320	122	3.9	921	2	B62334	hypothetical prote	393	118	3.8	823	2	AD1935	general secretion
321	122	3.9	992	2	T05335	hypothetical prote	394	118	3.8	1134	1	JN0711	protein-tyrosine k

395	118	3.8	2471	2	A49128	cell-fate determin	458	114	3.6	378	2	S00842	leukosialin precu
396	117.5	3.7	473	2	D85041	hypothetical prote	459	114	3.6	413	1	A34888	transcription fact
397	117.5	3.7	624	2	A55576	collagen alpha 2(X	470	114	3.6	555	1	S20100	mullerian inhibiti
398	117.5	3.7	660	2	JW0067	chitinase (EC 3.2.	471	114	3.6	586	2	T29695	hypothetical prote
399	117.5	3.7	996	2	T10725	protein kinase Xa2	472	114	3.6	633	2	S62057	proline-rich prote
400	117.5	3.7	1075	2	D70568	hypothetical prote	473	114	3.6	634	2	T00388	hypothetical prote
401	117.5	3.7	1706	2	I84499	zinc finger protei	474	114	3.6	656	2	E75468	hypothetical prote
402	117	3.7	431	2	T27904	hypothetical prote	475	114	3.6	768	2	A42755	p-selectin precurs
403	117	3.7	431	1	A46688	hepatocyte growth	476	114	3.6	1290	2	T00018	period protein hom
404	117	3.7	655	1	H96707	probable receptor	477	114	3.6	2225	2	T26063	hypothetical prote
405	117	3.7	678	2	JC4245	transcription fact	478	113.5	3.6	317	2	S55316	myc (clone PGM-2
406	117	3.7	743	2	C84633	probable disease r	479	113.5	3.6	330	2	T46256	brevican - human (
407	117	3.7	801	2	T29018	hypothetical prote	480	113.5	3.6	538	2	T01102	disease resistance
408	117	3.7	1007	2	C84668	probable receptor-	481	113.5	3.6	896	2	B43817	transforming prote
409	117	3.7	1009	2	D75399	probable penicilli	482	113.5	3.6	907	2	A86460	99.9K hypothetical
410	117	3.7	1328	2	T43060	agrin - electric r	483	113.5	3.6	938	1	Q0BE24	nuclear antigen EB
411	117	3.7	1450	2	T32073	hypothetical prote	484	113.5	3.6	1286	2	T33476	hypothetical prote
412	117	3.7	1574	2	T13954	MEGF6 protein - ra	485	113.5	3.6	1907	2	S50893	protein-tyrosine-p
413	117	3.7	2082	2	T37056	probable multi-dom	486	113.5	3.6	2911	2	T05666	hypothetical prote
414	117	3.7	2232	2	T34434	hypothetical prote	487	113	3.6	371	2	T49908	hypothetical prote
415	116.5	3.7	279	2	S53363	myc SAC (clone J	488	113	3.6	377	2	A48018	hypothetical prote
416	116.5	3.7	439	2	S51939	chitinase (EC 3.2.	489	113	3.6	382	2	E84527	hypothetical prote
417	116.5	3.7	621	2	I38467	low density lipopr	490	113	3.6	419	2	A90888	hypothetical prote
418	116.5	3.7	787	2	T27632	hypothetical prote	491	113	3.6	419	2	H85729	hypothetical prote
419	116.5	3.7	794	2	T27633	hypothetical prote	492	113	3.6	603	2	A75373	probable N-acetyl
420	116.5	3.7	828	2	A88860	protein ZC518.3 [i	493	113	3.6	979	2	A35913	regulatory factor
421	116.5	3.7	1048	1	A45344	C-terminal domain-	494	113	3.6	982	2	A53253	microtubule-associ
422	116.5	3.7	1446	1	A45344	immediate-early pr	495	113	3.6	1002	2	T46033	receptor protein k
423	116.5	3.7	2229	2	T16199	hypothetical prote	496	113	3.6	1025	2	T45647	receptor protein k
424	116	3.7	232	2	S24169	myc - rat	497	113	3.6	1069	2	S27922	nuclear antigen EB
425	116	3.7	652	2	S71753	repellent protein	498	113	3.6	1247	2	T42209	neural plakophilin
426	116	3.7	660	2	A82348	hypothetical prote	499	113	3.6	1343	2	AF0611	cell division prot
427	116	3.7	729	2	H66308	Similar to disease	500	113	3.6	2688	2	I49477	alpha-A-crystallin
428	116	3.7	771	2	T02565	disease resistance	501	113	3.6	3381	2	T42389	versican precursor
429	116	3.7	808	2	B97303	hypothetical prote	502	112.5	3.6	347	2	S10571	myc 1 precursor,
430	116	3.7	845	2	T07039	Hcr9-0 protein - t	503	112.5	3.6	581	2	G68811	unknown protein T1
431	116	3.7	907	2	A24938	hypothetical T2 pr	504	112.5	3.6	731	2	B63169	hypothetical prote
432	116	3.7	1291	2	T00019	period protein hom	505	112.5	3.6	1075	2	A57377	transcription fact
433	116	3.7	1494	2	T14355	protein-tyrosine-p	506	112.5	3.6	1237	2	AC1583	transcription fact
434	116	3.7	1840	2	T30250	GT1 protein - mous	507	112.5	3.6	1680	2	T01367	internalin protein
435	116	3.7	2531	2	A46019	notch-1 protein -	508	112.5	3.6	2479	2	H87386	hypothetical prote
436	116	3.7	2555	2	A40343	notch protein homo	509	112.5	3.6	4006	2	T09070	conserved hypotet
437	116	3.7	2774	2	A40359	microtubule-associ	510	112	3.6	241	2	S32359	probable tenascin
438	115.5	3.7	322	2	A53715	apomucin precursor	511	112	3.6	252	2	T01787	glial growth facto
439	115.5	3.7	513	2	AC3061	hypothetical prote	512	112	3.6	253	1	JC1319	thyrotropin recept
440	115.5	3.7	513	2	D98225	hypothetical prote	513	112	3.6	285	2	A41826	thyrotropin recept
441	115.5	3.7	528	2	I47141	gastric mucin (clo	514	112	3.6	383	2	S53716	probable pheromone
442	115.5	3.7	696	2	T42559	hypothetical prote	515	112	3.6	413	2	S48756	delta-like homeoti
443	115.5	3.7	805	2	T49385	hypothetical prote	516	112	3.6	704	2	AE2107	transcription fact
444	115.5	3.7	946	2	S27921	hypothetical prote	517	112	3.6	731	2	T04455	serine/threonine k
445	115.5	3.7	1093	2	T38533	nuclear antigen EB	518	112	3.6	742	2	F84643	hypothetical prote
446	115.5	3.7	1268	2	S52781	AF17 protein - hum	519	112	3.6	764	1	QRHURH	thyrotropin recept
447	115.5	3.7	1460	1	EDBE1F	neurocan - mouse	520	112	3.6	883	2	S49126	hypothetical prote
448	115.5	3.7	2214	2	T16305	immediate-early pr	521	112	3.6	960	2	G84652	brevican precursor
449	115.5	3.7	3421	1	WZBE86	hypothetical prote	522	112	3.6	990	2	T03784	probable receptor-
450	115	3.7	404	2	T08549	367K tegument prot	523	112	3.6	1032	2	T34433	hypothetical prote
451	115	3.7	451	2	S74728	hypothetical prote	524	112	3.6	1289	2	AB2217	hypothetical prote
452	115	3.7	461	2	S22542	hypothetical prote	525	111.5	3.6	224	2	D72861	AcOrf-91 protein -
453	115	3.7	473	1	S22542	transcription fact	526	111.5	3.6	224	2	D72861	gene BCRF2 protein
454	115	3.7	539	2	AH1216	extensin-like prot	527	111.5	3.6	383	2	S32975	transcription fact
455	115	3.7	766	2	T01817	transcription fact	528	111.5	3.6	478	1	I47154	transcription fact
456	115	3.7	838	2	T08423	internalin, probab	529	111.5	3.6	645	2	T05251	probable disease r
457	115	3.7	980	2	T05414	hypothetical prote	530	111.5	3.6	649	2	T46500	hypothetical prote
458	115	3.7	1133	2	E86308	protein kinase hom	531	111.5	3.6	1047	2	A55817	thyrotropin recept
459	115	3.7	1220	2	A56136	jagged protein pre	532	111.5	3.6	1253	2	T45787	immediate-early pr
460	114.5	3.7	328	2	JQ0985	aggregran precursor	533	111.5	3.6	1298	1	EDBE75	restriccin precurs
461	114.5	3.7	409	2	T11743	pp47 protein - pig	534	111.5	3.6	1353	1	JH0675	hypothetical prote
462	114.5	3.7	505	2	AC1469	internalin like pr	535	111.5	3.6	2649	2	T51023	heart-restricted l
463	114.5	3.7	606	2	T51880	hypothetical prote	536	111	3.5	274	2	JC8063	hypothetical prote
464	114.5	3.7	627	2	T27123	hypothetical prote	537	111	3.5	478	2	H86459	hypothetical prote
465	114.5	3.7	638	2	T05606	protein kinase hom	538	111	3.5	509	2	T05260	probable disease r
466	114.5	3.7	638	2	T05606	disease resistance	539	111	3.5	518	2	S50465	PAC2 protein - yea
467	114	3.6	218	2	T01104		540	111	3.5	548	2	E70546	hypothetical prote
										603	2	S28941	coagulation factor

541 111 3.5 610 2 S35049 mucin JER57 - huma
542 111 3.5 620 2 T50150 yeast nrd1-like pr
543 111 3.5 699 1 QRHUUT lutropin-choriogon
544 111 3.5 853 2 T17461 disease resistance
545 111 3.5 932 2 T21338 hypohetical prote
546 111 3.5 984 2 T48216 retinoblastoma bin
547 111 3.5 1721 1 I38902 xotchin protein - Af
548 111 3.5 2524 2 A35844 tyrosine decarboxy
549 110.5 3.5 359 2 C55066 neural cell adhesi
550 110.5 3.5 421 2 A60058 Hypohetical 55.6
551 110.5 3.5 512 2 G86459 neurotrophin-3 rec
552 110.5 3.5 525 1 A58674 aromatic-L-amino-a
553 110.5 3.5 533 2 T07970 Prizzled-2 protei
554 110.5 3.5 565 2 JEO338 leucine-rich repea
555 110.5 3.5 684 2 T01267 neurotrophin-3 rec
556 110.5 3.5 803 1 S35695 extracellular sign
557 110.5 3.5 815 2 B56708 Cf-4A protein - to
558 110.5 3.5 855 2 T07015 hypohetical prote
559 110.5 3.5 872 2 S33015 hypohetical prote
560 110.5 3.5 922 2 A31666 hypohetical prote
561 110.5 3.5 1207 2 T00378 K1AA0641 protein -
562 110.5 3.5 1295 2 A32901 glp1 protein precu
563 110.5 3.5 1344 2 T14316 rig-1 protein - mo
564 110.5 3.5 1346 2 T17412 polyketide synthas
565 110.5 3.5 1736 2 T00391 hypohetical prote
566 110.5 3.5 2476 2 T34022 zonadhesin - pig
567 110 3.5 275 2 T51437 hypohetical prote
568 110 3.5 391 2 T04609 hypohetical prote
569 110 3.5 549 2 S32987 hypohetical prote
570 110 3.5 691 2 D84889 probable receptor-
571 110 3.5 708 2 D96711 hypohetical prote
572 110 3.5 719 2 T02154 protein kinase hom
573 110 3.5 764 2 I48882 thyrotropin recept
574 110 3.5 846 2 H70599 hypohetical prote
575 110 3.5 846 2 T21700 hypohetical prote
576 110 3.5 951 2 A96770 hypohetical prote
577 110 3.5 1123 2 D96756 receptor-like prot
578 110 3.5 1483 2 E86143 F6F3.12 protein -
579 110 3.5 1711 1 A55148 protein-tyrosine-p
580 110 3.5 2703 1 A24420 notch protein - fr
581 110 3.5 2715 2 T13049 eyelid - fruit fly
582 110 3.5 342 2 T42730 Bassoon protein -
583 109.5 3.5 213 2 A86228 hypohetical prote
584 109.5 3.5 279 2 T10361 hypohetical prote
585 109.5 3.5 318 2 T29479 hypohetical prote
586 109.5 3.5 428 2 E71415 probable coll wall
587 109.5 3.5 473 2 S36553 I2 protein - huma
588 109.5 3.5 507 2 T44768 antifreeze glycope
589 109.5 3.5 538 2 S57459 hook-containing pr
590 109.5 3.5 558 2 JCS878 plasma hyaluronan-
591 109.5 3.5 583 1 S22544 transcription fact
592 109.5 3.5 612 2 I73633 gene trkC protein
593 109.5 3.5 825 2 A55178 neurotrophin recep
594 109.5 3.5 839 1 I73632 neurotrophin-3 rec
595 109.5 3.5 874 2 E97302 hypohetical prote
596 109.5 3.5 878 2 T21621 hypohetical prote
597 109.5 3.5 954 2 T19765 hypohetical prote
598 109.5 3.5 1299 2 T47182 hypohetical prote
599 109.5 3.5 1776 1 RRWPYM genome polypeptid
600 109.5 3.5 2531 2 T31070 notch homolog - se
601 109.5 3.5 2717 2 A34203 DNA-binding protei
602 109 3.5 379 2 T05441 proline-rich prote
603 109 3.5 379 2 D85257 extensin-like prot
604 109 3.5 395 2 I52842 CD43 Lp-3 antigen
605 109 3.5 395 2 A43545 leukostalin CD43 p
606 109 3.5 403 2 S52796 prp2 protein - hu
607 109 3.5 426 2 JQ1696 pistil extensin-11
608 109 3.5 431 2 T04868 hypohetical prote
609 109 3.5 437 2 A54595 transcription fact
610 109 3.5 598 2 C96756 receptor-like prot
611 109 3.5 613 2 T42671 hypohetical prote
612 109 3.5 833 2 S19087 gene Delta protein
613 109 3.5 1611 2 T38236 hypohetical prote

2809 2 T30213 G-cadherin - sea u
308 2 JC7125 epidermal growth f
389 2 S27200 proline-rich prote
402 2 A84581 probable disease r
418 2 T15142 hypohetical prote
499 2 A11107 internatin E limpo
514 2 H70699 probable ppp prote
548 1 I37577 islet cell antigen
662 2 A45155 mucin FIM-C.1 - Af
698 2 I39713 celB protein - Agr
710 1 Q0BE22 membrane antigen g
740 2 B84741 hypohetical prote
756 2 G86308 Similar to disease
764 2 A35956 thyrotropin recept
783 1 A38637 Ras interactor RIN
825 1 A40026 neurotrophin-3 rec
855 2 C82983 hypohetical prote
1011 2 C84524 probable disease r
1125 2 B41206 microtubule-associ
1176 2 T49482 hypohetical prote
1384 2 G01763 atrophin-1 - huma
1357 2 T29265 mucin 1 precursor,
1487 2 T02850 hypohetical prote
3707 2 S18252 heparan sulfate pr
348 2 JQ0431 flagellar hook-len
409 2 AG0752 hypohetical 35.5K
511 1 VGBE1K glycoprotein C - h
542 2 I39540 chitinase [EC 3.2.
544 2 T17547 proline-rich prote
550 2 T36746 probable serine/th
638 1 XXAV dihydroilpoamide S
741 2 T05250 veracan - pig-tai
862 2 S43922 probable disease r
996 2 JE0237 apolipoprotein E r
1017 2 T31354 probable potassium
1217 2 T51140 disease resistance
1414 2 A41948 alpha-fetoprotein
3511 2 A59295 unconventinal myo
4613 2 T17409 polyketide synthas
7576 2 T17428 FK506 polyketide s
363 2 H87702 hypohetical prote
369 2 S20500 hydroxyproline-ric
414 2 C96770 hypohetical prote
427 2 S74211 PAS-6/7 protein pr
536 2 H71563 hypohetical prote
604 2 S25203 smr protein - Str
655 2 G96524 protein T1N15.9 [1
832 2 A31246 neurogenic protein
880 2 S00670 neurogenic repetit
881 2 B98320 cellulose synthase
1009 2 T45645 receptor kinase-li
1099 2 A56155 tumor suppressor P
1206 2 S24407 formin isoform IV
1324 2 S52863 DNA-binding protei
1468 2 T11515 formin - mouse
3534 2 T42567 tegument protein 2
176 1 A46606 platelet glycoprot
228 2 S23504 extensin-like prot
273 2 A28512 fibronectin - chic
354 2 A48931 transmembrane gly
358 1 WMBE38 infected cell prot
416 1 SKXLAG dermal gland prote
447 2 A39321 mucin - rat (fragm
452 2 C41602 transcription fact
518 2 F75460 hypohetical prote
615 1 KFHU12 coagulation factor
650 2 S59630 dysroglycan alpha
840 1 S69204 pheromone response
915 2 T12526 hypohetical prote
1063 1 GNWVR4 structural polypro
1376 2 G00043 osteonitrogen - hum

687	3.4	1389	2	I58157	periaxin - rat	760	105	3.3	1133	2	A54164	sterol regulatory
688	107	2723	2	T03221	probable polyketid	761	105	3.3	1135	2	T30561	Scythe protein - A
689	107	7463	2	T36248	CDA peptide synthe	762	105	3.3	1136	1	S57845	protein-tyrosine k
690	106.5	304	2	A23993	transcription fact	763	105	3.3	1456	2	T01397	LTR gag/pol polypr
691	106.5	353	2	A41558	N-syndecan - rat (764	105	3.3	1658	2	D75489	hypothetical prote
692	106.5	505	2	B46629	mucin 6, gastric (765	105	3.3	1844	2	S01956	hypothetical prote
693	106.5	509	2	D86911	conserved hypothet	766	105	3.3	2133	2	T30637	hypothetical prote
694	106.5	509	2	T10013	probable phosphopr	767	105	3.3	2409	1	A50979	vesicular precursor
695	106.5	517	2	AD1570	internalin, probab	768	105	3.3	2769	1	UIBO	thyroglobulin prec
696	106.5	620	2	S06733	hydroxyproline-ric	769	104.5	3.3	329	2	T17033	leucine rich repea
697	106.5	827	2	A23963	cellB protein (limp	770	104.5	3.3	407	2	C70816	hypothetical prote
698	106.5	925	2	H96638	protein TIF9.20 li	771	104.5	3.3	464	2	T35943	probable hydrolyti
699	106.5	998	2	C75489	conserved hypothet	772	104.5	3.3	530	2	T32812	hypothetical prote
700	106.5	1003	2	T13856	ksr protein - frui	773	104.5	3.3	639	2	G02919	transcription fact
701	106.5	1161	2	S57180	probable membrane	774	104.5	3.3	662	2	T04856	hypothetical prote
702	106.5	1184	2	S08332	atrophin-1 - human	775	104.5	3.3	700	2	A42395	luteolin receptor
703	106.5	1305	2	AB0168	probable cell divi	776	104.5	3.3	707	1	A34458	gelatinase B (EC 3
704	106.5	1442	2	T42607	transcription acti	777	104.5	3.3	707	1	A53796	gelatinase B (EC 3
705	106.5	1892	2	T18314	hypothetical prote	778	104.5	3.3	744	2	T35192	probable ABC trans
706	106.5	2090	2	S26058	hypothetical prote	779	104.5	3.3	755	2	T20950	hypothetical prote
707	106.5	2453	2	S60254	nuclear receptor c	780	104.5	3.3	909	1	QRXLL1	LDL receptor 1 pre
708	106	135	2	T42996	AtGRP4 - Arabidops	781	104.5	3.3	960	1	S28262	kinesin-related pr
709	106	167	2	A33532	mucin SMUC-40 - hu	782	104.5	3.3	1117	2	JC4934	delta-crystallin/E
710	106	216	2	I51920	mucin - rhesus mac	783	104.5	3.3	1194	2	E96624	hypothetical prote
711	106	287	2	S65765	chitinase (EC 3.2.	784	104.5	3.3	1241	2	T37190	nephlin - human
712	106	405	2	S78691	flagellar hook-len	785	104.5	3.3	1505	2	JC4851	hypoxia-inducible
713	106	431	2	S47538	acrosin (EC 3.4.21	786	104.5	3.3	1851	2	T19964	leukocyte antigen-
714	106	435	2	D41602	transcription fact	787	104.5	3.3	1898	2	S46216	CDA peptide synthe
715	106	443	2	B39794	transcription fact	788	104.5	3.3	2117	2	T36180	larval glue protei
716	106	449	2	A24993	cellulase (EC 3.2.	789	104	3.3	232	2	A60095	lymphotoxin-beta -
717	106	567	2	A45977	Rab geranylgeranyl	790	104	3.3	306	2	I49139	hypothetical prote
718	106	666	2	B70803	gag polypeptide -	791	104	3.3	318	2	B64900	CD68 homolog macro
719	106	701	2	D48613	hypothetical prote	792	104	3.3	326	2	A46676	protein phosphatas
720	106	818	2	T01105	disease resistance	793	104	3.3	332	2	S43988	sds22 protein homo
721	106	822	2	T51049	related to nucleol	794	104	3.3	360	2	S68209	serum response fac
722	106	850	2	S56015	gastric mucin MUC5	795	104	3.3	365	2	A39481	protein W10G11.6 l
723	106	901	2	A49227	sialidase - Actino	796	104	3.3	426	2	D88103	glyceroldehyde-3-p
724	106	914	2	T17233	fibropellin Ia - s	797	104	3.3	440	2	I49681	l2 protein - human
725	106	1064	2	A40136	gag/pol polypeptei	798	104	3.3	470	2	S36536	myosin-binding pro
726	106	1603	2	A48613	hypothetical prote	799	104	3.3	537	2	A46611	chitinase (EC 3.2.
727	106	1958	2	B40505	kinase-related pro	800	104	3.3	538	2	S65764	glycoprotein G - s
728	106	2554	1	TVFF7L	Bassoon protein -	801	104	3.3	593	2	S49525	gelatinase B (EC 3
729	106	3938	2	T42761	leucine-rich repea	802	104	3.3	712	1	I46031	dystrophin-associa
730	105.5	395	2	T01392	DNA-binding protei	803	104	3.3	895	2	S20582	hypothetical prote
731	105.5	486	2	A41537	probable disease r	804	104	3.3	927	2	T24031	hypothetical prote
732	105.5	510	2	A42750	protein kinase hom	805	104	3.3	1045	2	T16275	blackjack protein,
733	105.5	668	2	T05257	amphiphysin (Clon	806	104	3.3	1547	2	T28657	synaptotagmin, 170K
734	105.5	688	2	T04568	KIAA0992 protein -	807	104	3.3	1575	2	S68448	1,4-beta-glucanase
735	105.5	695	2	S62400	HF-1 regulatory el	808	104	3.3	1711	2	T31337	tensin, cardiac mu
736	105.5	772	2	T13078	hypothetical prote	809	104	3.3	1744	2	A54370	hypothetical prote
737	105.5	780	2	A48143	MHC class III hist	810	104	3.3	3507	2	T34513	platelet glycoprot
738	105.5	952	2	S32954	hypothetical prote	811	103.5	3.3	206	1	NBHUIB	pistil extensin-li
739	105.5	1132	2	A35098	hypothetical prote	812	103.5	3.3	264	2	PQ0478	hypothetical prote
740	105.5	1172	2	T00065	hypothetical prote	813	103.5	3.3	281	2	D70845	pistil extensin-li
741	105.5	1621	2	T15264	masking protein pr	814	103.5	3.3	333	2	PQ0479	platelet glycoprot
742	105.5	1712	2	A38261	genome polypeptei	815	103.5	3.3	411	1	I55604	hypothetical prote
743	105.5	1839	1	RWPBPM	fibronectin precur	816	103.5	3.3	419	2	T49292	transcription fact
744	105.5	2477	2	S14428	genome polypeptei	817	103.5	3.3	444	1	A39794	P49 secreted prote
745	105.5	3033	1	QJ01303	hypothetical prote	818	103.5	3.3	489	2	F75591	nicotinic acetylch
746	105	349	2	T05857	hypothetical prote	819	103.5	3.3	625	2	A26456	hypothetical prote
747	105	422	2	I37891	interleukin-11 rec	820	103.5	3.3	654	2	T33044	hypothetical prote
748	105	454	2	E75291	probable cell wall	821	103.5	3.3	869	2	T20123	hypothetical prote
749	105	460	2	T33110	hypothetical prote	822	103.5	3.3	889	2	T00353	hypothetical prote
750	105	486	1	A57601	transcription fact	823	103.5	3.3	975	2	I48974	receptor-protein t
751	105	511	1	VGBEF4	glycoprotein C - h	824	103.5	3.3	980	2	S54986	fibronectin - chic
752	105	566	2	T34842	probable transfe	825	103.5	3.3	1020	2	A29355	TMV resistance pro
753	105	620	2	A70525	hypothetical prote	826	103.5	3.3	1144	2	A54810	hypothetical prote
754	105	658	2	T08153	cysteine protease	827	103.5	3.3	1171	2	T35548	hypothetical prote
755	105	730	2	JC1456	gelatinase B (EC 3	828	103.5	3.3	1268	2	T31420	C-terminal domain-
756	105	764	2	JC5643	thyroid stimulat	829	103.5	3.3	1590	2	B86398	protein TTN9.24 fi
757	105	847	1	A33800	mixed-lineage prot	830	103.5	3.3	1603	2	S23810	collagen alpha 1(I
758	105	895	2	I54343	dystroglycan - hum	831	103.5	3.3	1638	2	A42091	transcription acti
759	105	976	2	A36355	protein-tyrosine k	832	103.5	3.3				

833	103.5	3.3	1733	1	B45344	probable nuclear a	906	102	3.3	567	2	JC5538	Rab geranylgeranyl
834	103.5	3.3	3739	2	T17410	polyketide synthas	907	102	3.3	585	1	B70747	probable serine/th
835	103	3.3	168	2	S52994	arabinogalactan-li	908	102	3.3	650	2	B87791	protein B0207.1 (i
836	103	3.3	191	2	E84740	hypothetical prote	909	102	3.3	670	2	T22293	zinc finger protei
837	103	3.3	227	2	T27905	hypothetical prote	910	102	3.3	715	2	T12534	hypothetical prote
838	103	3.3	263	2	S01360	salivary glue prot	911	102	3.3	722	2	I48324	DELTA-like 1 mou
839	103	3.3	362	2	A44083	meq protein - Mare	912	102	3.3	728	2	D86278	hypothetical prote
840	103	3.3	367	2	AC1328	internalin protein	913	102	3.3	890	2	E84846	hypothetical recep
841	103	3.3	379	2	T16213	APX-1 protein homo	914	102	3.3	896	1	A35782	cytokine receptor
842	103	3.3	394	2	C84905	probable extensin	915	102	3.3	923	2	A39596	progesterone recep
843	103	3.3	515	2	F70904	hypothetical prote	916	102	3.3	963	2	A55926	DNA binding protei
844	103	3.3	535	1	S76953	protein kinase (EC	917	102	3.3	1008	2	T04462	hypothetical prote
845	103	3.3	550	2	G70597	probable proteinas	918	102	3.3	1021	2	H75423	hypothetical prote
846	103	3.3	575	2	JG0181	Kill2 protein - hu	919	102	3.3	1032	2	D83637	serine/threonine p
847	103	3.3	611	2	B86387	unknown protein (i	920	102	3.3	1052	2	B49120	protein-tyrosine k
848	103	3.3	648	2	T35120	hypothetical prote	921	102	3.3	1069	2	D85383	hypothetical prote
849	103	3.3	701	2	F48613	gag polyprotein -	922	102	3.3	1137	2	A86335	T20H2.9 protein -
850	103	3.3	793	2	JC7390	thyroid stimulatn	923	102	3.3	1166	2	T13958	syncAP-bl protein
851	103	3.3	799	1	TVRTTB	nerve growth facto	924	102	3.3	1249	2	T14270	Ras-GTPase activat
852	103	3.3	813	2	T04313	protein kinase Xa2	925	102	3.3	1293	2	T14259	ras GTPase activat
853	103	3.3	851	2	S67285	NUD1 protein - yea	926	102	3.3	1692	2	A33988	adenylate cyclase
854	103	3.3	863	2	A55173	cf-9 protein precu	927	102	3.3	1985	2	S19151	hypothetical prote
855	103	3.3	915	2	S36327	clathrin assembly	928	102	3.3	2218	2	B84683	hypothetical prote
856	103	3.3	1040	2	T29092	TSC-22 protein hom	929	102	3.3	2437	2	S42612	transmembrane prot
857	103	3.3	1121	2	A82809	exodeoxyribonuclea	930	102	3.3	2440	2	S39162	transcription coac
858	103	3.3	1199	2	A40670	nuclear envelope p	931	102	3.3	2441	2	S39161	CREB-binding prote
859	103	3.3	1201	2	G86441	unknown protein (i	932	102	3.3	3124	2	A40020	collagen alpha 1(X
860	103	3.3	1275	2	T33369	hypothetical prote	933	102	3.3	5147	1	IJFPTM	cadherin-related t
861	103	3.3	1340	2	A39808	proteoglycan core	934	101.5	3.2	98	2	S53367	mucin SAC (clone M
862	103	3.3	1541	2	T02831	AAA protein L4171.	935	101.5	3.2	173	2	T47176	hypothetical prote
863	103	3.3	1894	2	C54689	protein-tyrosine-p	936	101.5	3.2	244	2	A40428	nonspecific cross-
864	103	3.3	2207	1	GNNY5P	genome polyprotein	937	101.5	3.2	372	2	T29359	hypothetical prote
865	103	3.3	2481	2	A43908	fibronectin - Afri	938	101.5	3.2	409	2	T43599	yop targeted effec
866	103	3.3	3133	2	S52093	hemocytin - silkw	939	101.5	3.2	547	2	B56573	nuclear pore compl
867	102.5	3.3	217	2	S01358	salivary glue prot	940	101.5	3.2	654	2	C87587	hypothetical prote
868	102.5	3.3	252	2	T04739	hypothetical prote	941	101.5	3.2	657	2	B84869	probable Sfl6 prot
869	102.5	3.3	316	2	T31880	hypothetical prote	942	101.5	3.2	710	2	T44753	hypothetical prote
870	102.5	3.3	338	2	I53043	transforming prote	943	101.5	3.2	728	2	I50719	C-Delta-1 - chicke
871	102.5	3.3	352	2	S17313	transcription fact	944	101.5	3.2	733	2	A87168	conserved hypotet
872	102.5	3.3	371	2	F70555	hypothetical prote	945	101.5	3.2	833	2	AF2089	hypothetical prote
873	102.5	3.3	379	2	S31719	proline-rich prote	946	101.5	3.2	869	2	A55384	transcription fact
874	102.5	3.3	383	2	B62722	protein F16A14.12	947	101.5	3.2	921	2	S40495	collagen alpha 1(I
875	102.5	3.3	385	2	S53718	homeotic protein d	948	101.5	3.2	947	2	G86420	probable receptor-
876	102.5	3.3	385	2	A54785	preadipocyte facto	949	101.5	3.2	977	2	I52657	seizure-related pr
877	102.5	3.3	421	2	T30709	core protein homol	950	101.5	3.2	984	1	A34076	protein-tyrosine k
878	102.5	3.3	507	1	A32385	erythropoietin rec	951	101.5	3.2	1034	2	JC5569	serine proteinase
879	102.5	3.3	627	2	D75393	serine proteinase,	952	101.5	3.2	1039	2	A85096	hypothetical prote
880	102.5	3.3	674	2	T05264	probable serine/ch	953	101.5	3.2	1429	2	S06434	homeotic protein 1
881	102.5	3.3	706	2	S04411	synapsin Ia - bowi	954	101.5	3.2	1668	2	T13748	sex comb protein -
882	102.5	3.3	730	1	I52580	gelatinase B (EC 3	955	101.5	3.2	1733	2	S27939	tensin - chicken
883	102.5	3.3	760	1	S07896	transcription fact	956	101.5	3.2	4543	1	A53102	alpha-2-macroglobu
884	102.5	3.3	904	2	T46170	disease resistance	957	101	3.2	240	2	B24264	proline-rich prote
885	102.5	3.3	907	2	E96636	hypothetical prote	958	101	3.2	249	2	S72619	hypothetical prote
886	102.5	3.3	942	1	JQ1674	protein kinase TWK	959	101	3.2	294	2	T34537	hypothetical prote
887	102.5	3.3	964	2	JC5545	integrin beta-4 pr	960	101	3.2	360	2	S25561	transcription fact
888	102.5	3.3	1013	2	A46422	hypothetical prote	961	101	3.2	373	2	A44478	probable cell grow
889	102.5	3.3	1115	1	IJMSNL	neural cell adhesi	962	101	3.2	401	2	A48423	engrailed homeodom
890	102.5	3.3	1223	1	T15316	hypothetical prote	963	101	3.2	482	2	A44997	mezoote surface
891	102.5	3.3	1350	2	S36793	hypothetical prote	964	101	3.2	492	2	B86911	probable penicilli
892	102.5	3.3	1367	1	S48478	glucan 1,4-alpha-g	965	101	3.2	574	2	B87619	sensor histidine k
893	102.5	3.3	1678	2	T35547	hypothetical prote	966	101	3.2	610	2	A28798	myosin-light-chain
894	102.5	3.3	1779	2	T31085	xylanase - Caldice	967	101	3.2	613	2	A40497	dihydrolipoamide S
895	102.5	3.3	1813	2	T30564	resistance protein	968	101	3.2	615	1	XXHU	dihydrolipoamide S
896	102.5	3.3	1863	2	S46217	protein-tyrosine-p	969	101	3.2	628	2	JQ0110	hypothetical 69K p
897	102.5	3.3	1875	2	A36429	integrin beta-4 ch	970	101	3.2	671	2	D84648	probable disease r
898	102.5	3.3	2207	2	S09553	genome polyprotein	971	101	3.2	688	2	T18263	S-layer protein -
899	102	3.3	301	2	JQ1663	hybrid proline-ric	972	101	3.2	700	2	D70951	probable UvrD - My
900	102	3.3	307	2	S36779	ribosome-binding p	973	101	3.2	739	2	I56187	transcription fact
901	102	3.3	317	2	A28996	proline-rich prote	974	101	3.2	796	2	T14460	hypothetical prote
902	102	3.3	353	2	B36963	bcsA 5'-region pro	975	101	3.2	846	1	Q0BEC3	HORP1 protein - hu
903	102	3.3	413	2	T49545	hypothetical prote	976	101	3.2	1043	2	A56037	DNA-binding protei
904	102	3.3	532	2	S74453	hypothetical prote	977	101	3.2	1127	2	T32404	hypothetical prote
905	102	3.3	554	1	FQHUMP	macrophage colony-	978	101	3.2	1257	2	S28764	neurocan precursor

979	101	3.2	1367	2	T33819	hypothetical prote	1052	99.5	3.2	352	2	S05500	Ig alpha-1 chain C
980	101	3.2	1513	2	A54895	mucin 2, intestina	1053	99.5	3.2	353	1	AIHU	Ig alpha-1 chain C
981	101	3.2	1792	2	A57075	tensin - chicken (1054	99.5	3.2	353	2	S36438	EpR protein - hyd
982	101	3.2	2946	2	T15840	hypothetical prote	1055	99.5	3.2	375	1	TDHUN4	monocyte surface g
983	101	3.2	3176	2	CGH03A	collagen alpha 3(V	1056	99.5	3.2	383	1	VBEBKG	glycoprotein precu
984	100.5	3.2	138	2	D96715	protein F4N2.10 (I	1057	99.5	3.2	387	2	B49175	Motch A protein -
985	100.5	3.2	262	2	T33408	hypothetical prote	1058	99.5	3.2	392	2	B48423	homeotic protein e
986	100.5	3.2	262	2	E88400	protein H34124.2 (1059	99.5	3.2	393	1	VBEBD2	glycoprotein D - h
987	100.5	3.2	269	2	T26957	hypothetical prote	1060	99.5	3.2	420	2	T46910	hypothetical prote
988	100.5	3.2	274	2	T46041	hypothetical prote	1061	99.5	3.2	451	2	JC4199	heat-shock protein
989	100.5	3.2	283	2	E88597	protein Y47D3B.6 (1062	99.5	3.2	476	1	C70986	probable serine/th
990	100.5	3.2	314	2	T48514	hypothetical prote	1063	99.5	3.2	491	2	F70699	probable pbpA prot
991	100.5	3.2	384	2	T50921	carbamoyl-phosphat	1064	99.5	3.2	530	2	S52215	hypothetical prote
992	100.5	3.2	401	2	S65138	glycoprotein antig	1065	99.5	3.2	539	2	T28770	hypothetical prote
993	100.5	3.2	440	2	UC7807	Wiskott-Aldrich sy	1066	99.5	3.2	647	2	T43952	hypothetical prote
994	100.5	3.2	504	2	AG2373	hypothetical prote	1067	99.5	3.2	665	2	S62328	kinesin-like DNA b
995	100.5	3.2	504	2	S56745	mucin (clone PGW31	1068	99.5	3.2	702	2	A86383	hypothetical prote
996	100.5	3.2	512	2	E59437	F02569_2 protein (1069	99.5	3.2	802	2	T24293	76.4K protein kina
997	100.5	3.2	597	2	JQ0107	hypothetical 66K p	1070	99.5	3.2	851	2	AD1427	hypothetical prote
998	100.5	3.2	677	2	T39713	zinc finger protei	1071	99.5	3.2	853	1	TUBONC	internalin, probab
999	100.5	3.2	798	2	T34248	hypothetical prote	1072	99.5	3.2	886	2	T35469	neural cell adhesi
1000	100.5	3.2	906	2	A43817	transforming prote	1073	99.5	3.2	903	2	T19209	probable ATP/GTP-
1001	100.5	3.2	975	2	S33121	homotic protein C	1074	99.5	3.2	932	2	T24294	probable protein k
1002	100.5	3.2	1024	2	T27631	hypothetical prote	1075	99.5	3.2	949	2	T24294	hypothetical prote
1003	100.5	3.2	1030	1	H88859	protein ZC518.2 (I	1076	99.5	3.2	958	2	E82994	glycine cleavage s
1004	100.5	3.2	1106	1	TVHUGL	transforming prote	1077	99.5	3.2	961	1	TSHP4	thrombospondin 4 p
1005	100.5	3.2	1131	2	F96662	hypothetical prote	1078	99.5	3.2	1013	2	T33470	hypothetical prote
1006	100.5	3.2	1138	1	S24066	hypothetical prote	1079	99.5	3.2	1016	2	T41720	hypothetical prote
1007	100.5	3.2	1220	2	T48928	protein-tyrosine k	1080	99.5	3.2	1056	2	A53767	mucin MUC5B, trach
1008	100.5	3.2	1273	2	S58782	disease resistance	1081	99.5	3.2	1122	2	T47424	hypothetical prote
1009	100.5	3.2	1323	2	T30253	SEC31 protein - ye	1082	99.5	3.2	1220	2	T06403	hypothetical prote
1010	100.5	3.2	2327	2	T42630	spalt protein - mo	1083	99.5	3.2	1390	2	T31353	resistance complex
1011	100.5	3.2	2562	2	T14266	aggrecan - bovine	1084	99.5	3.2	1473	2	T31422	polyprotein - Arab
1012	100.5	3.2	3562	2	A47171	Xin protein - chic	1085	99.5	3.2	1742	2	T17120	C-terminal domain-
1013	100.5	3.2	4548	1	S00657	chondroitin sulfat	1086	99	3.2	3869	2	A48205	cellulase (EC 3.2.
1014	100	3.2	230	2	A56210	apoprotein(a) (EC	1087	99	3.2	214	2	T09854	All-1 protein +GTE
1015	100	3.2	311	2	B86211	neu differentiatio	1088	99	3.2	307	1	GSF3	pistil extensin-li
1016	100	3.2	334	2	G02409	hypothetical prote	1089	99	3.2	329	2	B41344	proline-rich cell
1017	100	3.2	366	2	S61796	protein kinase C-b	1090	99	3.2	329	2	D41344	salivary glue prot
1018	100	3.2	367	2	A33950	T-cell-specific tr	1091	99	3.2	331	2	C41344	lutropin-choriogon
1019	100	3.2	474	2	S15921	yopM protein - Yer	1092	99	3.2	358	2	T01296	lutropin-choriogon
1020	100	3.2	476	2	C39481	protein IFX-VI3 -	1093	99	3.2	415	1	A34170	leucine-rich repea
1021	100	3.2	510	2	H84824	serum response fac	1094	99	3.2	428	2	S45361	acrosin (EC 3.4.21
1022	100	3.2	535	2	T17212	En/Spm-like transp	1095	99	3.2	447	2	T34992	LRR47 protein - fr
1023	100	3.2	549	2	C87719	hypothetical prote	1096	99	3.2	511	2	AC0941	probable lipoprote
1024	100	3.2	556	2	D70940	protein R119.6 (Im	1097	99	3.2	543	2	S25128	cysteine proteinas
1025	100	3.2	562	2	G75457	probable PPE prote	1098	99	3.2	564	2	F75381	probable ABC trans
1026	100	3.2	596	2	T51915	DNA ligase (EC 6.5	1099	99	3.2	569	2	C75588	61K protein - Auto
1027	100	3.2	628	2	S44138	tetratricopeptide	1100	99	3.2	616	2	C75588	gene gli protein -
1028	100	3.2	673	2	AF1143	polyadenylate-bind	1101	99	3.2	638	2	T51383	probable two-compo
1029	100	3.2	688	2	T51915	internalin protein	1102	99	3.2	641	2	C84726	conserved hypotet
1030	100	3.2	698	2	T17261	hypothetical prote	1103	99	3.2	686	2	F96542	receptor protein k
1031	100	3.2	699	2	T09069	probable cAMP-resp	1104	99	3.2	696	2	A41344	probable protein k
1032	100	3.2	713	2	T44447	neuregulin-3 (limp	1105	99	3.2	701	2	S61239	lutropin-choriogon
1033	100	3.2	725	2	T01268	leucine-rich repea	1106	99	3.2	770	1	JC0293	hypothetical prote
1034	100	3.2	756	2	C87432	hypothetical prote	1107	99	3.2	814	2	JC7389	transcription fact
1035	100	3.2	776	2	A46583	neuroendocrine-spe	1108	99	3.2	860	2	C86203	thyroid stimulat
1036	100	3.2	881	2	T01269	serine/threonine-s	1109	99	3.2	940	2	H86420	hypothetical prote
1037	100	3.2	1109	2	C84545	probable disease r	1110	99	3.2	963	2	C82630	hypothetical prote
1038	100	3.2	1161	2	T45294	hypothetical prote	1111	99	3.2	1000	2	C82630	serine proteinase
1039	100	3.2	1182	2	T48378	hairless protein -	1112	99	3.2	1097	2	T49187	hypothetical prote
1040	100	3.2	1240	2	T06404	resistance complex	1113	99	3.2	1147	2	T42627	ADP-ribosylation f
1041	100	3.2	1420	2	T37781	probable cytoskele	1114	99	3.2	1217	2	T52348	disease resistance
1042	100	3.2	1687	2	T30176	EGR repeat transme	1115	99	3.2	1317	2	T03748	apoptosis associat
1043	100	3.2	1791	2	T02345	hypothetical prote	1116	99	3.2	1405	2	T04426	hypothetical prote
1044	100	3.2	1802	2	T00020	bacterial blight-r	1117	99	3.2	1532	2	A61262	collagen alpha 1(X
1045	100	3.2	1897	1	TDHULK	leukocyte antigen-	1118	99	3.2	1538	2	E70874	probable ppsb prot
1046	100	3.2	2459	2	S08315	peptide synthetase	1119	99	3.2	1594	2	S50065	sialoadhesin - mou
1047	99.5	3.2	108	2	S08315	cell wall protein	1120	99	3.2	1694	2	S50065	probable ppsb prot
1048	99.5	3.2	177	2	T07642	pEARL1 protein h	1121	99	3.2	1799	1	S44920	Zk688.5 protein - p
1049	99.5	3.2	230	2	A44074	Probable EGF-like	1122	99	3.2	2029	1	TDFFLK	protein-tyrosine-p
1050	99.5	3.2	280	2	I48713	Phox2 homeodomain	1123	99	3.2	2088	2	E71436	hypothetical prote
1051	99.5	3.2	293	2	C75421	hypothetical prote	1124	99	3.2	6420	2	T30283	polyketide synthas

1125	98.5	3.1	230	2	T22763	hypothetical prote	1198	97.5	3.1	362	2	S23395	fetuin precursor -
1126	98.5	3.1	234	2	D88560	protein F58A4.1 [i	1199	97.5	3.1	429	2	JC4365	elk1 protein - mou
1127	98.5	3.1	242	2	I77461	lutinizing hormon	1200	97.5	3.1	460	2	T23087	hypothetical prote
1128	98.5	3.1	349	2	T15422	hypothetical prote	1201	97.5	3.1	464	2	S22697	extensin - Volvox
1129	98.5	3.1	379	2	S50125	larval glue protei	1202	97.5	3.1	497	2	F83634	hypothetical prote
1130	98.5	3.1	385	2	T18180	proline-rich prote	1203	97.5	3.1	511	2	T43282	alp21 protein - fi
1131	98.5	3.1	393	2	S62335	I71-7 protein - fr	1204	97.5	3.1	521	2	S54266	glycoprotein gc -
1132	98.5	3.1	434	1	A35005	u-plasminogen acti	1205	97.5	3.1	531	2	B55066	tyrosine decarboxy
1133	98.5	3.1	464	2	T2853	hypothetical prote	1206	97.5	3.1	563	2	A75594	ferredoxin-nitrite
1134	98.5	3.1	486	2	B39481	serum response fac	1207	97.5	3.1	574	1	A48501	probable protein-1
1135	98.5	3.1	514	2	A44100	cell adheson mole	1208	97.5	3.1	587	2	T41653	probable transcrip
1136	98.5	3.1	633	2	T47346	receptor protein k	1209	97.5	3.1	614	2	T33149	hypothetical prote
1137	98.5	3.1	700	2	I77463	lutinizing hormon	1210	97.5	3.1	626	2	B70754	probable serine/th
1138	98.5	3.1	700	2	A49744	lutropin-choriogon	1211	97.5	3.1	627	1	JC6534	protein kinase 1 (
1139	98.5	3.1	707	2	A46302	FTB-associated spl	1212	97.5	3.1	627	2	AB0535	hypothetical prote
1140	98.5	3.1	770	2	T22808	hypothetical prote	1213	97.5	3.1	631	1	A36749	transcription fact
1141	98.5	3.1	803	2	F59433	RhoGAP protein [im	1214	97.5	3.1	662	2	D40228	neurexin II-beta p
1142	98.5	3.1	837	2	A42112	mucin-like peptide	1215	97.5	3.1	676	1	EDBE23	immediate-early pr
1143	98.5	3.1	862	2	B88594	protein Y48A6B.11	1216	97.5	3.1	710	2	D96728	hypothetical prote
1144	98.5	3.1	885	2	B86257	NBS/LRR disease re	1217	97.5	3.1	754	2	AC2807	OmpA family protei
1145	98.5	3.1	921	2	D86293	F7H2.22 protein -	1218	97.5	3.1	754	2	B97586	hypothetical prote
1146	98.5	3.1	947	2	T26314	hypothetical prote	1219	97.5	3.1	814	2	G02390	disintegrin-like m
1147	98.5	3.1	1087	2	T31100	probable potassium	1220	97.5	3.1	817	2	S51342	verprolin - yeast
1148	98.5	3.1	1272	2	T30248	fragile X mental r	1221	97.5	3.1	830	2	T17672	chitinase-like pro
1149	98.5	3.1	1281	2	T00346	hypothetical prote	1222	97.5	3.1	893	2	H96651	protein T3P18.19 [
1150	98.5	3.1	1309	2	T00078	probable RNA-direc	1223	97.5	3.1	909	1	A54809	disease resistance
1151	98.5	3.1	1396	2	A44453	translation initia	1224	97.5	3.1	921	2	AE0332	conserved hypotet
1152	98.5	3.1	1774	2	B56101	collagen alpha 1(X	1225	97.5	3.1	929	2	T52517	hypothetical prote
1153	98.5	3.1	2180	2	T29764	hypothetical prote	1226	97.5	3.1	948	2	F87693	peptidase, M16 fam
1154	98.5	3.1	2339	2	A42566	omega-conotoxin-se	1227	97.5	3.1	1006	2	G86292	hypothetical prote
1155	98	3.1	182	2	T07641	PEARL1 protein h	1228	97.5	3.1	1258	2	UC5765	inositol polyphosp
1156	98	3.1	291	2	AF0123	probable antigenic	1229	97.5	3.1	1392	2	T51947	probable transcrip
1157	98	3.1	296	2	A56943	sensory/motor neur	1230	97.5	3.1	1715	2	C40228	neurexin II-alpha
1158	98	3.1	303	2	S40973	hypothetical prote	1231	97.5	3.1	1748	1	JQ1555	genome polyprotein
1159	98	3.1	352	2	S09266	Ig alpha chain C r	1232	97	3.1	191	2	F84522	probable proline-r
1160	98	3.1	416	1	A42879	advanced glycosyla	1233	97	3.1	238	2	T23867	hypothetical prote
1161	98	3.1	442	2	S50062	cell wall glycopro	1234	97	3.1	238	2	T26419	hypothetical prote
1162	98	3.1	499	2	A12449	hypothetical prote	1235	97	3.1	330	2	T05717	probable extensin
1163	98	3.1	514	2	A56201	transcription fact	1236	97	3.1	355	2	B26883	neural cell adhesi
1164	98	3.1	534	2	S21961	proline-rich prote	1237	97	3.1	357	2	A39364	GDF-1 embryonic gr
1165	98	3.1	535	2	S65762	chitinase (EC 3.2.	1238	97	3.1	379	2	AE3003	conserved hypotet
1166	98	3.1	538	2	I68093	PRR2 delta - human	1239	97	3.1	395	2	A86166	protein F21B7.6 [i
1167	98	3.1	538	2	A70836	hypothetical prote	1240	97	3.1	397	2	T00914	leucine-rich repea
1168	98	3.1	553	1	A42499	mullerian inhibiti	1241	97	3.1	400	1	A28172	spasmolysin precu
1169	98	3.1	560	1	WFH0M	mullerian inhibiti	1242	97	3.1	421	1	SL1674	acrosin (EC 3.4.21
1170	98	3.1	605	2	S48940	hypothetical prote	1243	97	3.1	428	1	TVHUEK	transforming prote
1171	98	3.1	614	2	S27962	modulator recognit	1244	97	3.1	452	2	D98280	hypothetical 28.0K
1172	98	3.1	631	2	C89243	protein F28C1.3 [i	1245	97	3.1	459	2	T35317	probable serine/th
1173	98	3.1	631	2	T21471	hypothetical prote	1246	97	3.1	483	2	T02226	NBS-LRR type resis
1174	98	3.1	715	2	S76492	lipoprotein nlppd -	1247	97	3.1	500	2	D97302	hypothetical prote
1175	98	3.1	728	2	H59435	phosphoinositide-3	1248	97	3.1	530	2	G70904	hypothetical prote
1176	98	3.1	750	2	T42614	probable envelope	1249	97	3.1	601	2	D89711	protein F40E10.4 [
1177	98	3.1	788	1	Q0BEE3	HHLF1 protein - hu	1250	97	3.1	601	2	T22025	hypothetical prote
1178	98	3.1	856	2	T43631	serine/threonine k	1251	97	3.1	632	2	T02627	hypothetical prote
1179	98	3.1	889	2	C86257	resistance to Pseu	1252	97	3.1	701	1	FOFV1R	gag polyprotein -
1180	98	3.1	896	2	S36326	ciathrin assembly	1253	97	3.1	860	2	JC4566	chitinase (EC 3.2.
1181	98	3.1	1006	2	JC5526	kinase-defective E	1254	97	3.1	966	2	D96662	hypothetical prote
1182	98	3.1	1216	2	T34101	hypothetical prote	1255	97	3.1	967	2	G96637	hypothetical prote
1183	98	3.1	1372	2	T25933	hypothetical prote	1256	97	3.1	1123	2	A39962	kinase-related tra
1184	98	3.1	1522	2	H88360	protein T22F7.3 [i	1257	97	3.1	1214	2	T47438	disease resistance
1185	98	3.1	1873	2	A55645	calcium channel, v	1258	97	3.1	1265	1	A37967	neural cell adhesi
1186	98	3.1	2115	2	S38480	CREB-binding prote	1259	97	3.1	1690	2	T35694	ATP dependent DNA
1187	98	3.1	3190	2	T13828	nonstructural prote	1260	97	3.1	1734	2	A54602	microtubule-associ
1188	98	3.1	3623	2	T08618	intrinsic factor-B	1261	97	3.1	2055	2	T00093	hypothetical prote
1189	98	3.1	3635	2	T10053	laminin alpha 5 ch	1262	97	3.1	2205	1	GNVY2W	genome polyprotein
1190	98	3.1	3871	2	T22812	hypothetical prote	1263	97	3.1	3034	2	T14119	seven-pass transme
1191	98	3.1	5069	2	T17464	rifamycin polyketi	1264	96.5	3.1	346	2	S19129	proline-rich prote
1192	97.5	3.1	215	2	S55925	probable arabinoga	1265	96.5	3.1	350	2	B75341	peptidyl-prolyl ci
1193	97.5	3.1	266	1	A35037	insulin-like growt	1266	96.5	3.1	419	2	G70602	hypothetical prote
1194	97.5	3.1	268	2	S71830	transcription coac	1267	96.5	3.1	430	2	I48755	msAPla - mouse
1195	97.5	3.1	287	2	A46241	interferon respons	1268	96.5	3.1	444	2	B36389	transcription fact
1196	97.5	3.1	306	2	T09067	extensin-like prot	1269	96.5	3.1	485	1	S22543	transcription fact
1197	97.5	3.1	338	1	TVMSFB	transforming prote	1270	96.5	3.1	487	2	F70765	hypothetical prote

1271	96.5	3.1	514	2	A31643	cell adhesion 80K	1344	95.5	3.0	1159	2	I38465	probable potassium
1272	96.5	3.1	528	2	B75310	conserved hypotnet	1345	95.5	3.0	1255	2	T31065	diaphanous protein
1273	96.5	3.1	574	2	B35149	ipaH protein - Shi	1346	95.5	3.0	1256	2	T03096	CDO protein - rat
1274	96.5	3.1	598	2	T42070	protein serine/thr	1347	95.5	3.0	1331	2	T49813	related to gastric
1275	96.5	3.1	635	2	F70874	probable membrane	1348	95.5	3.0	1630	2	T00390	KIAA0614 protein -
1276	96.5	3.1	637	2	A75342	hypothetical prote	1349	95.5	3.0	2761	2	T21064	hypothetical prote
1277	96.5	3.1	646	2	T34532	hypothetical prote	1350	95	3.0	175	2	I38408	neu differentiation
1278	96.5	3.1	654	2	T45017	chemotaxis histidi	1351	95	3.0	227	2	C29149	proline-rich prote
1279	96.5	3.1	669	2	T08827	hypothetical prote	1352	95	3.0	227	2	G70555	hypothetical prote
1280	96.5	3.1	796	2	E96654	hypothetical prote	1353	95	3.0	239	2	D43273	hergulin precursor
1281	96.5	3.1	825	1	EDBEXD	hypothetical prote	1354	95	3.0	241	2	D43273	hypothetical prote
1282	96.5	3.1	1021	2	A86421	Receptor-like seri	1355	95	3.0	273	2	C70551	ABA-responsive pro
1283	96.5	3.1	1209	2	T00373	hypothetical prote	1356	95	3.0	326	2	A59232	proline-rich prote
1284	96.5	3.1	1241	2	T18311	hypothetical prote	1357	95	3.0	338	2	T08336	GTP cyclohydrolase
1285	96.5	3.1	1557	2	T02859	probable serine/th	1358	95	3.0	385	1	I39498	GTP cyclohydrolase
1286	96.5	3.1	2282	2	T42717	DNA-binding protei	1359	95	3.0	413	2	T52617	hypothetical prote
1287	96.5	3.1	2352	2	T30201	Notch homolog prot	1360	95	3.0	477	2	A53362	mucin SAC (clone J
1288	96.5	3.1	26926	1	I38344	titin, cardiac mus	1361	95	3.0	494	1	A29079	lymphocyte surface
1289	96	3.1	214	2	T10737	extensin-like cell	1362	95	3.0	502	2	A55197	Wiskott-Aldrich sy
1290	96	3.1	240	2	A24264	proline-rich prote	1363	95	3.0	636	2	I61718	neu differentiation
1291	96	3.1	287	2	C75494	cell division prot	1364	95	3.0	653	2	E84682	hypothetical prote
1292	96	3.1	346	2	JA0159	cysteine proteinas	1365	95	3.0	662	2	I61722	neu differentiation
1293	96	3.1	445	2	T05987	hypothetical prote	1366	95	3.0	667	2	T17221	hypothetical prote
1294	96	3.1	451	2	D88395	protein F53A3_6 li	1367	95	3.0	673	2	T49012	hypothetical prote
1295	96	3.1	483	2	S12741	transcription fact	1368	95	3.0	705	2	A35621	spore germination
1296	96	3.1	537	1	F0MVGV	gag polyprotein -	1369	95	3.0	712	2	G02512	interleukin-1 rece
1297	96	3.1	580	2	T43481	probable mucin DKF	1370	95	3.0	760	2	T16726	hypothetical prote
1298	96	3.1	594	2	S33561	ref(2)P protein -	1371	95	3.0	776	2	C96554	unknown protein [
1299	96	3.1	598	2	T48822	hypothetical prote	1372	95	3.0	799	2	T48889	serine/threonine p
1300	96	3.1	635	1	WMBEW6	capsid protein - h	1373	95	3.0	846	2	S52418	GTP-binding regula
1301	96	3.1	858	1	IJRTNC	neural cell adhesi	1374	95	3.0	891	2	G84693	probable proline-r
1302	96	3.1	883	2	A96662	hypothetical prote	1375	95	3.0	901	2	A44825	phosphoprotein, sy
1303	96	3.1	907	2	AD2951	cell division prot	1376	95	3.0	903	2	S60257	meltrin alpha, mo
1304	96	3.1	910	2	H98331	cell division prot	1377	95	3.0	943	2	T34847	probable transcrip
1305	96	3.1	959	2	A75634	McrB-related prote	1378	95	3.0	1024	2	S18251	collagen alpha 1(X
1306	96	3.1	1216	2	T26104	hypothetical prote	1379	95	3.0	1209	2	T13153	brhma associated
1307	96	3.1	1231	2	S30185	insulin receptor s	1380	95	3.0	1324	2	T14070	peptide synthetase
1308	96	3.1	1544	2	E59431	phosphoinositide-b	1381	95	3.0	1474	2	B85188	retrotransposon li
1309	96	3.1	1615	2	B49502	protein-tyrosine-p	1382	95	3.0	1616	2	G70668	polyketide synthas
1310	96	3.1	1737	2	T00209	MEGF8 protein - hu	1383	95	3.0	1731	2	AB3045	ice nucleation pro
1311	96	3.1	1767	2	A49502	protein-tyrosine-p	1384	95	3.0	1731	2	B98241	hypothetical prote
1312	96	3.1	1844	1	RRWPTM	genome polyprotein	1385	95	3.0	1770	2	T18551	saframycin Mx1 syn
1313	96	3.1	2529	2	A56523	transcription fact	1386	95	3.0	1806	1	CGHUIE	collagen alpha 1(X
1314	96	3.1	5376	2	T42215	zonadhesin - mouse	1387	95	3.0	2090	2	T30075	hypothetical prote
1315	95.5	3.0	188	2	D29149	proline-rich prote	1388	95	3.0	2148	2	A56011	transcription fact
1316	95.5	3.0	284	2	F95320	conserved hypotnet	1389	95	3.0	2274	2	T30258	adenomatous polyo
1317	95.5	3.0	366	1	TDMSM4	monocyte surface g	1390	95	3.0	3084	1	MMMSA	laminin alpha-1 ch
1318	95.5	3.0	382	2	S75923	threonine synthase	1391	94.5	3.0	211	2	T03381	high sulfur zein p
1319	95.5	3.0	384	2	S51796	vasodilator-stimul	1392	94.5	3.0	255	2	B75309	hypothetical prote
1320	95.5	3.0	435	2	T46443	hypothetical prote	1393	94.5	3.0	255	2	S31096	proline-rich prote
1321	95.5	3.0	451	2	S71754	cellular hepatitis	1394	94.5	3.0	270	2	I38857	hypothetical prote
1322	95.5	3.0	479	2	D70676	probable PE protei	1395	94.5	3.0	277	2	I38857	microtubule-associ
1323	95.5	3.0	486	2	AB2975	succinate semialde	1396	94.5	3.0	298	2	H87533	peptidase, M23/M37
1324	95.5	3.0	486	2	A98308	artK protein (U594	1397	94.5	3.0	301	2	D87684	transcription regu
1325	95.5	3.0	501	2	S76563	hypothetical prote	1398	94.5	3.0	358	2	A61188	probable transcrip
1326	95.5	3.0	507	1	A46713	erythropoietin rec	1399	94.5	3.0	376	2	H82988	hypothetical prote
1327	95.5	3.0	553	2	C75318	hypothetical prote	1400	94.5	3.0	393	2	B82283	conserved hypotnet
1328	95.5	3.0	570	2	A48836	fibropellin C prec	1401	94.5	3.0	464	2	A83557	hypothetical prote
1329	95.5	3.0	571	2	T43456	hypothetical prote	1402	94.5	3.0	569	2	T19128	probable amidase P
1330	95.5	3.0	573	2	B70726	probable secD - My	1403	94.5	3.0	630	2	A39344	hypothetical prote
1331	95.5	3.0	624	2	T49366	myocyte-specific e	1404	94.5	3.0	665	2	B75461	tetrasin-X - mouse
1332	95.5	3.0	630	2	T31798	hypothetical prote	1405	94.5	3.0	708	2	T33170	collagen alpha 1(I
1333	95.5	3.0	650	2	S44806	F10E9.6 protein -	1406	94.5	3.0	719	2	T33170	collagen alpha 1(I
1334	95.5	3.0	685	2	C56591	E75 B steroid rece	1407	94.5	3.0	860	2	I48839	hypothetical prote
1335	95.5	3.0	710	1	S70965	serine/threonine-s	1408	94.5	3.0	921	2	S42617	hypothetical prote
1336	95.5	3.0	722	2	T22359	hypothetical prote	1409	94.5	3.0	985	2	T06049	hypothetical prote
1337	95.5	3.0	749	2	B87559	hypothetical prote	1410	94.5	3.0	1006	2	T00050	hypothetical prote
1338	95.5	3.0	790	1	TVHUT	nerve growth facto	1411	94.5	3.0	1092	1	UN0635	neural cell adhesi
1339	95.5	3.0	880	2	D89756	protein T23E7.2b [1412	94.5	3.0	1131	2	T13850	gene u-shaped prot
1340	95.5	3.0	943	2	B84429	probable receptor-	1413	94.5	3.0	1487	1	EDBEE1	immediate-early pr
1341	95.5	3.0	987	2	A54092	protein-tyrosine k	1414	94.5	3.0	1690	1	CGHUIB	collagen alpha 4(I
1342	95.5	3.0	1027	2	I38759	zinc finger/leucin	1415	94.5	3.0	2062	2	G96602	probable receptor
1343	95.5	3.0	1054	2	A30239	hydroxymethylgluta	1416	94.5	3.0	2302	2	T14328	protein-tyrosine-p

QY 215 LRLLAARNPFCVCLPSWFGWRES-----HVTLASPEETRC----- 253
DB 216 AFLHG---NPWLCNCEILYFRRWLQDAENVYVMKQGVDFKAMTSNVASVQCDNSDKFPV 272
QY 254 -HFPKKNAGRLLE--LDVADFGCPATTTATVPTTRPVVREP-----TA 295
DB 273 KYFPGKCTGLDGGDTLDYDPEDETDGDKVRATRTVKPPTKAHTPWGLFYGSWSTA 332
QY 296 LSSSLAPTWSPTAPATE-----APSPSTAPPTVGPV---PQ 330
DB 333 SLDSQMPSSLHPTQESTKQOTFFPRWTFNFTLHMSITFSKTPKSTTEPTSPPTSEPV 392
QY 331 PQDCPSTCLNGTCHLGRHHLACLPFGFTGLYCESOMGQGTSPSPVTPRPPRSLT 390
DB 393 PEPAPNMTTLEPTP-----SPTTPE-----PTSEPAPSPPTPEPTPIPT 431
QY 391 LGIEP---VSPSLRVLQRYLOGSS--VOLRSRLTYRNLSPGDKRLVTLR--LPASLA 443
DB 432 IATSPILVSATSLITPKSTFLTITTKPVSLLESTKTIPELDQPPKLRGVQLQHLESSRN 491
QY 444 EYTVTLQRLNATYSVCVMPLG-----PGRV-PEGEEACGEAHT 480
DB 492 D---PFLHPD---FCLLPLGFVVLGLFWLLPASVVLILLSSVGHVKPQALDSSGOGAL 545
QY 481 PPAVHSHNAPVQAREGNLP---LLI-----APALAAVLLAALAAVGAAYCVRRGRAMAA 533
DB 546 ITATQTTLELQROGROTVPRAWLLFLRGSLPTFRSSFLWVRPNRGVGLVAGRRPSAL 605
QY 534 AODKGO 539
DB 606 SOGRGO 611

RESULT 4
JC1282
insulin-like growth factor-binding protein acid labile chain precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
R:Daai, J.; Baxter, R.C.
Biochem. Biophys. Res. Commun. 188, 304-309, 1992
A:Title: Molecular cloning of the acid-labile subunit of the rat insulin-like growth factor
A:Reference number: JC1282; MUID:93038676; PMID:1384485
A:Accession: JC1282
A:Molecule type: mRNA
A:Residues: 1-603 <DAI>
A:Cross-references: UNIPROT:P35859; UNIPARC:UPI0000125918; GB:S46785; NID:G258002; PIDN:
A:Experimental source: liver
A>Note: the authors translated the codon AAG for residue 63 as Arg, AAA for residue 205
F:1-27/Domain: signal sequence #status predicted <SIG>
F:28-603/Product: insulin-like growth factor binding protein, acid labile chain #status
F:267-290/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR>

Query Match 9.0%; Score 281.5; DB 2; Length 603;
Best Local Similarity 32.4%; Pred. No. 4.5e-09;
Matches 92; Conservative 49; Mismatches 106; Indels 37; Gaps 11;

QY 6 PLLLLPLL-LALGP-GVQG-----CPSGCOCQPO-----TVFCTARQGT 45
DB 8 PALVLLAFWALGPGCYLQGTDPGASADAEQPCQVCTCSDYDDYDELVSFVCSRNLTQ 67

QY 46 VPRDVPDVTGLYVFPENGITMLDASSFAGLPGQLQLDLSONQIATSLRLPRLLL----- 98
DB 68 LPDDIPVSTRALWLDGNNLSSIPSAFQNLSSLDLFLNLOGSWLSLE-PQALLGLQNLVYH 126
QY 99 DLSHNSLLALEPGIL-DTANVEALRLAGLQQLDEGLFSRLRNHLHDVSDNQLERVP 157
DB 127 LHLERNLRNLAVGLFTHPTPSLASLSLGNLGRLEEGFLRGLSHLWDLNLGWSNLVLP 186
QY 158 PVIRGLRGLTRLAGNTRIAOLRPEDLAGLAALQELDVNSLSLOALPGDLSGLFPRLR 216
DB 187 DTVFOGLGNLHELVLGN-KLTYLOPALFCGLGELRDLNRLNALSRSKANVFHLPRLQ 245
QY 217 LLAAARNPFCVCLPSWFG-----PWVRESHTLA 246
DB 246 KLYLDRLNLTAVAPRAFLGKALRWLDLSHNRVA 279

RESULT 6
T42218
slit-1 protein homolog - rat
N:Alternate names: MEGF4 protein
C:Species: Rattus norvegicus (Norway rat)
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
R:Kakayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.
Genomics 51, 27-34, 1998
A:Title: Identification of high-molecular-weight proteins with multiple EGF-like motifs
A:Reference number: Z14126; MUID:98360089; PMID:9693030
A:Accession: T42218
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1531 <NAK>
A:Cross-references: UNIPROT:O88279; UNIPARC:UPI000004F20B; EMBL:AB011530; NID:G3449289;
A:Experimental source: strain Sprague-Dawley; brain
C:Genetics:
A:Gene: MEGF4
C:Superfamily: fruit fly slit protein; EGF homology; leucine-rich alpha-2-glycoprotein r

Query Match 8.9%; Score 278; DB 2; Length 1531;
Best Local Similarity 25.8%; Pred. No. 2.1e-08;

QY 218 LAAARNPFCVCLPSWFG-----PWVRESHTLAS-PEETRCCHPP 256
DB 247 LYLDRLNLTAVAPGAFGLGKALRWLDLSHNRVAGLMEDT---FP 287

RESULT 5
JC6128
insulin-like growth factor binding complex acid labile chain - mouse
C:Species: Mus musculus (house mouse)
C:Date: 23-Mar-1997 #sequence_revision 09-May-1997 #text_change 09-Jul-2004
C:Accession: JC6128
R:Boisclair, Y.R.; Seto, D.; Hsieh, S.; Hurst, K.R.; Ooi, G.T.
Proc. Natl. Acad. Sci. U.S.A. 93, 10028-10033, 1996
A:Title: Organization and chromosomal localization of the gene encoding the mouse acid labile
A:Reference number: JC6128; MUID:96413591; PMID:8816745
A:Accession: JC6128
A:Molecule type: DNA
A:Residues: 1-603 <BOI>
A:Cross-references: UNIPROT:P70389; UNIPARC:UPI0000000891; GB:U66900; NID:G1621612; PIDN:
C:Comment: This protein is a serum protein and it is of the ternary complex in the physical
C:Genetics:
A:Gene: als
A:Map position: 17

Query Match 8.9%; Score 278.5; DB 2; Length 603;
Best Local Similarity 32.8%; Pred. No. 6.7e-09;
Matches 90; Conservative 48; Mismatches 101; Indels 35; Gaps 10;

QY 6 PLLLLPLL-LALGP-GVQG-----CPSGCOCQPO-----TVFCTARQGT 45
DB 8 PALVLLAFWALGPGCYLQGTDPGASADAEQPCQVCTCSDYDDYDELVSFVCSRNLTQ 67

QY 46 VPRDVPDVTGLYVFPENGITMLDASSFAGLPGQLQLDLSONQIATSLRLPRLLL----- 98
DB 68 LPDGPVSTRALWLDGNNLSSIPSAFQNLSSLDLFLNLOGSWLSLE-PQALLGLQNLVYH 126
QY 99 DLSHNSLLALEPGIL-DTANVEALRLAGLQQLDEGLFSRLRNHLHDVSDNQLERVP 157
DB 127 LHLERNLRNLAVGLFTHPTPSLASLSLGNLGRLEEGFLRGLSHLWDLNLGWSNLVLP 186
QY 158 PVIRGLRGLTRLAGNTRIAOLRPEDLAGLAALQELDVNSLSLOALPGDLSGLFPRLR 216
DB 187 DTVFOGLGNLHELVLGN-KLTYLOPALFCGLGELRDLNRLNALSRSKANVFHLPRLQ 245
QY 217 LLAAARNPFCVCLPSWFG-----PWVRESHTLA 246
DB 246 KLYLDRLNLTAVAPRAFLGKALRWLDLSHNRVA 279

RESULT 6
T42218
slit-1 protein homolog - rat
N:Alternate names: MEGF4 protein
C:Species: Rattus norvegicus (Norway rat)
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
R:Kakayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.
Genomics 51, 27-34, 1998
A:Title: Identification of high-molecular-weight proteins with multiple EGF-like motifs
A:Reference number: Z14126; MUID:98360089; PMID:9693030
A:Accession: T42218
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1531 <NAK>
A:Cross-references: UNIPROT:O88279; UNIPARC:UPI000004F20B; EMBL:AB011530; NID:G3449289;
A:Experimental source: strain Sprague-Dawley; brain
C:Genetics:
A:Gene: MEGF4
C:Superfamily: fruit fly slit protein; EGF homology; leucine-rich alpha-2-glycoprotein r

Query Match 8.9%; Score 278; DB 2; Length 1531;
Best Local Similarity 25.8%; Pred. No. 2.1e-08;

Matches 127; Conservative 56; Mismatches 207; Indels 102; Gaps 16;	
QY	6 PLILPLLALLALPGVQGGPSGCQSQPQTFFCTARQGTTPRDVPPDTVGLYVFENGIT 65
Db	16 PELWLLWAAWRLGATACPALCTCT-GTIVDCHGTGLQAIKNIPIRTERLELNGNIT 74
QY	66 MLDASSFAGLPGQLLDLSONQIASURLPRLLLDLSHNSLLALEPGIIL-DTANVEALRL 124
Db	75 RIHKNDFAGLKQRLVQLMENQIG-----AVERGAFDDMKELERLR 116
QY	125 AGLGLOQDEGLFSRLNLHDLVDSDNQLERVP-PVIRGLRGLTRLRLAGNTRIAOLRPE 183
Db	117 NRNLQVLPELLFQNNQALSRLDSLSLQAVPRKAFRGATDLKNQLQDN-QIISIEEG 175
QY	184 DLAGLAALQELVDNSLSLOALPGDLGLFPRRLALAAARNPNCVCLSWFGPFWRESHV 243
Db	176 AFRALRGLEVLTLNNNIITIPVSSFNMHPKLTFRLLSHNLFCDCHLAWLSQMLRQ-RP 234
QY	244 TLASPBETRCHPPKKNAGRLLLLELDVADFGCPATTTTATVTPTRPVVREPTALSSSLAPT 303
Db	235 TIGL--FTQCSGPASRLGNVAEVQKSEFSCSQGGEAAQVPA-----CTLSSGSCPA 284
QY	304 WLSPTAPATEAPSPSTAPTPVGPVQPO-----DCPSTCLNGGTCHLG----- 348
Db	285 MCSCSNGIVDCRGKGLTAPANLPETWTEIRLELNGIKSIPP-----GAFSPYR 333
QY	349 -----TRHHLACLCPPEGTGLHYCESQMGQGTTPVTPRPPRSLTLGIEPVGS--PT 399
Db	334 KLRRIDLSNNQIAEIPADFQGL-----RSLNSLVLYGNKITDLPR 374
QY	400 SLRVGLQRYLQGSVQLRSURLTYRLNSGPD--KRLVTLRLLPA-----SLAEYVTQL 450
Db	375 GVFGGLY-----TLQILLNANKINCIRDPADFQDLQNLSLSLYDNKIQSLAKGFTSL 428
QY	451 RPNATYSVCVMP 462
Db	429 RAIQTLHLAQN 440
RESULT 7	
A53531	
N;Alternate names: oncofetal protein 5T4 precursor - human	
C;Species: Homo sapiens (man)	
C;Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004	
C;Accession: A53531; S40087	
R;Myers K.A.; Rahi-Saund, V.; Davison, M.D.; Young, J.A.; Cheater, A.J.; Stern, P.L.	
J. Biol. Chem. 269, 9319-9324, 1994	
A;Title: Isolation of a cDNA encoding 5T4 oncofetal trophoblast glycoprotein. An antigen	
A;Reference number: A53531; MUID:94179356; PMID:8132670	
A;Accession: A53531	
A;Status: preliminary	
A;Molecule type: mRNA	
A;Residues: 1-420 <MEY>	
A;Cross-references: UNIPROT:Q13641; UNIPARC:UPI000004CAD5; EMBL:Z29083; NID:9435654; PID	
F;1-31/Domain: signal sequence #status predicted <SIG>	
F;32-420/Product: oncofetal trophoblast glycoprotein 5T4 #status predicted <MAT>	
Query Match 8.4%; Score 264.5; DB 2; Length 420;	
Best Local Similarity 28.1%; Pred. No. 2.9e-08;	
Matches 103; Conservative 44; Mismatches 121; Indels 99; Gaps 15;	
QY	2 CSRVV-----LLPLLLLALG-----PGVQCPS 26
Db	5 CSRGPAAGDGLRLRLALVLVLGWSSSPSSASSFSSAPFLASAVSQPLPDQCPA 64
QY	27 GCQCSQ-PQNVFCTARQGTTPRDVPPDTVGLYVFENGITMLDASSFAGL---GLQLLD 82
Db	65 LCEGSEARTVKCVNRNLTEVPTDLPAYVRNLFTLGNQLAVLPAGAFARRPPLAELALN 124
QY	83 LSQNIQIASLR-----LPRLLLDLSHNSLLALEPGILDNTANVEALRLAGLGLQLDEGL 136

Db	125 LSGSRLDVRAAGAEHLPSLRQLDLSHNPDLADLSPPAFSGSNASV-----SAPSPL 175
QY	137 FSRLRLNLHDLVDSDNQLER-----VPPVI--RGLRGITRLRLAGNTRIAQLRPEDLAGL 188
Db	176 VELILN-HIVPPEDERQNRSEFGMVVAALLAGRALQGLRLRLASN-HFLYLPYPRDVLQAL 233
QY	189 ALQELVDNSLSLOALP-----GDLISGLFPRRLRLAA 220
Db	234 PSRLHLDSLNSLSVLTVVSFRNLTHLSLHUEDNALKVLHNGTIAELQGL-PHIRVF-L 291
QY	221 ANPNPCVCLPSLWFGPFWRESHVTLASPEETRCHPPKKNAGRLLELDVADFGC-----PA 276
Db	292 DNNPVVCDCHWADMTWLKETE-VQGRDLTCAYPEKMRNRVLELNSADLDCDPIPPP 350
QY	277 TTTTATV 283
Db	351 SLQTSV 357
RESULT 8	
MEGF5 protein - rat	
N;Alternate names: slit protein homolog	
C;Species: Rattus norvegicus (Norway rat)	
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004	
C;Accession: T13953	
R;Nakayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.	
Genomics 51, 27-34, 1998	
A;Title: Identification of high-molecular-weight proteins with multiple EGF-like motifs	
A;Reference number: Z14126; MUID:98360089; PMID:9693030	
A;Accession: T13953	
A;Status: preliminary; translated from GB/EMBL/DBJ	
A;Molecule type: mRNA	
A;Residues: 1-1523 <NAK>	
A;Cross-references: UNIPROT:O88280; UNIPARC:UPI000005E57A; EMBL:AB011531; NID:93449291; F	
C;Genetics:	
C;Superfamily: fruit fly slit protein; EGF homology; leucine-rich alpha-2-glycoprotein re	
Query Match 8.3%; Score 261; DB 2; Length 1523;	
Best Local Similarity 26.3%; Pred. No. 2e-07;	
Matches 93; Conservative 41; Mismatches 126; Indels 94; Gaps 14;	
QY	24 CPSGCGCQSQPQTVFCTARQGTTPRDVPPDTVGLYVFENGITMLDASSFAGLPGQLQLDL 83
Db	725 CPEQCTCBE-TVVRCSNRGLHTLPKMPKDVTELYLEGHNLTA----- 767
QY	84 SQNQIASLRPLRLLLDLGSHNSLLALEPGILDNTANVEALRLAGLGLQLDEGLFSRLNL 143
Db	768 -PKELSTFR-QUTLIDLNSNS-----ISMLTNHTFSNMSHL 801
QY	144 HDLDVSDNQLERVP-PVIRGLRGLTRLRLAGNTRIAQLRPEDLAGLAALQELVDNSLSLQ 202
Db	802 STLILSYNRLRCIPVHAFNGLRSLRVLTLGN-----DISSVPEGSFNDLTSL-- 850
QY	203 ALPGLDLSGLFPRRLILAAARNPNCVCLSWFGPFWRESHVTLASPEETRCHPPKKNAGR 262
Db	851 -----HLALGINPLHCDCSRMLSEWIRAGY---KEPGIARCSSPESWADR 893
QY	263 LLLLELDVADFGCPATTTTATVTPTRPVVREPTALSSSLAPTTLSPATAPATEAPSPSTAP 322
Db	894 LLTTTTHRFQCKG-----PVDINIVAKCNACLS--PCKNNGTCSQDPVEQYRCTCP 944
QY	323 PTVGVPVQPODC--PPSTCL-----NGGTCHLGRHH--LACLCPBEGFTGLYCE 367
Db	945 YSY---KGKDCVTPINTCVQPCQGGTCHLSHRDGFSCSCPLGFEQORCE 994
RESULT 9	
B36665	
slit protein 2 precursor - fruit fly (Drosophila melanogaster)	
C;Species: Drosophila melanogaster	
C;Date: 30-Apr-1991 #sequence_revision 30-Apr-1991 #text_change 02-Aug-2002	

C;Accession: B36665
 R;Rothberg, J.M.; Jacobs, J.R.; Goodman, C.S.; Artavanis-Tsakonas, S.
 Genes Dev. 4, 2169-2187, 1990
 A;Title: slit: an extracellular protein necessary for development of midline glia and co
 A;Reference number: A36665; MUID:91099665; PMID:2176636
 A;Accession: B36665
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-1469 <ROT>
 A;Cross-references: UNIPARC:UPI0000177454; GB:X53959
 C;Genetics:
 A;Gene: FlyBase:sl
 A;Cross-references: FlyBase:FBgn0003425
 C;Superfamily: fruit fly slit protein; EGF homology; leucine-rich alpha-2-glycoprotein r
 F;66-91/Domain: proteoglycan amino-terminal homology <PAH1>
 F;101-124/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
 F;125-148/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
 F;149-172/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
 F;173-196/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>
 F;197-220/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>
 F;228-272/Domain: proteoglycan carboxyl-terminal homology <PCS1>
 F;288-313/Domain: proteoglycan amino-terminal homology <PAH2>
 F;323-346/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>
 F;347-370/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>
 F;371-394/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>
 F;395-418/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR9>
 F;419-442/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR10>
 F;450-494/Domain: proteoglycan carboxyl-terminal homology <PCS2>
 F;512-537/Domain: proteoglycan amino-terminal homology <PAH3>
 F;547-571/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR11>
 F;572-595/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR12>
 F;596-619/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR13>
 F;620-643/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR14>
 F;651-695/Domain: proteoglycan carboxyl-terminal homology <PCS3>
 F;708-733/Domain: proteoglycan amino-terminal homology <PAH4>
 F;743-766/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR15>
 F;767-790/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR16>
 F;846-890/Domain: proteoglycan carboxyl-terminal homology <PCS4>
 F;1028-1061/Domain: EGF homology <EGF>
 F;1068-1099/Domain: EGF homology <EGF2>
 F;1115-1148/Domain: EGF homology <EGF1>

Query Match 8.1%; Score 255.5; DB 2; Length 1469;
 Best Local Similarity 21.4%; Pred. No. 3.9e-07;
 Matches 105; Conservative 52; Mismatches 168; Indels 165; Gaps 14;
 QY 24 CPSCGCSQPTVCTARQTTVPDVP-----PDTVGLY 58
 DB 519 CPAMCHC-EGTVDCTGRRLKEIPRDIPLHTTELLNDNLGRISDGLFRLPHLVKLE 577
 QY 59 VFENGITMLDASSFAGLPGLQLDLSONQIAS-----LRLPRLLLDLHNSLLALEPG 112
 DB 578 LKRNQLTGTPNFAEGASHIQELQNGENKIKETISNKFGLHQLKTLNLDNQISCVMPG 637
 QY 113 ILDTAN-----VEALRLAGLQLOQDLGFLSRLNLHDLV--- 148
 DB 638 SFEHLNLSLNLASPNFNCNCHLAWPAECVRKKSLLNGGAARCAPSKVRDQVKDLPHS 697
 QY 149 -----SDNLERVP---PV----- 159
 DB 698 EFKCSSENSEGGCDGVCPPSCCTGTGTVACSRNQLKEIPRGTPAETSLEYLESNEIEQI 757
 QY 160 ----IRGLRGLRLRLAGNTRIAQLRPEDLAGLAALQELDVS-----NL 199
 DB 758 HYERIRHRSLSRLDLS-NNQITLSNYTANLTKLSTLISYNKLOCLQRHALSGLNLL 816
 QY 200 SLQALPGDLGLFFR-----LRLAAARNPFCNPLSWFGPWWRESHVTLASPEET 251
 DB 817 RVVSLHGNRISMLPEGSFEDLKSITHIALGNSNPLYCCGCKWFSMDIKLDV---EGIA 873
 QY 252 RCHFPNKNAGRLLELDYADGCPATTTATVPTTRPVREPTALSSSLAPTWLSPTAPA 311
 DB 874 RCAEPEQMKDKLILSTPSSSFVCRGRVRNDILAKNCNACFEQPCQONQOCV-----ALPQ 927

QY 312 TEAPSPSTAPPVGVVPOP-----QDCPPSTCLNGTCHLGRHHLACLCEP 360
 DB 928 REYQC-----LCOPGVGHKCEFMIDACYGNPCRNATCTVLEEGRFSCQCAPG 976
 QY 361 FTGLYCESOM 370
 DB 977 YTGARCTNI 986
 RESULT 10
 A36665
 A;Title: protein 1 precursor - fruit fly (Drosophila melanogaster)
 C;Species: Drosophila melanogaster
 C;Date: 30-Apr-1991 #sequence revision 30-Apr-1991 #text_change 02-Aug-2002
 C;Accession: A36665; A31640; S13523
 R;Rothberg, J.M.; Jacobs, J.R.; Goodman, C.S.; Artavanis-Tsakonas, S.
 Genes Dev. 4, 2169-2187, 1990
 A;Title: slit: an extracellular protein necessary for development of midline glia and co
 A;Reference number: A36665; MUID:91099665; PMID:2176636
 A;Accession: A36665
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-1480 <ROT>
 A;Cross-references: UNIPARC:UPI0000150FD1; GB:X53959; NID:98614; PIDN:CAA37910.1; PID:98
 R;Rothberg, J.M.; Hartley, D.A.; Walther, Z.; Artavanis-Tsakonas, S.
 Cell 55, 1047-1059, 1988
 A;Title: slit: An EGF-homologous locus of D. melanogaster involved in the development of
 A;Reference number: A31640; MUID:89077533; PMID:3144436
 A;Accession: A31640
 A;Molecule type: DNA
 A;Residues: 881-1182, 'G', 1185-1404, 'GT', 1463-1464, 'YHA', 'RO2'
 C;Cross-references: UNIPARC:UPI000016BD7A; GB:M23543; NID:G340939; PID:G514357
 C;Genetics:
 A;Gene: FlyBase:sl
 A;Cross-references: FlyBase:FBgn0003425
 A;Introns: 1351/3
 C;Superfamily: fruit fly slit protein; EGF homology; leucine-rich alpha-2-glycoprotein r
 C;Keyfams: alternative splicing; growth factor
 F;66-91/Domain: proteoglycan amino-terminal homology <PAH1>
 F;101-124/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
 F;125-148/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
 F;149-172/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
 F;173-196/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>
 F;197-220/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>
 F;228-272/Domain: proteoglycan carboxyl-terminal homology <PCS1>
 F;288-313/Domain: proteoglycan amino-terminal homology <PAH2>
 F;323-346/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>
 F;347-370/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>
 F;371-394/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>
 F;395-418/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR9>
 F;419-442/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR10>
 F;450-494/Domain: proteoglycan carboxyl-terminal homology <PCS2>
 F;512-537/Domain: proteoglycan amino-terminal homology <PAH3>
 F;547-571/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR11>
 F;572-595/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR12>
 F;596-619/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR13>
 F;620-643/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR14>
 F;651-695/Domain: proteoglycan carboxyl-terminal homology <PCS3>
 F;708-733/Domain: proteoglycan amino-terminal homology <PAH4>
 F;743-766/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR15>
 F;767-790/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR16>
 F;846-890/Domain: proteoglycan carboxyl-terminal homology <PCS4>
 F;1028-1061/Domain: EGF homology <EGF>
 F;1068-1099/Domain: EGF homology <EGF2>
 F;1115-1148/Domain: EGF homology <EGF1>

Query Match 8.1%; Score 255.5; DB 2; Length 1480;
 Best Local Similarity 21.4%; Pred. No. 4e-07;
 Matches 105; Conservative 52; Mismatches 168; Indels 165; Gaps 14;

A;Gene: GDB:GPI5
A;Cross-references: GDB:230236; OMIM:173511
A;Map position: 5pter-5qter
C;Keywords: blocked amino end; glycoprotein; platelet; tandem repeat; transmembrane protein

Query Match 7.7%; Score 240; DB 2; Length 560;
Best Local Similarity 27.2%; Pred. No. 1e-06;
Matches 109; Conservative 28; Mismatches 111; Indels 152; Gaps 14;

QY 57 LYVPENGITMIDASSFAGLPGQLDLSQNOI-----ASL--RLPRLLLDLSHNSLLALE 110
Db 127 LFLDHNALRGIDQNMFKLVNLQELALNQQLDPLPASLFTNLENLKLDDLSGNLTHLP 186
QY 111 PGILDT-ANVEALRLAGLGLOOLDEGL-----FSRLNLHD 145
Db 187 KGLGAQAKLERLLHSHNRVLSLDSGLNSLGAELTELOFHRNHIRSIAPGAFDRLPNLSS 246
QY 146 LDVSS-----DNQLERVPPVIRG----- 162
Db 247 LTLSRNHLAFPLSFLHSHNLTLLTFENFLAEPLGVDFGEMGGLQELNLNRTQRLTP 306
QY 163 ---LRGLTRLRAGNT---RIAQLRPEDLAGLAALQELDV----- 196
Db 307 AAAPRNLRLRYLGVTLSPRLSALPQGAQFQGLGELQVLALHNSGLTALPDGLLRGLGKLR 366
QY 197 -----SNLS-----LQALPGDLSGLFPRRLRLAARNPFCNV 228
Db 367 QVSLRRNRLRALPRALFRNLSSLESVQLDHNQLETPGDGVFCALPRLTEVLLGHNSWRCD 426
QY 229 CPLSWFGPVRSHVTLASPEE-TRCHEPPKNAGRLLELDYADFCCPATTITATVPTTR 287
Db 427 CGLGPFGLWLRQ-HLGLVGGBEPRCAGPGAAGLPLMALPGGDACPCG-----PRGP 478
QY 288 PVVREPTALSSSLAPTWLSPTAPATEAPSPSTAPPTVGP 327
Db 479 P--PRPADSSS-----EAPVHPALPNSSEP 503

RESULT 14
JC7763
neuronal leucine-rich repeat protein-3 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C;Accession: JC7763
R;Fukamachi, K.; Matsuo, Y.; Kitanaka, C.; Kuchino, Y.; Tsuda, H.
Biochem. Biophys. Res. Commun. 287, 257-263, 2001
A;Title: Rat neuronal leucine-rich repeat protein-3: Cloning and regulation of the gene
A;Reference number: JC7763; PMID:11549284
A;Contents: Fibrosarcoma cells
A;Accession: JC7763
A;Molecule type: mRNA
A;Residues: 1-707 <FUK>
C;Cross-references: UNIPROT:Q9ESY6; UNIPARC:UPI000004F0F2; GB:AF291437
C;Comment: This protein, a new member of the neuronal leucine-rich repeat protein family,
in protein-protein interaction and functions as a cell adhesion molecule or soluble ligand
C;Genetics:
A;Gene: nlrr-3
C;Keywords: cell adhesion

Query Match 7.6%; Score 237; DB 2; Length 707;
Best Local Similarity 20.7%; Pred. No. 2e-06;
Matches 127; Conservative 80; Mismatches 222; Indels 186; Gaps 22;

QY 6 PLLPLPLALLALGPGVGG-----CPSCQCS-----QPQTVFCTARQGTTPV 47
Db 5 PLQIHVLGLGAIATLVAQGDKKVDCPQCTCEIRPWFTRPSIYMEASTVDCNDLGLLNPP 64
QY 48 RDVPPDVTGLYVFENGITMLDASSFAGLP-GLQLDLSQNIASL----- 91
Db 65 ARLPADTQILLQTNNTARIIEHST--DFPVLTLGLDLSQNNLSSVTNNVQKMSQLLSVY 122
QY 92 -----RLPRLLLDLS-----HNSLLALEPGIL----- 114

Db	123	LEENKLTPEKCLYGLSNLOELYVNHLLSAISPGAFVGLHNLRLHLNSNRLOMINSK	182
QY	115	-----DTANVEALRL-----AGLGLOOLDEGLFSRLRNLDLD	147
Db	183	WFEPALFNLEILMLGDNPIRLIKDMNFQPLKLSLSLVIAGINLTVDPD DALVGLNLESIS	242
QY	148	VSDNQLERVP-----PVIRGLRG-----	165
Db	243	FYDNRNLNKVPOVALQKAVNLKFLDLNKNPINRIRGDFSNMLHLKELGINNMPELVSDS	302
QY	166	-----LTRLRAGNTRIAQRPELAGLAALQELDVSNLSLQAL-PQDLSGLFPRLR	216
Db	303	LAVDNLPDLRKIEATNPNRLSYTHPNAFFRLPKLESMLNSALSXYHGTTESL-PNLK	361
QY	217	LAAARNPNCVPLSWFGPWVRESHVTLASPEETCHFPKPKNAGRLILLELDYADFGCPA	276
Db	362	EISIHNPIRCDCVIRWIN--MNKTNIRFMBPDSLCFVDPPEFQGGQVRQVHFRDM----	415
QY	277	TTTTATVPTTRPVVREPTALSSSL---APTMLSPATAPAEAPSPSTAPTPTVGPVPOPD	333
Db	416	-----MEICLPLI-APESPSPILDVDEADSVSLHCRATAEPQ-----PEIYWITPSGKR	463
QY	334	CPSTCLNGGTCHL-GTRHHLACLCEPFGTGLY---CESQMGQGTTPSPPTVTPRPPR--	387
Db	464	LENTLREKFPVHSEGLTDIRGTPKEG--GLVTCIATNLVAGADLKSIMIKVGGFVPODN	521
QY	388	--SITLGIEPVSTSLRVGLQRYLQSSVOLRSRLTYRNLSGPDKRLVTLRLPASLAEY	445
Db	522	NGSLNLIKIRDIRANSVLVS---WKANSKILKSSVKMTAFVKTEDSQAASARIPSDVKVY	578
QY	446	TVTQLRPNATYSVCV	460
Db	579	NLTHLKPSTBYKICI	593

RESULT 15

T42626

secreted leucine-rich repeat-containing protein SLIT2 - mouse (fragment)

N;Alternate names: neurogenic extracellular slit protein

C;Species: Mus musculus (house mouse)

C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004

C;Accession: T42626

R;Holmes, G.P.; Negus, K.; Burridge, L.; Raman, S.; Algar, E.; Yamada, T.; Little, M.H. Mech. Dev. 79, 57-72, 1998

A;Title: Distinct but overlapping expression patterns of two vertebrate slit homologs in

A;Reference number: Z22177; MUID:99279238; PMID:10349621

A;Accession: T42626

A;Status: preliminary; translated from GR/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-1025 <HOL>

A;Cross-references: UNIPROT:Q9R1B9; UNIPARC:UPI000000E8104; EMBL:AF074960; NID:g4151258;

C;Genetics:

A;Gene: Slit2

C;Superfamily: fruit fly slit protein; EGF homology; leucine-rich alpha-2-glycoprotein x

Query Match 7.4%; Score 231; DB 2; Length 1025;

Best Local Similarity 24.0%; Pred. No. 6.9e-06;

Matches 89; Conservative 32; Mismatches 122; Indels 128; Gaps 13;

QY	24	CPSCGCSQPTVFCTARQGTTPRDPVDPDTVGLYFPENGITMLDASSFAGLPGLQLLDL	83
Db	223	CPSECTCLD-TXVRCNKGKLVLPKGPDKDVTELYLDGNQFTLV-PKELSNYKHLTLIDL	280
QY	84	SQNOIASL-----RLPRLLLDLSHNSLLALEPGILDRTANVEALRIAGLQQLDEGLF	137
Db	281	SNNRISTLSNQXFSNMTQLTLILSYNRLRCIPRTFD-----GLKSL-----	323
QY	138	SLRLNHLQVSDNQLSERVPPVIRGLRGLTELRLAGNTRIAQLRPEDLAGLAALQELDVS	197
Db	324	-RLSLHGNDIS-----VVP-----	337
QY	198	NLSIQALFGDLSGLFPRLRLIAARNPNCVPLSWFGPWVRESHVTLASPEETRCHFPF	257

Db	338	-----EGAFNDLSA-----LSHLAIGANPLYCDNCMOWLSDWKSEY---KEPGIARCAGPG	386
QY	258	KNAGRLILLELDYADFGCPATTTTATVPTTRPVVREPTALSSSLAPTMLSPATAPATEAPSP	317
Db	387	EWADKLLLTTPSKKFTCQ-----GPMDDITIQAKCNPCLSN	421
QY	318	PSTAPPTVGPVP-----QPQDCP-----PSTCLNGGTCHL--GTRHHLACL	356
Db	422	PKNDGTCNNDPVDVFRCTCPYGFKGQDCDVIHACISNPKHGSGTCHLKEGENAGFWCT	481
QY	357	CPEGFTGLYCE	367
Db	482	CADGFEENCE	492

Search completed: July 27, 2006, 12:06:49
Job time : 62 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: July 27, 2006, 12:00:33 ; Search time 301 Seconds
(without alignments)
1837.739 Million cell updates/sec

Title: US-10-677-669-69

Perfect score: 3135

Sequence: 1 MCSRPVLLPLLLLLALGPG.....PLMGPPGQLQSLHAKPYI 598

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database : UniProt 7.2.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	3135	100.0	598	2	Q6UXL5_HUMAN	Q6uxl5 homo sapien
2	3083.5	98.4	673	2	Q6UXL4_HUMAN	Q6uxl4 homo sapien
3	3078.5	98.2	673	2	Q6EMK4_HUMAN	Q6emk4 homo sapien
4	2697.5	86.0	601	2	Q96CX1_HUMAN	Q96cx1 homo sapien
5	2491	79.5	673	2	Q8BJJ0_MOUSE	Q8bjj0 m 9 days em
6	2490	79.4	673	2	Q8RZG5_MOUSE	Q8rzg5 mus musculus
7	2484	79.2	673	2	Q9CZT5_MOUSE	Q9czts mus musculus
8	1213.5	38.7	661	2	Q6DF55_XENTR	Q6df55 xenopus tro
9	972.5	31.0	688	2	Q3MKM9_BRARE	Q3mkm9 brachydanio
10	927.5	29.6	643	2	Q503G2_BRARE	Q503g2 brachydanio
11	914.5	29.2	962	2	Q4S068_TETNG	Q4s068 tetraodon n
12	368.5	11.8	513	2	Q50LQ9_HUMAN	Q50lq9 homo sapien
13	359.5	11.5	635	1	LRFN4_HUMAN	Q6pj99 homo sapien
14	351	11.2	636	1	LRFN4_MOUSE	Q80xu8 mus musculus
15	351	11.2	636	2	Q3TOG8_MOUSE	Q3tog8 mus musculus
16	348	11.1	636	2	Q460G5_MOUSE	Q460g5 mus musculus
17	341	10.9	634	2	Q3UVS6_MOUSE	Q3uvs6 mus musculus
18	341	10.9	660	2	Q8LUJ0_MOUSE	Q8luu0 m adult mal
19	339	10.8	521	2	Q8BHA1_MOUSE	Q8bhla m 0 day neo
20	338	10.8	655	2	Q4SGV9_TETNG	Q4sgv9 tetraodon n
21	332	10.6	637	2	Q6A073_MOUSE	Q6a073 mus musculus
22	331.5	10.6	622	2	Q59GV4_HUMAN	Q59gv4 homo sapien
23	330	10.5	653	1	LRRC4_HUMAN	Q9hbw1 homo sapien
24	329.5	10.5	648	2	Q6DDY0_XENLA	Q6ddy0 xenopus lae
25	325.5	10.4	570	2	Q70AK2_XENLA	Q70ak2 xenopus lae
26	324	10.3	626	1	LRFN3_MOUSE	Q8bly3 mus musculus
27	324	10.3	626	2	Q505E2_MOUSE	Q505e2 mus musculus
28	323	10.3	732	2	Q4RPB8_TETNG	Q4rpb8 tetraodon n
29	322.5	10.3	682	2	Q6DJD2_XENLA	Q6djd2 xenopus lae
30	322.5	10.3	811	2	Q7LOX0_HUMAN	Q7lox0 homo sapien
31	322.5	10.3	887	2	Q75139_HUMAN	Q75139 homo sapien

32	322	10.3	605	1	ALS_PAPHA	002833 papio hamad
33	321	10.2	628	1	LRFN3_HUMAN	Q9bnc0 homo sapien
34	321	10.2	762	2	Q5JY13_HUMAN	Q5jy13 homo sapien
35	320.5	10.2	597	2	Q310Y3_BOVIN	Q310y3 bos taurus
36	320	10.2	660	1	FLRT2_HUMAN	Q43155 homo sapien
37	320	10.2	674	2	Q6RKD8_MOUSE	Q6rk8 m fibronect
38	319	10.2	602	2	Q58CS0_BOVIN	Q58cs0 bos taurus
39	319	10.2	652	2	Q4SR42_RAT	Q4s42 rattus norv
40	318.5	10.2	652	1	LRRC4_MOUSE	Q99ph1 mus musculus
41	317	10.1	778	2	Q6NU16_HUMAN	Q6nu16 homo sapien
42	312.5	10.0	648	2	Q70AK3_XENLA	Q70ak3 xenopus lae
43	312.5	10.0	935	2	Q4SBT7_TETNG	Q4sbt7 tetraodon n
44	311.5	9.9	420	1	R4RL2_MOUSE	Q7ms20 mus musculus
45	310.5	9.9	420	1	R4RL2_RAT	Q80wd1 rattus norv
46	310.5	9.9	646	1	FLRT1_HUMAN	Q9nzul homo sapien
47	308	9.8	627	2	Q8NC95_HUMAN	Q8nc95 homo sapien
48	308	9.8	649	1	FLRT3_HUMAN	Q9nzul0 homo sapien
49	308	9.8	649	2	Q542Z5_HUMAN	Q542z9 homo sapien
50	307.5	9.8	626	2	Q4TBM8_TETNG	Q4t8m8 tetraodon n
51	307.5	9.8	674	2	Q8WVA2_HUMAN	Q8wva2 homo sapien
52	307	9.8	637	2	Q68F21_XENLA	Q68f21 xenopus lae
53	307	9.8	649	2	Q5R6T0_PONPY	Q5r6t0 pongo pygma
54	306.5	9.8	730	2	Q6PHP6_MOUSE	Q6php6 mus musculus
55	306.5	9.7	730	2	Q6US92_MOUSE	Q6us92 mus musculus
56	303.5	9.7	692	2	Q4GOS0_HUMAN	Q4g080 homo sapien
57	302.5	9.6	420	1	R4RL2_HUMAN	Q86un3 homo sapien
58	302.5	9.6	618	2	Q4SHD7_TETNG	Q4shd7 tetraodon n
59	302	9.6	605	1	ALS_HUMAN	P35858 homo sapien
60	302	9.6	605	2	Q8TAY0_HUMAN	Q8tay0 homo sapien
61	299.5	9.6	677	2	Q28256_CANFA	Q28256 canis famil
62	298.5	9.5	649	2	Q88GT1_MOUSE	Q88gt1 m 12 days e
63	298.5	9.5	663	2	Q62PQ1_MOUSE	Q62pq1 mus musculus
64	295.5	9.4	640	1	NGLI_MOUSE	Q80c31 mus musculus
65	295.5	9.4	640	2	Q505E5_MOUSE	Q505e5 mus musculus
66	294.5	9.4	647	2	Q50317_BRARE	Q50317 brachydanio
67	293.5	9.4	372	2	Q499C1_BRARE	Q499c1 brachydanio
68	293.5	9.4	809	2	Q9DBY4_MOUSE	Q9db4 m adult mal
69	292.5	9.3	640	1	NGLI_HUMAN	Q9hcj2 homo sapien
70	292.5	9.3	811	2	Q496Z2_RAT	Q496z2 rattus norv
71	292.5	9.3	837	2	Q80TV0_MOUSE	Q80tv0 mus musculus
72	288.5	9.2	372	2	Q7T2W3_BRARE	Q7t2w3 brachydanio
73	288.5	9.2	581	2	Q4SV17_TETNG	Q4sv17 tetraodon n
74	288.5	9.2	640	2	Q4JIW0_HUMAN	Q4jiw0 homo sapien
75	287.5	9.2	428	2	Q4S4W6_TETNG	Q4s4w6 tetraodon n
76	287.5	9.2	713	1	LRN5_HUMAN	Q93325 homo sapien
77	286	9.1	650	2	Q4RQ15_TETNG	Q4rq15 tetraodon n
78	285	9.1	640	2	Q4JIV9_HUMAN	Q4jiv9 homo sapien
79	284.5	9.1	457	2	Q6WZD1_BRARE	Q6wzd1 brachydanio
80	284	9.1	782	2	Q5T0V4_HUMAN	Q5t0v4 homo sapien
81	283.5	9.0	603	2	Q70211_RAT	Q70211 rattus norv
82	283	9.0	1515	2	Q9DE37_BRARE	Q9de37 brachydanio
83	282.5	9.0	745	2	Q6UXK2_HUMAN	Q6uxk2 homo sapien
84	282.5	9.0	785	2	Q9P263_HUMAN	Q9p263 homo sapien
85	282	9.0	626	1	GP1BA_HUMAN	P07359 homo sapien
86	281.5	9.0	603	1	ALS_RAT	P35859 rattus norv
87	281	9.0	738	2	Q90Z45_CHICK	Q90z45 gallus gall
88	280	8.9	633	2	Q4SR95_TETNG	Q4sr95 tetraodon n
89	279.5	8.9	331	2	Q2YDZ4_EPTST	Q2ydz4 eptatretus
90	279.5	8.9	619	2	Q570Z9_MOUSE	Q570z9 mus musculus
91	278.5	8.9	301	2	Q3KQP3_MOUSE	Q3kqp3 mus musculus
92	278.5	8.9	603	1	ALS_MOUSE	P70389 mus musculus
93	278.5	8.9	603	2	Q791Q5_MOUSE	Q791q5 mus musculus
94	278.5	8.9	687	2	Q9JIL0_MOUSE	Q9jil0 mus musculus
95	278	8.9	321	2	Q6S4K4_PETMA	Q6s4k4 petromyzon
96	278	8.9	1531	1	SLIT1_RAT	Q88279 rattus norv
97	277	8.8	330	2	Q4G1K3_EPTBU	Q4g1k3 eptatretus
98	277	8.8	1532	2	Q3Y6S4_BRARE	Q3y6s4 brachydanio
99	276.5	8.8	347	2	Q32QN8_EPTST	Q32qn8 eptatretus
100	276	8.8	1071	2	Q4RT16_TETNG	Q4rt16 tetraodon n
101	276	8.8	1531	1	SLIT1_MOUSE	Q80tr4 mus musculus
102	276	8.8	2623	2	Q6WR10_HUMAN	Q6wr10 homo sapien
103	275	8.8	358	2	Q2YE01_EPTST	Q2ye01 eptatretus
104	273.5	8.7	593	2	Q6UY18_HUMAN	Q6uy18 homo sapien

105	273.5	8.7	1504	1	SLIT DROME	P24014 drosophila	178	251	8.0	1021	2	Q9V430_DROME	Q9V430 drosophila
106	273	8.7	745	2	Q5RRK3_MOUSE	Q5rrkr3 mus musculus	179	250	8.0	412	2	Q4RRU8_TETNG	Q4rru8 tetraodon n
107	273	8.7	785	2	Q62PQ3_MOUSE	Q62pq3 mus musculus	180	249.5	8.0	347	2	Q32QQ1_EPTST	Q32qq1 eptatretus
108	272.5	8.7	1524	2	Q3S2J2_BRARE	Q3s2j2 brachydanio	181	249.5	8.0	789	1	LRFN2_HUMAN	Q9ulh4 homo sapien
109	272	8.7	372	2	Q32QO2_EPTST	Q32qo2 eptatretus	182	249.5	8.0	789	1	LRFN2_MACFA	Q9be71 macaca fasc
110	271.5	8.7	342	2	Q91XL1_MOUSE	Q91xl1 mus musculus	183	249.5	8.0	2597	2	Q6WRH9_RAT	Q6wrh9 rattus norv
111	271.5	8.7	347	2	Q32QO5_EPTST	Q32qo5 eptatretus	184	248.5	7.9	420	1	TPBG_MACFA	Q4t8y9 macaca fasc
112	271.5	8.7	1312	2	Q61PF0_CAEBR	Q61pf0 caenorhabdi	185	248	7.9	284	2	Q2YE15_EPTST	Q2ye15 eptatretus
113	271	8.6	372	2	Q32QO5_EPTST	Q32qo5 eptatretus	186	248	7.9	481	1	NYX_HUMAN	Q9gru5 homo sapien
114	271	8.6	473	1	RTN4R_HUMAN	Q9br2r homo sapien	187	248	7.9	481	2	Q2M1S4_HUMAN	Q2m1s4 homo sapien
115	271	8.6	473	1	Q6PK41_HUMAN	Q9noe3 macaca fasc	188	247.5	7.9	305	2	Q4G1L3_EPTBU	Q4g1l3 eptatretus
116	270.5	8.6	541	2	Q6WZD2_BRARE	Q6wzd2 brachydanio	189	247.5	7.9	323	2	Q32Q7_T_EPTST	Q32qt7 eptatretus
117	270	8.6	478	2	Q5VM18_HUMAN	Q5vm18 homo sapien	190	247.5	7.9	323	2	Q32QX2_EPTST	Q32qx2 eptatretus
118	270	8.6	1461	2	Q6IPL6_HUMAN	Q6ipl6 homo sapien	191	247.5	7.9	739	2	Q2PNW3_XENIA	Q2pnw3 xenopus lae
119	270	8.6	1534	1	SLIT1_HUMAN	Q75093 homo sapien	192	247.5	7.9	1521	1	SLIT2_MOUSE	Q9lib9 mus musculus
120	270	8.6	1534	2	Q5VM17_HUMAN	Q5vm17 homo sapien	193	247.5	7.9	1529	1	SLIT2_HUMAN	Q94813 homo sapien
121	268.5	8.6	409	2	Q5TOV2_HUMAN	Q5tov2 homo sapien	194	247.5	7.9	1530	2	Q90WZ3_XENIA	Q90wz3 xenopus lae
122	268	8.5	417	2	Q6E4J7_PETMA	Q6e4j7 petromyzon	195	247	7.9	794	2	Q4SK16_TETNG	Q4sk16 tetraodon n
123	267.5	8.5	1512	2	Q9DE36_BRARE	Q9de36 brachydanio	196	246.5	7.9	283	2	Q2YE14_EPTST	Q2ye14 eptatretus
124	266.5	8.5	1529	2	Q7ZX12_XENIA	Q7zx12 xenopus lae	197	246.5	7.9	323	2	Q2YE01_EPTST	Q2ye01 eptatretus
125	266	8.5	460	2	Q6IPL6_HUMAN	Q6ipl6 homo sapien	198	246.5	7.9	371	2	Q32QP6_EPTST	Q32qp6 eptatretus
126	266	8.5	734	2	Q35930_MOUSE	Q35930 mus musculus	199	246	7.8	264	2	Q2VGV6_PETMA	Q2vgv6 petromyzon
127	265.5	8.5	1044	2	Q5ISR9_MACFA	Q5isr9 macaca fasc	200	246	7.8	306	2	Q2YE10_EPTST	Q2ye10 eptatretus
128	265	8.5	298	2	Q4G1L7_EPTBU	Q4g1l7 eptatretus	201	246	7.8	308	2	Q4G1I3_EPTST	Q4g1i3 eptatretus
129	265	8.5	734	2	Q5SX47_MOUSE	Q5sx47 mus musculus	202	246	7.8	346	2	Q2KIF2_BOVIN	Q2kif2 bos taurus
130	264.5	8.4	420	1	TPBG_HUMAN	Q5sk41 homo sapien	203	245.5	7.8	331	2	Q3UYU1_MOUSE	Q3uyy1 m 6 days ne
131	264	8.4	334	2	Q5VSG2_HUMAN	Q5vsg2 homo sapien	204	245.5	7.8	331	2	Q91W20_MOUSE	Q91w20 m cdna sequ
132	264	8.4	334	2	Q2IOM4_HUMAN	Q2iom4 homo sapien	205	245.5	7.8	346	2	Q32QY6_EPTBU	Q32qy6 eptatretus
133	264	8.4	332	2	Q4G1L1_EPTBU	Q4g1l1 eptatretus	206	245.5	7.8	544	2	Q61X58_CAEBR	Q61x58 caenorhabdi
134	263	8.4	308	2	Q4G1L2_EPTST	Q4g1l2 eptatretus	207	245.5	7.8	788	2	Q460M5_RAT	Q460m5 rattus norv
135	263	8.4	332	2	Q5I0E1_RAT	Q5i0e1 rattus norv	208	245	7.8	306	2	Q4G1K6_EPTST	Q4g1k6 eptatretus
136	263	8.4	1253	2	Q4TOS1_TETNG	Q4tos1 tetraodon n	209	245	7.8	321	2	Q6E4J9_PETMA	Q6e4j9 petromyzon
137	262	8.4	346	2	Q4G1L9_EPTBU	Q4g1l9 eptatretus	210	245	7.8	708	1	LRN3_PONPY	Q6419 pongo pygma
138	261.5	8.3	347	1	A2GL_HUMAN	P02750 homo sapien	211	244.5	7.8	411	2	Q4S6L6_TETNG	Q4s6l6 tetraodon n
139	261	8.3	318	2	Q2YE28_EPTBU	Q2ye28 eptatretus	212	244.5	7.8	718	2	Q73675_XENIA	Q73675 xenopus lae
140	261	8.3	341	2	Q2YE06_EPTST	Q2ye06 eptatretus	213	244.5	7.8	766	1	LRN2_RAT	Q9wvc1 rattus norv
141	261	8.3	1523	1	SLIT3_RAT	Q2ye21 eptatretus	214	244.5	7.8	788	1	LRN2_MOUSE	Q80t99 mus musculus
142	260	8.3	306	2	Q2YE21_EPTST	Q2ye21 eptatretus	215	244.5	7.8	1593	2	Q5DTL5_MOUSE	Q5dtl5 mus musculus
143	259	8.3	370	2	Q2YE78_EPTST	Q2ye78 eptatretus	216	244	7.8	346	2	Q32QV4_EPTST	Q32qv4 eptatretus
144	258	8.2	321	2	Q6E4D1_PETMA	Q6e4d1 petromyzon	217	244	7.8	458	2	Q6WZD3_BRARE	Q6wzd3 brachydanio
145	258	8.2	370	2	Q2YE77_EPTST	Q2ye77 eptatretus	218	244	7.8	567	1	GPV_RAT	Q80770 rattus norv
146	258	8.2	370	2	SLIT3_HUMAN	Q9w094 homo sapien	219	244	7.8	708	1	LRN3_HUMAN	Q9h3w5 homo sapien
147	257.5	8.2	324	2	Q4S3K9_TETNG	Q4s3k9 tetraodon n	220	243.5	7.8	347	2	Q32QO8_EPTST	Q32qo8 eptatretus
148	257.5	8.2	347	2	Q32QX0_EPTST	Q32qx0 eptatretus	221	243.5	7.8	476	1	NYX_MOUSE	P83503 mus musculus
149	257.5	8.2	501	2	Q4S2C5_TETNG	Q4szc5 tetraodon n	222	243	7.8	242	2	Q2VGV4_PETMA	Q2vgv4 petromyzon
150	257	8.2	306	2	Q2YD26_EPTST	Q2ydz6 eptatretus	223	243	7.8	290	2	Q2VGV3_PETMA	Q2vgv3 petromyzon
151	257	8.2	473	1	RTN4R_RAT	Q9sm75 rattus norv	224	243	7.8	321	2	Q6E4L4_PETMA	Q6e4l4 petromyzon
152	257	8.2	739	2	Q8BKM5_MOUSE	Q8bkm5 mus musculus	225	243	7.8	323	2	Q32QY0_EPTST	Q32qy0 eptatretus
153	256.5	8.2	342	2	Q4SGG5_TETNG	Q4sgg5 tetraodon n	226	242.5	7.7	355	2	Q2YE75_EPTST	Q2ye75 eptatretus
154	255.5	8.1	1095	2	Q90XG4_CHICK	Q90xg4 gallus gall	227	242.5	7.7	371	2	Q32QW7_EPTST	Q32qw7 eptatretus
155	254.5	8.1	1196	2	Q3V1M1_MOUSE	Q3v1m1 mus musculus	228	242.5	7.7	388	2	Q6ZM54_BRARE	Q6zm54 brachydanio
156	254	8.1	528	2	Q8N644_HUMAN	Q8n644 homo sapien	229	242.5	7.7	545	1	CPN2_HUMAN	P22732 homo sapien
157	254	8.1	1523	1	SLIT3_MOUSE	Q9wvb4 mus musculus	230	242.5	7.7	718	2	Q6PCK4_XENIA	Q6pck4 xenopus lae
158	254	8.1	1523	2	Q3UHN1_MOUSE	Q3uhn1 mus musculus	231	242	7.7	220	2	Q2VGH4_PETMA	Q2vgh4 petromyzon
159	254	8.1	1523	2	Q5SS56_MOUSE	Q5ss56 mus musculus	232	242	7.7	266	2	Q2VGF4_PETMA	Q2vgf4 petromyzon
160	253.5	8.1	347	2	Q68CK4_HUMAN	Q68ck4 homo sapien	233	242	7.7	380	2	Q5TOV3_HUMAN	Q5tov3 homo sapien
161	253.5	8.1	429	2	Q3UPM4_MOUSE	Q3upm4 mus musculus	234	242	7.7	652	2	Q7PVZ3_ANOGA	Q7pvr3 anopheles g
162	253.5	8.1	589	2	Q6GQ06_MOUSE	Q6gq06 mus musculus	235	241.5	7.7	272	2	Q4KPI2_LAMAP	Q4kpi2 lampetra ap
163	253.5	8.1	1410	2	Q20204_CAEBL	Q20204 caenorhabdi	236	241.5	7.7	311	2	Q6E4L3_PETMA	Q6e4l3 petromyzon
164	253	8.1	368	2	Q32QF3_EPTST	Q32qf3 eptatretus	237	241	7.7	330	2	Q2YD29_EPTST	Q2ydz9 eptatretus
165	253	8.1	426	1	TPBG_MOUSE	Q9z010 mus musculus	238	240.5	7.7	299	2	Q2YD23_EPTST	Q2ydz3 eptatretus
166	253	8.1	426	2	Q3UP12_MOUSE	Q3up12 mus musculus	239	240.5	7.7	323	2	Q2YB62_EPTST	Q2yeb2 eptatretus
167	253	8.1	567	1	GPV_MOUSE	Q08742 mus musculus	240	240.5	7.7	323	2	Q32QX5_EPTST	Q32qx5 eptatretus
168	252.5	8.1	323	2	Q2YEO8_EPTST	Q2ye08 eptatretus	241	240.5	7.7	332	2	Q32QY1_EPTST	Q32qy1 eptatretus
169	252	8.0	311	2	Q6E4L1_PETMA	Q6e4l1 petromyzon	242	240	7.7	308	2	Q2YD22_EPTST	Q2ydz2 eptatretus
170	252	8.0	426	1	TPBG_RAT	Q9pqr5 rattus norv	243	240	7.7	560	1	GPV_HUMAN	P40197 homo sapien
171	252	8.0	567	2	Q9QZ03_MOUSE	Q9qz03 mus musculus	244	239.5	7.6	307	2	Q2YEO4_EPTST	Q2ye04 eptatretus
172	252	8.0	567	2	Q3TA66_MOUSE	Q3ta66 mus musculus	245	239.5	7.6	370	2	Q8BGX3_MOUSE	Q8bgx3 m adult mal
173	251.5	8.0	309	2	Q2YD28_EPTST	Q2ydz8 eptatretus	246	239.5	7.6	786	2	Q5TU01_ANOGA	Q5tu01 anopheles g
174	251	8.0	473	1	RTN4R_MOUSE	Q99pi8 mus musculus	247	239.5	7.6	1256	2	Q7QCT2_ANOGA	Q7qct2 anopheles g
175	251	8.0	542	2	Q9N4G6_CAEBL	Q9n4g6 caenorhabdi	248	238.5	7.6	347	2	Q2YB56_EPTST	Q2yeb6 eptatretus
176	251	8.0	622	2	Q7Z2Q7_HUMAN	Q7z2q7 homo sapien	249	238	7.6	323	2	Q4KPI3_9PETR	Q4kpi3 ichtthyomyzo
177	251	8.0	622	2	Q6ZW15_HUMAN	Q6zw15 homo sapien	250	238	7.6	348	2	Q2YE73_EPTST	Q2ye73 eptatretus

251	238	7.6	453	2	Q86XY1_HUMAN	Q86xy1 homo sapien	324	227	7.2	324	2	Q2YE58_EPTST	Q2ye58 eptatretus
252	238	7.6	544	2	Q8UV23_9PERC	Q8uv23 spheroioides	325	227	7.2	326	2	Q4KLL3_RAT	Q4kll3 rattus norv
253	237.5	7.6	343	2	Q2YE74_EPTST	Q2ye74 eptatretus	326	227	7.2	371	2	Q32R26_EPTBU	Q32r26 eptatretus
254	237.5	7.6	346	2	Q32R39_EPTBU	Q32r39 eptatretus	327	227	7.2	783	2	Q90XG2_CHICK	Q90xg2 gallus gall
255	237.5	7.6	391	2	Q9D3K0_MOUSE	Q9d3k0 m 6 days ne	328	227	7.2	950	2	Q90Z44_CHICK	Q90z44 gallus gall
256	237.5	7.6	1174	2	Q4S4C0_TETNG	Q4s4c0 tetraodon n	329	226.5	7.2	209	2	Q2VGN5_PETMA	Q2vgn5 petromyzon
257	237	7.6	289	2	Q4K906_LAMAP	Q4kp06 lampetra ap	330	226.5	7.2	283	2	Q4G111_EPTST	Q4g111 eptatretus
258	237	7.6	370	2	Q8N967_HUMAN	Q8n967 homo sapien	331	226.5	7.2	298	2	Q4KP15_9PETR	Q4kpl15 ichthyomyzo
259	237	7.6	578	1	LRC15_RAT	LRC15 rattus norv	332	226.5	7.2	299	2	Q4G119_EPTST	Q4g119 eptatretus
260	237	7.6	707	1	LRRN3_RAT	LRRN3 rattus norv	333	226.5	7.2	323	2	Q32QU1_EPTST	Q32qu1 eptatretus
261	237	7.6	1046	2	Q7PZJ7_ANOGA	Q7pzj7 anophelies g	334	226.5	7.2	557	1	LG11_HUMAN	LG11 homo sapien
262	236.5	7.5	461	2	Q4SA12_TETNG	Q4sa12 tetraodon n	335	226.5	7.2	719	1	LRFN5_HUMAN	LRFN5 homo sapien
263	236.5	7.5	715	2	Q4RY04_TETNG	Q4ry04 tetraodon n	336	226	7.2	321	2	Q4KP16_9PETR	Q4kpl16 ichthyomyzo
264	236	7.5	366	2	Q2YZD7_EPTST	Q2yzd7 eptatretus	337	226	7.2	322	2	Q3QON1_EPTST	Q3qon1 eptatretus
265	236	7.5	707	1	LRRN3_MOUSE	LRRN3 mus musculu	338	226	7.2	364	2	Q4SQ63_TETNG	Q4sq63 tetraodon n
266	236	7.5	718	2	Q6PEZ7_XENILA	Q6pez7 xenopus lae	339	225.5	7.2	210	2	Q4SCF1_TETNG	Q4scf1 tetraodon n
267	235.5	7.5	283	2	Q2YE20_EPTST	Q2ye20 eptatretus	340	225.5	7.2	257	2	Q2VGS2_PETMA	Q2vgs2 petromyzon
268	235.5	7.5	296	2	Q4GIH6_EPTST	Q4gih6 eptatretus	341	225.5	7.2	298	2	Q6E4J3_PETMA	Q6e4j3 petromyzon
269	235.5	7.5	307	2	Q2YE00_EPTST	Q2ye00 eptatretus	342	225	7.2	733	2	Q2M032_DROPS	Q2m032 drosophila
270	235.5	7.5	307	2	Q2YE19_EPTST	Q2ye19 eptatretus	343	224.5	7.2	323	2	Q3QSO0_EPTST	Q3qso0 eptatretus
271	235.5	7.5	579	1	LRC15_MOUSE	LRC15 mus musculu	344	224.5	7.2	347	2	Q32QO0_EPTST	Q32qo0 eptatretus
272	235	7.5	574	2	Q4RRR5_TETNG	Q4rrr5 tetraodon n	345	224	7.1	218	2	Q2VGM8_PETMA	Q2vgm8 petromyzon
273	234.5	7.5	346	2	Q32R33_EPTBU	Q32r33 eptatretus	346	224	7.1	322	2	Q32QR2_EPTST	Q32qr2 eptatretus
274	234.5	7.5	488	2	Q4RK86_TETNG	Q4rk86 tetraodon n	347	223.5	7.1	209	2	Q2VGS5_PETMA	Q2vgs5 petromyzon
275	233.5	7.4	288	2	Q6EAJ4_PETMA	Q6eaj4 petromyzon	348	223.5	7.1	283	2	Q4GIH8_EPTST	Q4gih8 eptatretus
276	233.5	7.4	322	2	Q32QZ1_EPTBU	Q32qz1 eptatretus	349	223.5	7.1	323	2	Q2YE55_EPTST	Q2ye55 eptatretus
277	233.5	7.4	346	2	Q32QY9_EPTBU	Q32qy9 eptatretus	350	223.5	7.1	323	2	Q32QR0_EPTST	Q32qr0 eptatretus
278	233.5	7.4	545	2	Q5RS34_PONPY	Q5rs34 pongo pygma	351	223.5	7.1	647	2	Q4S1N0_TETNG	Q4s1n0 tetraodon n
279	233	7.4	393	2	Q32R29_EPTBU	Q32r29 eptatretus	352	223	7.1	289	2	Q6E4C8_PETMA	Q6e4c8 petromyzon
280	233	7.4	1316	2	Q9VQ25_DROME	Q9vq25 drosophila	353	223	7.1	345	2	Q2VEB3_EPTBU	Q2veb3 eptatretus
281	232.5	7.4	323	2	Q2YE85_EPTST	Q2ye85 eptatretus	354	223	7.1	349	2	Q4SH52_TETNG	Q4sh52 tetraodon n
282	232	7.4	487	2	Q4SA13_TETNG	Q4sa13 tetraodon n	355	222.5	7.1	323	2	Q2YE67_EPTST	Q2ye67 eptatretus
283	232	7.4	766	2	Q2WF71_MOUSE	Q2wf71 mus musculu	356	222.5	7.1	323	2	Q32QV2_EPTST	Q32qv2 eptatretus
284	231.5	7.4	283	2	Q4GIH4_EPTST	Q4gih4 eptatretus	357	222.5	7.1	323	2	Q32QW5_EPTST	Q32qw5 eptatretus
285	231.5	7.4	323	2	Q32Q59_EPTST	Q32q59 eptatretus	358	222.5	7.1	413	2	Q64Z15_MOUSE	Q64z15 mus musculu
286	231.5	7.4	323	2	Q2YE66_EPTST	Q2ye66 eptatretus	359	222.5	7.1	557	1	LG11_RAT	LG11 rattus norv
287	231.5	7.4	598	2	Q2PPR9_MACFA	Q2ppr9 macaca fasc	360	222.5	7.1	557	2	Q5R945_PONPY	Q5r945 pongo pygma
288	231.5	7.4	840	1	SLIK6_MOUSE	SLIK6 mus musculu	361	222.5	7.1	557	2	Q5FWS7_RAT	Q5fws7 rattus norv
289	231	7.4	294	2	Q5VT99_HUMAN	Q5vt99 homo sapien	362	222.5	7.1	792	2	Q90Z43_CHICK	Q90z43 gallus gall
290	231	7.4	324	2	Q32QP7_EPTST	Q32qp7 eptatretus	363	222	7.1	269	2	Q6E4L0_PETMA	Q6e4l0 petromyzon
291	231	7.4	347	2	Q32R08_EPTBU	Q32r08 eptatretus	364	222	7.1	348	2	Q32QN3_EPTST	Q32qn3 eptatretus
292	231	7.4	547	1	CPN2_MOUSE	Q9dbb9 mus musculu	365	222	7.1	348	2	Q32QP2_EPTST	Q32qp2 eptatretus
293	231	7.4	581	2	Q495Q6_HUMAN	Q495q6 homo sapien	366	222	7.1	348	2	Q95J38_MACFA	Q95j38 macaca fasc
294	231	7.4	619	2	Q7QBW2_ANOGA	Q7qbw2 anophelies g	367	222	7.1	722	2	Q5PPU2_XENILA	Q5ppu2 xenopus lae
295	231	7.4	766	2	Q460M4_MOUSE	Q460m4 mus musculu	368	221.5	7.1	249	2	Q2VGK2_PETMA	Q2vgk2 petromyzon
296	231	7.4	787	2	Q4SW26_TETNG	Q4sw26 tetraodon n	369	221.5	7.1	323	2	Q32QW6_EPTST	Q32qw6 eptatretus
297	230.5	7.4	257	2	Q2VGP9_PETMA	Q2vgp9 petromyzon	370	221.5	7.1	323	2	Q32QV6_EPTST	Q32qv6 eptatretus
298	230.5	7.4	323	2	Q32QO3_EPTST	Q32qo3 eptatretus	371	221.5	7.1	475	2	Q4T109_TETNG	Q4t109 tetraodon n
299	230.5	7.4	323	2	Q4SCK3_TETNG	Q4scx3 tetraodon n	372	221.5	7.1	557	1	LG11_MOUSE	LG11 mus musculu
300	230	7.3	332	2	Q8QFN6_ELAQU	Q8qfn6 elaphe quad	373	221.5	7.1	719	1	LRFN5_MOUSE	LRFN5 mus musculu
301	230	7.3	332	2	Q8QFN7_ELAQU	Q8qfn7 elaphe quad	374	221.5	7.1	721	2	Q5DTH4_MOUSE	Q5dth4 mus musculu
302	230	7.3	872	2	Q4S2Q4_TETNG	Q4sz04 tetraodon n	375	221	7.0	286	2	Q2YE07_EPTST	Q2ye07 eptatretus
303	230	7.3	1229	2	Q4T7S0_TETNG	Q4t7s0 tetraodon n	376	221	7.0	322	2	Q32QS5_EPTST	Q32qs5 eptatretus
304	229.5	7.3	223	2	Q2VGE3_PETMA	Q2vge3 petromyzon	377	221	7.0	345	2	Q32QZ9_EPTBU	Q32qz9 eptatretus
305	229.5	7.3	323	2	Q2YE65_EPTST	Q2ye65 eptatretus	378	221	7.0	348	2	Q32QU7_EPTST	Q32qu7 eptatretus
306	229.5	7.3	323	2	Q2YE70_EPTST	Q2ye70 eptatretus	379	221	7.0	1093	1	LRIG1_HUMAN	LRIG1 homo sapien
307	229.5	7.3	323	2	Q32QW0_EPTST	Q32qw0 eptatretus	380	221	7.0	1528	2	Q6Z4U6_AEDAE	Q6z4u6 aedes aegyp
308	229.5	7.3	370	2	Q32R18_EPTBU	Q32r18 eptatretus	381	220.5	7.0	210	2	Q6Z4M1_PETMA	Q6z4m1 petromyzon
309	229.5	7.3	828	2	Q8C8T7_MOUSE	Q8c8t7 mus musculu	382	220.5	7.0	306	2	Q4KP04_LAMAP	Q4kp04 lampetra ap
310	229	7.3	240	2	Q2VGN7_PETMA	Q2vgn7 petromyzon	383	220.5	7.0	322	2	Q6E4K1_PETMA	Q6e4k1 petromyzon
311	229	7.3	324	2	Q32QT5_EPTST	Q32qt5 eptatretus	384	220.5	7.0	323	2	Q32QN5_EPTST	Q32qn5 eptatretus
312	229	7.3	347	2	Q32R44_EPTBU	Q32r44 eptatretus	385	220.5	7.0	342	2	Q4RW94_TETNG	Q4rw94 tetraodon n
313	229	7.3	348	2	Q32QW2_EPTST	Q32qw2 eptatretus	386	220.5	7.0	515	1	LRTM2_MOUSE	LRTM2 mus musculu
314	229	7.3	581	1	LRC15_HUMAN	LRC15 homo sapien	387	220.5	7.0	515	2	Q8C8L1_MOUSE	Q8c8l1 mus musculu
315	228.5	7.3	294	2	Q6E416_PETMA	Q6e416 petromyzon	388	220.5	7.0	733	2	Q24250_DROME	Q24250 drosophila
316	228.5	7.3	341	2	Q6ZSA7_HUMAN	Q6zsa7 homo sapien	389	220.5	7.0	841	1	SLIK6_HUMAN	SLIK6 homo sapien
317	228.5	7.3	342	2	Q4RRU5_TETNG	Q4rru5 tetraodon n	390	220	7.0	345	2	Q32R13_EPTBU	Q32r13 eptatretus
318	228	7.3	310	2	Q4RRQ4_TETNG	Q4rrq4 tetraodon n	391	220	7.0	347	2	Q32R23_EPTBU	Q32r23 eptatretus
319	228	7.3	322	2	Q32QP0_EPTST	Q32qp0 eptatretus	392	220	7.0	582	1	LRTM3_MOUSE	LRTM3 mus musculu
320	228	7.3	838	2	Q4SP99_TETNG	Q4sp99 tetraodon n	393	220	7.0	582	2	Q3TOA3_MOUSE	Q3tga3 m adult mal
321	227.5	7.3	356	2	Q8BXQ3_MOUSE	Q8bxq3 m adult ret	394	220	7.0	582	2	Q8BZA0_MOUSE	Q8bza0 mus musculu
322	227	7.2	311	2	Q3UY51_MOUSE	Q3uy51 m adult mal	395	220	7.0	603	2	Q4SJ27_TETNG	Q4sj27 tetraodon n
323	227	7.2	321	2	Q32R27_EPTBU	Q32r27 eptatretus	396	219.5	7.0	323	2	Q32QT4_EPTST	Q32qt4 eptatretus

397	219.5	7.0	323	2	Q32QV3_EPTST	Q32qv3 eptatretus	470	212	6.8	216	2	Q2VQU4_PETMA	Q2vqu4 petromyzon
398	219.5	7.0	323	2	Q32QW4_EPTST	Q32qw4 eptatretus	471	212	6.8	218	2	Q2VGI6_PETMA	Q2vgi6 petromyzon
399	219.5	7.0	323	2	Q32QR3_EPTST	Q32qr3 eptatretus	472	212	6.8	276	2	Q4GJ9_EPTST	Q4gj9 eptatretus
400	219.5	7.0	593	2	Q4SNQ0_TETNG	Q4snq0 tetraodon n	473	212	6.8	324	2	Q32QM9_EPTST	Q32qm9 eptatretus
401	219	7.0	218	2	Q2VH13_PETMA	Q2vh13 petromyzon	474	212	6.8	445	1	R4RL1_RAT	R4rl1 rat
402	219	7.0	264	2	Q2VH48_PETMA	Q2vh48 petromyzon	475	212	6.8	918	2	Q7Q3F0_ANOGA	Q7q3f0 anopheles g
403	219	7.0	324	2	Q2YB60_EPTST	Q2yb60 eptatretus	476	211.5	6.7	192	2	Q6E419_PETMA	Q6e419 petromyzon
404	219	7.0	334	2	Q6P7C4_RAT	Q6p7c4 rattus norv	477	211.5	6.7	270	2	Q6E417_PETMA	Q6e417 petromyzon
405	218.5	7.0	322	2	Q32R19_EPTBU	Q32r19 eptatretus	478	211.5	6.7	322	2	Q32R35_EPTBU	Q32r35 eptatretus
406	218.5	7.0	323	2	Q6YU76_EPTST	Q6yu76 eptatretus	479	211.5	6.7	323	2	Q32Q57_EPTST	Q32q57 eptatretus
407	218.5	7.0	359	2	Q6GTU0_HUMAN	Q6gtu0 homo sapien	480	211.5	6.7	323	2	Q2YE72_EPTST	Q2ye72 eptatretus
408	218.5	7.0	618	1	LRC21_MOUSE	Q8k099 mus musculus	481	211.5	6.7	323	2	Q32QU9_EPTST	Q32qu9 eptatretus
409	218	7.0	216	2	Q2VGN7_PETMA	Q2vgn7 petromyzon	482	211.5	6.7	518	2	Q5F712_PONPY	Q5f712 pongo pygma
410	218	7.0	264	2	Q2VGT2_PETMA	Q2vgt2 petromyzon	483	211	6.7	187	2	Q6E412_PETMA	Q6e412 petromyzon
411	218	7.0	323	2	Q32R09_EPTST	Q32r09 eptatretus	484	211	6.7	218	2	Q2VGR7_PETMA	Q2vgr7 petromyzon
412	218	7.0	347	2	Q32R14_EPTBU	Q32r14 eptatretus	485	211	6.7	581	1	LRTM3_HUMAN	Q86vh5 homo sapien
413	217.5	6.9	288	2	Q8BR15_MOUSE	Q8br15 mus musculus	486	211	6.7	581	1	LRTM3_MACFA	Q9b9p6 macaca fasc
414	217.5	6.9	615	2	Q4SL87_TETNG	Q4sl87 tetraodon n	487	211	6.7	581	1	Q2NKK7_HUMAN	Q2nkk7 homo sapien
415	217.5	6.9	695	2	Q4T1Y8_TETNG	Q4t1y8 tetraodon n	488	210.5	6.7	209	2	Q2VGR9_PETMA	Q2vgr9 petromyzon
416	217.5	6.9	1335	2	Q61OC7_CAEBR	Q61oc7 caenorhabdi	489	210.5	6.7	257	2	Q4G1M3_EPTBU	Q4gm3 eptatretus
417	217	6.9	322	2	Q2YB64_EPTST	Q2yb64 eptatretus	490	210.5	6.7	321	2	Q6E415_PETMA	Q6e415 petromyzon
418	217	6.9	348	2	Q32QW4_EPTST	Q32qw4 eptatretus	491	210.5	6.7	322	2	Q32R10_EPTBU	Q32r10 eptatretus
419	217	6.9	637	2	Q6DCV7_XENLA	Q6dcv7 xenopus lae	492	210.5	6.7	322	2	Q32R37_EPTBU	Q32r37 eptatretus
420	216.5	6.9	209	2	Q2VGT8_PETMA	Q2vgt8 petromyzon	493	210.5	6.7	403	1	PKD1_HUMAN	P98161 homo sapien
421	216	6.9	283	2	Q6E4C7_PETMA	Q6e4c7 petromyzon	494	210	6.7	264	2	Q2VGI2_PETMA	Q2vgi2 petromyzon
422	216	6.9	282	2	Q4G1I6_EPTST	Q4gi16 eptatretus	495	210	6.7	324	2	Q32QS2_EPTST	Q32qs2 eptatretus
423	216	6.9	324	2	Q32Q54_EPTST	Q32q54 eptatretus	496	210	6.7	324	2	Q32QTO_EPTST	Q32qt0 eptatretus
424	216	6.9	324	2	Q32QW1_EPTST	Q32qw1 eptatretus	497	210	6.7	324	2	Q32QU4_EPTST	Q32qu4 eptatretus
425	215	6.9	514	2	Q4VBX1_MOUSE	Q4vbx1 mus musculus	498	210	6.7	324	2	Q2YE50_EPTST	Q2ye50 eptatretus
426	215.5	6.9	322	2	Q32R32_EPTBU	Q32r32 eptatretus	499	210	6.7	358	1	CHAD_RAT	Q70210 rattus norv
427	215.5	6.9	323	2	Q2YB61_EPTST	Q2yb61 eptatretus	500	210	6.7	1028	2	Q865R7_PIG	Q865r7 sus scrofa
428	215.5	6.9	323	2	Q32Q76_EPTST	Q32q76 eptatretus	501	209.5	6.7	214	2	Q6E4H0_PETMA	Q6e4h0 petromyzon
429	215.5	6.9	329	2	Q56NG5_CIOIN	Q56ng5 ciona intes	502	209.5	6.7	322	2	Q32R06_EPTBU	Q32r06 eptatretus
430	215.5	6.9	331	1	PLIB_AGBL	Q93233 agkistrodon	503	209.5	6.7	322	2	Q32R12_EPTBU	Q32r12 eptatretus
431	215.5	6.9	612	2	Q4SVK9_TETNG	Q4svk9 tetraodon n	504	209.5	6.7	323	2	Q32QS1_EPTST	Q32qs1 eptatretus
432	215.5	6.9	737	2	Q9VU51_DROME	Q9vu51 drosophila	505	209.5	6.7	323	2	Q32QU6_EPTST	Q32qu6 eptatretus
433	215	6.9	322	2	Q32QX8_EPTST	Q32qx8 eptatretus	506	209.5	6.7	323	2	Q32QO8_EPTST	Q32qo8 eptatretus
434	215	6.9	323	2	Q32Q00_EPTST	Q32q00 eptatretus	507	209.5	6.7	533	2	Q5E9T6_BOVIN	Q5e9t6 bos taurus
435	215	6.9	323	2	Q2YB53_EPTST	Q2yb53 eptatretus	508	209	6.7	211	2	Q6E4I3_PETMA	Q6e4i3 petromyzon
436	215	6.9	323	2	Q32QV8_EPTBU	Q32qv8 eptatretus	509	209	6.7	216	2	Q2VGO6_PETMA	Q2vgo6 petromyzon
437	215	6.9	324	2	Q32Q04_EPTST	Q32q04 eptatretus	510	209	6.7	257	2	Q6E4J6_PETMA	Q6e4j6 petromyzon
438	215	6.9	324	2	Q32Q04_EPTST	Q32q04 eptatretus	511	209	6.7	322	2	Q32QW8_EPTST	Q32qw8 eptatretus
439	215	6.9	743	2	Q6P1M7_HUMAN	Q6p1m7 homo sapien	512	209	6.7	323	2	Q32R01_EPTBU	Q32r01 eptatretus
440	214.5	6.8	215	2	Q2VH33_PETMA	Q2vh33 petromyzon	513	209	6.7	353	2	Q6UXK1_HUMAN	Q6uxk1 homo sapien
441	214.5	6.8	323	2	Q32QP5_EPTST	Q32qp5 eptatretus	514	209	6.7	358	1	CHAD_MOUSE	Q55226 mus musculus
442	214.5	6.8	323	2	Q32Q04_EPTST	Q32q04 eptatretus	515	209	6.7	358	2	Q5SUU4_MOUSE	Q5suu4 mus musculus
443	214.5	6.8	323	2	Q32Q06_EPTST	Q32q06 eptatretus	516	209	6.7	391	2	Q4S8B7_TETNG	Q4s8b7 tetraodon n
444	214.5	6.8	329	2	Q56NG6_CIOIN	Q56ng6 ciona intes	517	209	6.7	1091	1	LRI1_MOUSE	P70193 mus musculus
445	214.5	6.8	347	2	Q32QP1_EPTST	Q32qp1 eptatretus	518	208.5	6.7	350	2	Q5RH05_BRARE	Q5rh06 brachydanio
446	214.5	6.8	441	1	R4RL1_HUMAN	Q86un2 homo sapien	519	208.5	6.7	382	1	PRELP_HUMAN	P51898 homo sapien
447	214.5	6.8	716	1	LRRN1_HUMAN	Q6uxk5 homo sapien	520	208.5	6.7	382	2	Q6FHG6_HUMAN	Q6fhg6 homo sapien
448	214.5	6.8	731	2	Q4T149_TETNG	Q4t149 tetraodon n	521	208.5	6.7	382	2	Q6FG38_HUMAN	Q6fg38 homo sapien
449	214.5	6.8	1535	2	Q23991_DROME	Q23991 drosophila	522	208.5	6.7	445	1	R4RL1_MOUSE	Q8k0s5 mus musculus
450	214	6.8	295	2	Q6E4C9_PETMA	Q6e4c9 petromyzon	523	208.5	6.7	479	2	Q6X3Y5_BRARE	Q6x3y5 brachydanio
451	214	6.8	323	2	Q32R42_EPTBU	Q32r42 eptatretus	524	208.5	6.7	518	1	LRTM4_HUMAN	Q86vh4 homo sapien
452	214	6.8	324	2	Q2YB68_EPTST	Q2yb68 eptatretus	525	208.5	6.7	518	2	Q4F298_HUMAN	Q4fz98 homo sapien
453	214	6.8	516	1	LRTM2_HUMAN	Q33000 homo sapien	526	208.5	6.7	519	2	Q4F298_HUMAN	Q4fz98 homo sapien
454	214	6.8	716	1	LRRN1_RAT	Q32q07 rattus norv	527	208.5	6.7	537	1	Q4F298_HUMAN	Q4fz98 homo sapien
455	214	6.8	717	2	Q4SR34_TETNG	Q4sr34 tetraodon n	528	208.5	6.7	590	2	Q6UXJ7_HUMAN	Q6uxj7 homo sapien
456	214	6.8	2828	2	Q9NR99_HUMAN	Q9nr99 homo sapien	529	208	6.6	218	2	Q2VGF5_PETMA	Q2vgf5 petromyzon
457	213.5	6.8	238	2	Q6E4J5_PETMA	Q6e4j5 petromyzon	530	208	6.6	322	2	Q2YE51_EPTST	Q2ye51 eptatretus
458	213.5	6.8	259	2	Q2YE23_EPTST	Q2ye23 eptatretus	531	208	6.6	649	2	Q9VK22_DROME	Q9vk22 drosophila
459	213.5	6.8	273	2	Q4G1I2_EPTBU	Q4gi12 eptatretus	532	207.5	6.6	180	2	Q6E4F0_PETMA	Q6e4f0 petromyzon
460	213.5	6.8	323	2	Q32QW9_EPTST	Q32qw9 eptatretus	533	207.5	6.6	323	2	Q32QT2_EPTST	Q32qt2 eptatretus
461	213.5	6.8	359	1	CHAD_HUMAN	Q15335 homo sapien	534	207.5	6.6	330	2	Q4S074_TETNG	Q4s074 tetraodon n
462	213.5	6.8	361	1	CHAD_BOVIN	Q27972 bos taurus	535	207.5	6.6	518	2	Q6ZT31_HUMAN	Q6zt31 homo sapien
463	213	6.8	361	1	Q2VGT0_PETMA	Q2vgt0 petromyzon	536	207.5	6.6	1329	1	GP124_MOUSE	Q912v8 mus musculus
464	213	6.8	322	2	Q32QX1_EPTST	Q32qx1 eptatretus	537	207	6.6	313	1	LRC52_HUMAN	Q8n7c0 homo sapien
465	213	6.8	323	2	Q32QW5_EPTST	Q32qw5 eptatretus	538	207	6.6	323	2	Q2YB80_EPTBU	Q2yb80 eptatretus
466	213	6.8	347	2	Q32R04_EPTBU	Q32r04 eptatretus	539	207	6.6	323	2	Q32R43_EPTBU	Q32r43 eptatretus
467	213	6.8	716	1	LRRN1_MOUSE	Q61809 mus musculus	540	207	6.6	536	2	Q6P0D2_BRARE	Q6p0d2 brachydanio
468	212.5	6.8	323	2	Q32Q53_EPTST	Q32q53 eptatretus	541	207	6.6	613	2	Q501L4_CHICK	Q501l4 gallus gall
469	212.5	6.8	604	2	Q4SHB8_TETNG	Q4shb8 tetraodon n	542	207	6.6	740	2	Q5JWV6_HUMAN	Q5jwv6 homo sapien

543	207	6.6	4293	2	O08852_MOUSE	O08852_mus musculus	616	202.5	6.5	829	2	Q4RIG0_TETNG	Q4RIG0_tetraodon n
544	206.5	6.6	192	2	Q2VGE9_PETMA	Q2vge9 petromyzon	617	202	6.4	271	2	Q4RP11_LAWAP	Q4rp11 lampetra ap
545	206.5	6.6	270	2	Q6E4K6_PETMA	Q6e4k6 petromyzon	618	202	6.4	300	2	Q2YE57_EPTST	Q2ye57 eptatretus
546	206.5	6.6	274	2	Q6E4B9_PETMA	Q6e4b9 petromyzon	619	202	6.4	321	2	Q32R36_EPTBU	Q32r36 eptatretus
547	206.5	6.6	274	2	Q6E4C1_PETMA	Q6e4c1 petromyzon	620	202	6.4	321	2	Q32R38_EPTBU	Q32r38 eptatretus
548	206.5	6.6	294	2	Q6E4L2_PETMA	Q6e4l2 petromyzon	621	202	6.4	324	2	Q32Q58_EPTST	Q32q58 eptatretus
549	206.5	6.6	323	2	Q32Q08_EPTST	Q32q08 eptatretus	622	202	6.4	1117	2	Q5VQM7_ORYSA	Q5vqm7 oryza sativ
550	206.5	6.6	327	2	Q5UAS7_XENLA	Q5u487 xenopus lae	623	202	6.4	1501	2	Q2MIB4_DROPS	Q2mb4 drosophila
551	206.5	6.6	618	2	Q9DIT0_MOUSE	Q9dit0 mus musculus	624	201.5	6.4	187	2	Q6E4D7_PETMA	Q6e4d7 petromyzon
552	206	6.6	218	2	Q2VGU6_PETMA	Q2vgu6 petromyzon	625	201.5	6.4	275	2	Q4GIJ5_EPTST	Q4gij5 eptatretus
553	206	6.6	324	2	Q32QX7_EPTST	Q32qx7 eptatretus	626	201.5	6.4	372	2	Q8CBR6_MOUSE	Q8cbr6 m adult mal
554	206	6.6	353	2	Q8WU48_HUMAN	Q8wu48 homo sapien	627	201.5	6.4	457	2	Q960D1_DROME	Q960d1 drosophila
555	206	6.6	353	2	Q9ULX9_HUMAN	Q9ulx9 homo sapien	628	201.5	6.4	524	2	Q4RG59_TETNG	Q4rg59 tetraodon n
556	206	6.6	381	1	PRELP_BOVIN	Q9gkn8 bos taurus	629	201.5	6.4	551	2	Q4RF95_TETNG	Q4rf95 tetraodon n
557	206	6.6	428	2	O14498_HUMAN	O14498 homo sapien	630	201.5	6.4	606	2	Q9BZ20_HUMAN	Q9bz20 homo sapien
558	206	6.6	539	2	Q5TPW2_ANOGA	Q5tpw2 anopheles g	631	201.5	6.4	892	2	P91644_DROME	P91644 drosophila
559	206	6.6	606	2	Q3URE9_MOUSE	Q3ure9 mus musculus	632	201.5	6.4	1527	2	Q9VZZ4_DROME	Q9vzz4 drosophila
560	206	6.6	606	2	O8BLC0_MOUSE	O8blc0 m adult mal	633	201	6.4	213	2	Q6E4H6_PETMA	Q6e4h6 petromyzon
561	206	6.6	606	2	O8BZD4_MOUSE	O8bz44 mus musculus	634	201	6.4	218	2	Q6E4K9_PETMA	Q6e4k9 petromyzon
562	206	6.6	738	2	Q5UIA7_DROME	Q5uia7 drosophila	635	201	6.4	322	2	Q32QT1_EPTST	Q32qt1 eptatretus
563	206	6.6	1054	1	LRIIG2_MOUSE	Q52kr2 mus musculus	636	201	6.4	336	2	Q4S8M5_TETNG	Q4s8m5 tetraodon n
564	206	6.6	1127	2	Q4TAT9_TETNG	Q4tat9 tetraodon n	637	201	6.4	354	2	Q4W655_MOUSE	Q4w655 mus musculus
565	205.5	6.6	212	2	Q6E4H2_PETMA	Q6e4h2 petromyzon	638	201	6.4	430	2	Q58F20_HUMAN	Q58f20 homo sapien
566	205.5	6.6	479	2	Q6DH76_BRARE	Q6dh76 brachydanio	639	201	6.4	602	1	LRC40_HUMAN	LRC40 homo sapien
567	205.5	6.6	492	2	Q99KT6_MOUSE	Q99kt6 mus musculus	640	201	6.4	712	2	Q5BL20_BRARE	Q5bl20 brachydanio
568	205.5	6.6	590	1	LRTW4_MOUSE	Q80xg9 mus musculus	641	200.5	6.4	845	1	SLIK2_HUMAN	Q9h36 homo sapien
569	205	6.5	248	2	Q4GIX4_EPTST	Q4gix4 eptatretus	642	200.5	6.4	845	2	Q2KHN3_HUMAN	Q2khn3 homo sapien
570	205	6.5	256	2	Q4GIL6_EPTBU	Q4gil6 eptatretus	643	200.5	6.4	1336	2	Q2XXV6_DROYA	Q2xxv6 drosophila
571	205	6.5	320	2	Q32QR9_EPTST	Q32qr9 eptatretus	644	200.5	6.4	1337	2	Q2XXV7_DROYA	Q2xxv7 drosophila
572	205	6.5	322	2	Q2Y5E4_EPTST	Q2ye54 eptatretus	645	200	6.4	218	2	Q2XVG1_PETMA	Q2xvg1 petromyzon
573	205	6.5	322	2	Q2Y5E3_EPTST	Q2ye53 eptatretus	646	200	6.4	280	2	Q2YE26_EPTBU	Q2ye26 eptatretus
574	205	6.5	322	2	Q32QN6_EPTST	Q32qn6 eptatretus	647	200	6.4	460	2	Q4RK03_TETNG	Q4rk03 tetraodon n
575	205	6.5	324	2	Q2Y5E4_EPTST	Q2ye54 eptatretus	648	200	6.4	616	2	Q58A95_CABEL	Q58a95 caenorhabdi
576	205	6.5	486	2	Q4RU74_TETNG	Q4ru74 tetraodon n	649	200	6.4	653	2	Q02329_CABEL	Q02329 caenorhabdi
577	205	6.5	614	2	O5RDJ4_PONPY	O5rdj4 pongo pygma	650	199.5	6.4	227	2	Q4SP28_TETNG	Q4sp28 tetraodon n
578	205	6.5	614	2	O9N008_MACFA	O9n008 macaca fasc	651	199.5	6.4	261	2	Q4GIL4_EPTBU	Q4gil4 eptatretus
579	205	6.5	620	2	Q96PE5_HUMAN	Q96fe5 homo sapien	652	199.5	6.4	319	2	Q32QN9_EPTST	Q32qn9 eptatretus
580	205	6.5	740	1	CT075_HUMAN	Q8wu44 homo sapien	653	199.5	6.4	622	2	Q66HV9_BRARE	Q66hv9 brachydanio
581	204.5	6.5	322	2	Q32R03_EPTBU	Q32r03 eptatretus	654	199	6.3	260	2	Q2YE05_EPTST	Q2ye05 eptatretus
582	204.5	6.5	323	2	Q32QV2_EPTST	Q32qv2 eptatretus	655	199	6.3	298	2	Q32QW3_EPTST	Q32qw3 eptatretus
583	204.5	6.5	463	2	Q8CIV9_MOUSE	Q8civ9 mus musculus	656	199	6.3	322	2	Q32QV8_EPTST	Q32qv8 eptatretus
584	204	6.5	196	2	Q2VGM9_PETMA	Q2vgm9 petromyzon	657	199	6.3	322	2	Q32QV5_EPTST	Q32qv5 eptatretus
585	204	6.5	276	2	Q2Y5E2_EPTST	Q2ye52 eptatretus	658	199	6.3	323	2	Q32QV5_EPTBU	Q32qv5 eptatretus
586	204	6.5	323	2	Q2Y5E1_EPTST	Q2ye51 eptatretus	659	199	6.3	323	2	Q32R07_EPTBU	Q32r07 eptatretus
587	204	6.5	323	2	Q2Y5B1_EPTBU	Q32r20 eptatretus	660	199	6.3	323	2	Q32R24_EPTST	Q32r24 eptatretus
588	204	6.5	353	2	Q6QWY6_RAT	Q6qwy6 rattus norv	661	199	6.3	324	2	Q32QT9_EPTST	Q32qt9 eptatretus
589	204	6.5	1173	2	O9V7J8_DROME	O9v7j8 drosophila	662	199	6.3	846	1	SLIK2_MOUSE	Q810c0 mus musculus
590	204	6.5	1306	2	Q6P4S1_XENLA	Q6p4s1 xenopus lae	663	199	6.3	862	2	Q4S8T3_TETNG	Q4s8t3 tetraodon n
591	203.5	6.5	219	2	Q2VGZ2_PETMA	Q2vgz2 petromyzon	664	199	6.3	1328	2	Q21043_CABEL	Q21043 caenorhabdi
592	203.5	6.5	299	2	Q32QX3_EPTST	Q32qx3 eptatretus	665	198.5	6.3	259	2	Q4GIJ4_EPTST	Q4gij4 eptatretus
593	203.5	6.5	845	2	Q6AII3_HUMAN	Q6aill3 homo sapien	666	198.5	6.3	320	2	Q6YN44_HUMAN	Q6yn44 homo sapien
594	203.5	6.5	894	2	O9VKG1_DROME	O9vkg1 drosophila	667	198.5	6.3	322	2	Q32R17_EPTBU	Q32r17 eptatretus
595	203.5	6.5	1061	2	Q53ME4_ORYSA	Q53me4 oryza sativ	668	198.5	6.3	617	1	LRC21_RAT	Q9jmh2 rattus norv
596	203.5	6.5	1055	1	LRIIG2_HUMAN	Q94898 homo sapien	669	198.5	6.3	741	2	Q4SWG9_TETNG	Q4swg9 tetraodon n
597	203	6.5	218	2	Q2VGC8_PETMA	Q2vgc8 petromyzon	670	198.5	6.3	873	2	Q7XR24_ORYSA	Q7xr24 oryza sativ
598	203	6.5	269	2	Q6E4B6_PETMA	Q6e4b6 petromyzon	671	198.5	6.3	1331	1	GP124_HUMAN	Q96pe1 homo sapien
599	203	6.5	286	2	Q2Y5E17_EPTST	Q2ye17 eptatretus	672	198	6.3	192	2	Q2VH08_PETMA	Q2vh08 petromyzon
600	203	6.5	321	2	Q32QZ4_EPTBU	Q32qz4 eptatretus	673	198	6.3	298	2	Q32QV7_EPTST	Q32qv7 eptatretus
601	203	6.5	323	2	Q32R15_EPTBU	Q32r15 eptatretus	674	198	6.3	322	2	Q32QP4_EPTST	Q32qp4 eptatretus
602	203	6.5	324	2	Q2Y5E71_EPTST	Q2ye71 eptatretus	675	198	6.3	323	2	Q32R22_EPTBU	Q32r22 eptatretus
603	203	6.5	324	2	Q32QR5_EPTST	Q32qr5 eptatretus	676	198	6.3	323	2	Q32R16_EPTBU	Q32r16 eptatretus
604	203	6.5	428	2	O5NVQ6_PONPY	Q5nvq6 pongo pygma	677	198	6.3	324	2	Q32QP8_EPTST	Q32qp8 eptatretus
605	203	6.5	602	1	LRC40_MACFA	Q4r36 macaca fasc	678	198	6.3	363	2	Q7SYE5_BRARE	Q7sy5e5 brachydanio
606	203	6.5	703	2	Q4SLZ4_TETNG	Q4slz4 tetraodon n	679	198	6.3	602	1	LRC40_PONPY	Q5rife9 pongo pygma
607	203	6.5	1514	2	Q6NKA9_DROME	Q6nka9 drosophila	680	197.5	6.3	193	2	Q2VGP6_PETMA	Q2vgp6 petromyzon
608	203	6.5	1514	2	Q9NBK9_DROME	Q9nbk9 drosophila	681	197.5	6.3	280	2	Q6E4K3_PETMA	Q6e4k3 petromyzon
609	203	6.5	1514	2	Q9VUN0_DROME	Q9vun0 drosophila	682	197.5	6.3	300	2	Q6E4K8_PETMA	Q6e4k8 petromyzon
610	202.5	6.5	197	2	Q2VGR8_PETMA	Q2vgr8 petromyzon	683	197.5	6.3	323	2	Q32QU3_EPTST	Q32qu3 eptatretus
611	202.5	6.5	209	2	Q2VGV9_PETMA	Q2vgv9 petromyzon	684	197.5	6.3	441	2	Q4VBZ3_HUMAN	Q4vzb3 homo sapien
612	202.5	6.5	259	2	Q4G1K1_EPTST	Q4g1k1 eptatretus	685	197.5	6.3	537	2	Q9VE49_DROME	Q9ve49 drosophila
613	202.5	6.5	259	2	Q4GIH5_EPTST	Q4gih5 eptatretus	686	197.5	6.3	548	1	LG13_HUMAN	Q8n145 homo sapien
614	202.5	6.5	274	2	Q6E4J2_PETMA	Q6e4j2 petromyzon	687	197.5	6.3	548	2	Q4R4H3_MACFA	Q4r4h3 macaca fasc
615	202.5	6.5	322	2	Q32QZ8_EPTBU	Q32qz8 eptatretus	688	197.5	6.3	818	2	Q4SIX2_TETNG	Q4six2 tetraodon n

689	197.5	6.3	835	2	Q4SPB0_TETNG	Q4sfb0 tetraodon n	762	193	6.2	321	2	Q32R11_EPTBU	Q32r11 eptaretus
690	197.5	6.3	1321	1	GP125_HUMAN	Q8iwk6 homo sapien	763	193	6.2	327	2	Q32QX2_EPTST	Q32qn2 eptaretus
691	197	6.3	248	2	Q2YE16_EPTST	Q2ye16 eptaretus	764	193	6.2	394	2	Q4SZU8_TETNG	Q4szu8 tetraodon n
692	197	6.3	320	2	Q32Q09_EPTST	Q32qg9 eptaretus	765	193	6.2	538	2	Q2LZK6_DROPS	Q2lzk6 drosophila
693	197	6.3	342	2	Q32Q06_EPTST	Q32qg6 eptaretus	766	193	6.2	550	2	Q9VJN8_DROME	Q9vjn8 drosophila
694	197	6.3	335	2	Q9HBL6_HUMAN	Q9hbl6 homo sapien	767	192.5	6.1	185	2	Q2VGZ4_PETMA	Q2vgz4 petromyzon
695	197	6.3	345	2	Q6VYX5_ORYZA	Q6vyx5 oryza sativ	768	192.5	6.1	187	2	Q6E4D5_PETMA	Q6e4d5 petromyzon
696	197	6.3	694	2	Q6VYX5_ORYZA	Q6vyx5 oryza sativ	769	192.5	6.1	195	2	Q2VH18_PETMA	Q2vh18 petromyzon
697	196.5	6.3	1093	2	Q5XWD3_HUMAN	Q5xwd3 homo sapien	770	192.5	6.1	214	2	Q6E4G0_PETMA	Q6e4g0 petromyzon
698	196.5	6.3	209	2	Q2VGN6_PETMA	Q2vgn6 petromyzon	771	192.5	6.1	259	2	Q4G1H7_EPTST	Q4g1h7 eptaretus
699	196.5	6.3	259	2	Q2YE12_EPTST	Q2ye12 eptaretus	772	192.5	6.1	270	2	Q6E4K0_PETMA	Q6e4k0 petromyzon
700	196.5	6.3	259	2	Q4GIJ3_EPTST	Q4gi13 eptaretus	773	192.5	6.1	299	2	Q32QV1_EPTST	Q32qv1 eptaretus
701	196.5	6.3	261	2	Q4GIJ1_EPTST	Q4gi11 eptaretus	774	192.5	6.1	322	2	Q32QV3_EPTBU	Q32qv3 eptaretus
702	196.5	6.3	322	2	Q32QY4_EPTBU	Q32qy4 eptaretus	775	192.5	6.1	428	2	Q6GU68_MOUSE	Q6gu68 mus musculu
703	196.5	6.3	332	2	Q2L292_DROPS	Q2l292 drosophila	776	192.5	6.1	542	2	Q5QDZ7_MOUSE	Q5qdz7 mus musculu
704	196.5	6.3	1332	2	Q2XXW5_DROME	Q2xxw5 drosophila	777	192.5	6.1	575	2	Q32S80_CABEL	Q32s80 caenorhabdi
705	196	6.3	1333	2	Q2XXW0_DROME	Q2xxw0 drosophila	778	192.5	6.1	887	2	Q2XI21_DROER	Q2xi21 drosophila
706	196	6.3	263	2	Q6E4D0_PETMA	Q6e4d0 petromyzon	779	192.5	6.1	1093	2	Q6HA06_CRAGI	Q6ha06 crassostrea
707	196	6.3	300	2	Q32QX6_EPTST	Q32qx6 eptaretus	780	192	6.1	1265	2	Q6E4K2_PETMA	Q6e4k2 petromyzon
708	195.5	6.2	3638	2	Q15142_HUMAN	Q15142 homo sapien	781	192	6.1	273	2	Q6E4K5_PETMA	Q6e4k5 petromyzon
709	195.5	6.2	298	2	Q32QZ6_EPTBU	Q32qz6 eptaretus	782	192	6.1	300	2	Q2VE86_EPTST	Q2ve86 eptaretus
710	195.5	6.2	323	2	Q2YE59_EPTST	Q2ye59 eptaretus	783	192	6.1	548	1	LG13_MOUSE	Q8k406 mus musculu
711	195.5	6.2	378	1	PRELP_MOUSE	Q58d17 bos taurus	784	192	6.1	548	2	Q3VIR3_MOUSE	Q3vir3 mus musculu
712	195.5	6.2	378	2	Q543S0_MOUSE	Q543s0 mus musculu	785	192	6.1	627	2	Q6UN14_LEICH	Q6un14 leishmania
713	195.5	6.2	917	2	Q86PM1_DROME	Q86pm1 drosophila	786	191.5	6.1	185	2	Q2VGS8_PETMA	Q2vgs8 petromyzon
714	195.5	6.2	931	2	Q9VM16_DROME	Q9vm16 drosophila	787	191.5	6.1	187	2	Q6E417_PETMA	Q6e417 petromyzon
715	195	6.2	322	2	Q32QP9_EPTST	Q32qp9 eptaretus	788	191.5	6.1	193	2	Q2VGY8_PETMA	Q2vgy8 petromyzon
716	195	6.2	440	2	Q4RSH2_MACFA	Q4rsh2 macaca fasc	789	191.5	6.1	204	2	Q6E4J8_PETMA	Q6e4j8 petromyzon
717	195	6.2	614	2	Q6NKK3_HUMAN	Q6nuk3 homo sapien	790	191.5	6.1	915	2	Q9ERV7_MOUSE	Q9erv7 mus musculu
718	195	6.2	620	2	Q6UXM3_HUMAN	Q6uxm3 homo sapien	791	191.5	6.1	980	1	SLIK3_MOUSE	Q810b9 mus musculu
719	195	6.2	837	1	SLIK4_HUMAN	Q8iws2 homo sapien	792	191.5	6.1	980	2	Q6NZM5_MOUSE	Q6nzm5 mus musculu
720	195	6.2	837	2	Q5JXG3_HUMAN	Q5jxg3 homo sapien	793	191	6.1	192	2	Q2VGN8_PETMA	Q2vgn8 petromyzon
721	194.5	6.2	322	2	Q2YEB2_EPTBU	Q2yeb2 eptaretus	794	191	6.1	194	2	Q2VGE8_PETMA	Q2vge8 lampetra ap
722	194.5	6.2	323	2	Q32QV9_EPTST	Q32qv9 eptaretus	795	191	6.1	271	2	Q4RP00_LAMAP	Q4rp00 pongo pygma
723	194.5	6.2	369	2	Q65Z91_CHICK	Q65z91 gallus gall	796	191	6.1	440	2	Q5SRC8_PONPY	Q5src8 tetraodon n
724	194.5	6.2	680	2	Q3MH9_BOVIN	Q3mh9 bos taurus	797	191	6.1	610	2	Q4T1M0_TETNG	Q4t1m0 gallus gall
725	194.5	6.2	693	2	Q7Z3D0_HUMAN	Q7z3d0 homo sapien	798	191	6.1	868	2	Q2XQ10_CHICK	Q2xq10 gallus gall
726	194.5	6.2	699	1	ECM2_HUMAN	Q94769 homo sapien	799	190.5	6.1	251	2	Q5H721_EPTST	Q5h721 fugu rubrip
727	194.5	6.2	699	2	Q5T9F2_HUMAN	Q5t9f2 homo sapien	800	190.5	6.1	894	2	Q5H721_FUGRU	Q5h721 fugu rubrip
728	194.5	6.2	737	2	Q965M3_CABEL	Q965m3 caenorhabdi	801	190.5	6.1	1238	2	Q6NR19_DROME	Q6nr19 drosophila
729	194.5	6.2	881	2	Q965M2_CABEL	Q965m2 caenorhabdi	802	190.5	6.1	1535	2	Q9VPF0_DROME	Q9vpf0 drosophila
730	194.5	6.2	1630	1	LAP4_HUMAN	Q14150 homo sapien	803	190	6.1	191	2	Q6E4H3_PETMA	Q6e4h3 petromyzon
731	194	6.2	192	2	Q2VGG7_PETMA	Q2vg17 petromyzon	804	190	6.1	639	2	Q6E4H3_PETMA	Q6e4h3 petromyzon
732	194	6.2	258	2	Q4GI10_EPTST	Q4gi10 eptaretus	805	190	6.1	654	2	Q628N6_CABER	Q628n6 tetraodon n
733	194	6.2	258	2	Q4GIJ0_EPTST	Q4gi10 eptaretus	806	190	6.1	733	1	CT075_MOUSE	Q628n6 caenorhabdi
734	194	6.2	263	2	Q6E4C0_PETMA	Q6e4c0 petromyzon	807	190	6.1	1139	1	LRIG3_HUMAN	P59383 mus musculu
735	194	6.2	320	2	Q32Q73_EPTST	Q32q73 eptaretus	808	190	6.1	1346	2	Q9V477_DROME	Q9v477 drosophila
736	194	6.2	611	2	Q4RHK3_TETNG	Q4rhk3 tetraodon n	809	190	6.1	2800	2	Q6XHB1_DICDI	Q6xhb1 dictyosteli
737	194	6.2	692	2	Q4RV46_TETNG	Q4rv46 tetraodon n	810	189.5	6.0	252	2	Q4GIJ7_EPTST	Q4gi17 eptaretus
738	194	6.2	836	2	Q9V9V6_DROME	Q9v9v6 drosophila	811	189.5	6.0	370	2	Q4RSX9_TETNG	Q4rsx9 tetraodon n
739	193.5	6.2	186	2	Q6E4H8_PETMA	Q6e4h8 petromyzon	812	189.5	6.0	880	2	Q2XY23_DROYA	Q2xy23 drosophila
740	193.5	6.2	270	2	Q4KP03_LAMAP	Q4kp03 lampetra ap	813	189	6.0	192	2	Q2VGF2_PETMA	Q2vgf2 petromyzon
741	193.5	6.2	273	2	Q4G1M1_EPTBU	Q4g1m1 eptaretus	814	189	6.0	298	2	Q32QU2_EPTST	Q32qu2 eptaretus
742	193.5	6.2	377	1	PRELP_RAT	Q9eqp5 rattus norv	815	189	6.0	369	1	PGS1_MOUSE	P28653 mus musculu
743	193.5	6.2	378	2	Q8CAZ5_MOUSE	Q8caz5 mus musculu	816	189	6.0	369	1	PGS1_RAT	P47853 rattus norv
744	193.5	6.2	421	2	Q9NT99_HUMAN	Q9nt99 homo sapien	817	189	6.0	369	2	Q3TNV9_MOUSE	Q3tnv9 m 15 days e
745	193.5	6.2	433	2	Q6IDG7_DROME	Q6idg7 drosophila	818	189	6.0	627	2	Q4T5R5_TETNG	Q4t5r5 tetraodon n
746	193.5	6.2	545	1	LG12_HUMAN	Q9n0v4 homo sapien	819	189	6.0	760	2	Q4QGI8_LEIMA	Q4qgi8 leishmania
747	193.5	6.2	545	2	Q3MIN2_HUMAN	Q3min2 homo sapien	820	189	6.0	839	2	Q9SN46_ARATH	Q9sna46 arabidopsis
748	193.5	6.2	574	2	Q60W68_CABER	Q60w68 caenorhabdi	821	189	6.0	1392	2	Q9VAD1_DROME	Q9vad1 drosophila
749	193.5	6.2	721	1	Y2082_MYCTU	Q10690 mycobacteri	822	189	6.0	4311	2	Q7YQK5_CANFA	Q7yqk5 canis famil
750	193.5	6.2	721	2	Q7TZ24_MYCTO	Q7tz24 mycobacteri	823	188.5	6.0	348	2	Q32QV7_EPTST	Q32qv7 eptaretus
751	193.5	6.2	863	2	Q46A62_METBA	Q46a62 methanosarc	824	188.5	6.0	369	2	Q6GM15_BRARE	Q6gm15 brachydanio
752	193.5	6.2	881	2	Q2XY24_DROSI	Q2xy24 drosophila	825	188.5	6.0	370	2	Q5O4E0_BRARE	Q5o4e0 brachydanio
753	193.5	6.2	881	2	Q2XY26_DROME	Q2xy26 drosophila	826	188.5	6.0	410	2	Q9DDZ7_PETMA	Q9ddz7 petromyzon
754	193.5	6.2	893	2	Q96C25_HUMAN	Q96c25 homo sapien	827	188.5	6.0	433	2	Q5SYH5_MOUSE	Q5syh5 mus musculu
755	193.5	6.2	910	2	Q9HB75_HUMAN	Q9hb75 homo sapien	828	188.5	6.0	440	1	OMGP_MOUSE	Q3uvr3 mus musculu
756	193.5	6.2	967	2	Q3UUV5_MOUSE	Q3uuv5 mus musculu	829	188.5	6.0	440	2	Q3UVV3_MOUSE	Q3uvv3 mus musculu
757	193.5	6.2	977	1	SLIK3_HUMAN	Q94933 homo sapien	830	188.5	6.0	538	2	Q5Z8W0_ORYSA	Q5z8w0 oryza sativ
758	193.5	6.2	1333	2	Q2XXV8_DROSI	Q2xxv8 drosophila	831	188.5	6.0	655	2	Q4SBU9_TETNG	Q4sbu9 tetraodon n
759	193	6.2	1333	2	Q2XXV9_DROSI	Q2xxv9 drosophila	832	188.5	6.0	677	2	Q3KR19_HUMAN	Q3kr19 homo sapien
760	193	6.2	252	2	Q4GL12_EPTST	Q4gl12 eptaretus	833	188	6.0	218	2	Q2VGY9_PETMA	Q2vgy9 petromyzon
761	193	6.2	319	2	Q32R40_EPTBU	Q32r40 eptaretus	834	188	6.0	324	2	Q32QR1_EPTST	Q32qr1 eptaretus

835	188	6.0	368	2	Q53HU6_HUMAN	Q53hu6 homo sapien	908	184	5.9	253	2	Q6B4K5_PETMA	Q6eak5 petromyzon
836	188	6.0	369	1	PGS1_CANFA	O02678 canis famil	909	184	5.9	263	2	Q6B4K7_PETMA	Q6eak7 petromyzon
837	188	6.0	369	2	Q3UXK8_MOUSE	Q3uxk8 mus musculus	910	184	5.9	274	2	Q4G1M0_EPTBU	Q4g1m0 eptatretus
838	188	6.0	369	2	Q7TWM3_MOUSE	Q7tww3 mus musculus	911	184	5.9	291	2	Q4RF21_TETNG	Q4rf21 tetraodon n
839	188	6.0	369	2	LRTM1_MOUSE	Q8k377 mus musculus	912	184	5.9	368	1	PGS1_HUMAN	P21a10 homo sapien
840	188	6.0	522	2	Q3UVX1_MOUSE	Q3uxv1 mus musculus	913	184	5.9	368	2	Q53PF4_HUMAN	P21a14 homo sapien
841	188	6.0	626	2	Q4SE92_TETNG	Q4se92 tetraodon n	914	184	5.9	369	2	Q3TAF9_MOUSE	Q3taf9 mus musculus
842	188	6.0	818	2	Q5ZIH8_CHICK	Q5zih8 gallus gall	915	184	5.9	473	2	Q7QF76_ANOGA	Q7qf76 anopheles g
843	187.5	6.0	195	2	Q2VGR5_PETMA	Q2vg15 petromyzon	916	184	5.9	543	2	Q4RGC6_TETNG	Q4rgc6 tetraodon n
844	187.5	6.0	259	2	Q4G1L0_EPTBU	Q4g1l0 eptatretus	917	184	5.9	552	2	Q6K6X6_ORYSA	Q6k6x6 oryza sativ
845	187.5	6.0	310	2	Q5DDZ8_PETMA	Q5ddz8 petromyzon	918	184	5.9	565	2	Q7RJD0_ANOGA	Q7rjd0 anopheles g
846	187.5	6.0	350	2	Q5M7S9_XENTR	Q5m7s9 xenopus tro	919	184	5.9	837	1	SLIK4_MOUSE	Q8l0b8 mus musculus
847	187.5	6.0	352	2	Q4W6V7_CHICK	Q4w6v7 gallus gall	920	184	5.9	1058	2	Q3MNF2_BOVIN	Q3mnf2 bos taurus
848	187.5	6.0	363	2	Q9H5G9_HUMAN	Q9h5g9 homo sapien	921	183.5	5.9	187	2	Q6E4F6_PETMA	Q6e4f6 petromyzon
849	187.5	6.0	425	2	Q9VGH2_DROME	Q9vgh2 drosophila	922	183.5	5.9	287	2	Q9W2B9_DROME	Q9w2b9 drosophila
850	187.5	6.0	601	1	LRC40_BRARE	Q7sxx3 brachydanio	923	183.5	5.9	292	2	Q6NYE6_BRARE	Q6nye6 brachydanio
851	187.5	6.0	861	2	Q4ZJ82_CHICK	Q4zj82 gallus gall	924	183.5	5.9	652	2	Q7Q6Y6_ANOGA	Q7q6y6 anopheles g
852	187.5	6.0	885	2	Q2XY22_DROYA	Q2xy22 drosophila	925	183.5	5.9	727	2	Q6A0E8_MOUSE	Q6a0e8 mus musculus
853	187	6.0	260	2	Q4G1K7_EPTST	Q4g1k7 eptatretus	926	183.5	5.9	795	1	TLR1_MOUSE	Q9epq1 mus musculus
854	187	6.0	262	2	Q4G1K0_EPTST	Q4g1k0 eptatretus	927	183.5	5.9	824	2	Q5GGX1_PIG	Q5ggx1 sus scrofa
855	187	6.0	324	2	Q2VHC4_PETMA	Q2vhc4 petromyzon	928	183.5	5.9	841	1	TLR4_PIG	Q6h5y6 sus scrofa
856	187	6.0	592	2	Q61FG4_CAEER	Q61pg4 caenorhabdi	929	183.5	5.9	841	2	Q4O1C7_PIG	Q4o1c7 sus scrofa
857	187	6.0	615	2	Q9V284_DROME	Q9v284 drosophila	930	183.5	5.9	864	2	Q2XY30_DROSI	Q2xy30 drosophila
858	187	6.0	735	2	Q6E1I4_MOUSE	Q6e1i4 mus musculus	931	183.5	5.9	864	2	Q2XY31_DROSI	Q2xy31 drosophila
859	187	6.0	818	2	Q5WA51_CHICK	Q5wa51 gallus gall	932	183.5	5.9	867	2	Q2XY27_DROER	Q2xy27 drosophila
860	187	6.0	1741	2	Q5LJU2_DROME	Q5lj2 drosophila	933	183.5	5.9	871	2	Q2XY28_DROYA	Q2xy28 drosophila
861	186.5	5.9	193	2	Q2VHC4_PETMA	Q2vhc4 petromyzon	934	183.5	5.9	871	2	Q2XY29_DROYA	Q2xy29 drosophila
862	186.5	5.9	323	2	Q3QV0_EPTST	Q3qv0 eptatretus	935	183.5	5.9	1059	2	Q5ZJD0_CHICK	Q5zjd0 gallus gall
863	186.5	5.9	368	1	PGS1_XENLA	Q9ib75 xenopus lae	936	183.5	5.9	1322	2	Q2M1B0_DROPS	Q2mb0 drosophila
864	186.5	5.9	521	2	Q72UJ4_LEPIC	Q72uj4 leptospira	937	183.5	5.9	1537	1	LREC7_HUMAN	Q96nw7 homo sapien
865	186.5	5.9	639	2	Q5VZ17_HUMAN	Q5vz17 homo sapien	938	183	5.8	432	2	Q8BJ03_MOUSE	Q8bj09 mus musculus
866	186.5	5.9	799	2	Q5VZ18_HUMAN	Q5vz18 homo sapien	939	183	5.8	540	2	Q9VU53_DROME	Q9vu53 drosophila
867	186.5	5.9	839	1	TLR4_HUMAN	Q00206 homo sapien	940	183	5.8	568	2	Q6P3Y9_MOUSE	Q6p3y9 mus musculus
868	186.5	5.9	839	1	TLR4_PANPA	Q9ttn0 pan paniscu	941	183	5.8	662	1	LRC32_HUMAN	Q14392 homo sapien
869	186.5	5.9	839	2	Q5VZ19_HUMAN	Q5vz19 homo sapien	942	183	5.8	664	2	Q7ZT81_ONCMY	Q7zt81 oncorhynch
870	186	5.9	216	2	Q2VGR1_PETMA	Q2vgr1 petromyzon	943	183	5.8	972	2	Q5ZJ34_CHICK	Q5zj34 gallus gall
871	186	5.9	218	2	Q2VGR4_PETMA	Q2vgr4 petromyzon	944	182.5	5.8	187	2	Q6E4G1_PETMA	Q6e4g1 petromyzon
872	186	5.9	273	2	Q6E4B4_PETMA	Q6e4b4 petromyzon	945	182.5	5.8	187	2	Q6E4G7_PETMA	Q6e4g7 petromyzon
873	186	5.9	368	2	Q5RAY4_PONPY	Q5ray4 pongo pygma	946	182.5	5.8	219	2	Q2VGV7_PETMA	Q2vgv7 petromyzon
874	186	5.9	440	1	OMGP_HUMAN	P23515 homo sapien	947	182.5	5.8	257	2	Q4G1L8_EPTBU	Q4g1l8 eptatretus
875	186	5.9	440	2	Q53HB8_HUMAN	Q53hb8 homo sapien	948	182.5	5.8	261	2	Q2YE27_EPTBU	Q2ye27 eptatretus
876	186	5.9	552	2	Q9VT44_DROME	Q9vt44 drosophila	949	182.5	5.8	298	2	Q3QV7_EPTBU	Q3qv7 eptatretus
877	186	5.9	623	1	LRC21_HUMAN	Q9p2v4 homo sapien	950	182.5	5.8	379	1	ASEN_HUMAN	Q9bxn1 homo sapien
878	186	5.9	1029	1	TLR9_BOVIN	Q5i2m5 bos taurus	951	182.5	5.8	380	2	Q5TBF3_HUMAN	Q5tbf3 homo sapien
879	185.5	5.9	185	2	Q2VGV1_PETMA	Q2vgv1 petromyzon	952	182.5	5.8	384	2	Q6P528_HUMAN	Q6p528 homo sapien
880	185.5	5.9	191	2	Q2VGC6_PETMA	Q2vgc6 petromyzon	953	182.5	5.8	810	2	Q8T3J2_DROME	Q8t3j2 drosophila
881	185.5	5.9	191	2	Q2VGR0_PETMA	Q2vgr0 petromyzon	954	182.5	5.8	811	2	Q9VK54_DROME	Q9vk54 drosophila
882	185.5	5.9	191	2	Q2VGT6_PETMA	Q2vgt6 petromyzon	955	182.5	5.8	828	1	TLR4_PONPY	Q8spe9 pongo pygma
883	185.5	5.9	195	2	Q2VGR9_PETMA	Q2vgk9 petromyzon	956	182.5	5.8	837	1	TLR4_GORGO	Q8spe8 gorilla gor
884	185.5	5.9	251	2	Q2YE24_EPTST	Q2ye24 eptatretus	957	182.5	5.8	864	2	Q2XY32_DROME	Q2xy32 drosophila
885	185.5	5.9	369	2	Q4T3M1_TETNG	Q4t3m1 tetraodon n	958	182.5	5.8	880	2	P91643_DROME	P91643 drosophila
886	185.5	5.9	466	2	Q66IW3_XENLA	Q66iw3 xenopus lae	959	182.5	5.8	958	1	SLIK5_HUMAN	Q4q991 homo sapien
887	185.5	5.9	953	2	Q6MF87_PARUW	Q6mf87 parachlamyd	960	182.5	5.8	958	2	Q4QQH1_HUMAN	Q4qqh1 homo sapien
888	185	5.9	254	2	Q4S4N7_TETNG	Q4s4n7 tetraodon n	961	182.5	5.8	958	2	Q5VT81_HUMAN	Q5vt81 homo sapien
889	185	5.9	323	2	Q3ZR21_EPTBU	Q3zr21 eptatretus	962	182.5	5.8	1041	2	Q3HJ14_TRIER	Q3hj14 trichodesmi
890	185	5.9	389	2	Q6BP55_BRARE	Q6bpb5 brachydanio	963	182	5.8	192	2	Q2VGF9_PETMA	Q2vgf9 petromyzon
891	185	5.9	512	2	Q6PEZ8_HUMAN	Q6pez8 homo sapien	964	182	5.8	194	2	Q2VGR0_PETMA	Q2vgz0 petromyzon
892	185	5.9	603	1	LRC40_CHICK	Q5zln0 gallus gall	965	182	5.8	205	2	Q4BPX7_TETNG	Q4bp7 tetraodon n
893	184.5	5.9	257	2	Q4G1L5_EPTBU	Q4g1l5 eptatretus	966	182	5.8	252	2	Q4G1L8_EPTST	Q4g1l8 eptatretus
894	184.5	5.9	259	2	Q2YE09_EPTST	Q2ye09 eptatretus	967	182	5.8	271	2	Q6E4C4_PETMA	Q6e4c4 petromyzon
895	184.5	5.9	270	2	Q4KP09_LAMAP	Q4kp09 lampetra ap	968	182	5.8	297	2	Q4RU73_TETNG	Q4ru73 tetraodon n
896	184.5	5.9	724	2	Q5XWB9_HORSE	Q5xwb9 equus cabal	969	182	5.8	319	2	Q3ZR34_EPTBU	Q3zr34 eptatretus
897	184.5	5.9	799	2	Q9V964_DROME	Q9v964 drosophila	970	182	5.8	369	1	PGS1_SHEEP	Q46390 ovis aries
898	184.5	5.9	839	2	Q6ZTV6_MOUSE	Q6zv6 mus musculus	971	182	5.8	369	2	Q5BIM3_BOVIN	Q5bim3 bos taurus
899	184.5	5.9	841	2	Q2TNK4_PIG	Q2tnk4 sus scrofa	972	182	5.8	373	2	Q5B145_BRARE	Q5b145 brachydanio
900	184.5	5.9	841	2	Q5FAK7_PIG	Q5fak7 sus scrofa	973	182	5.8	373	2	Q8O3T7_BRARE	Q8o3t1 brachydanio
901	184.5	5.9	843	1	TLR4_HORSE	Q9myw3 equus cabal	974	182	5.8	428	2	Q8F3F8_LEPIN	Q8f3f8 leptospira
902	184.5	5.9	957	1	SLIK5_MOUSE	Q8l0b7 mus musculus	975	182	5.8	532	2	Q9G671_DROME	Q9g671 drosophila
903	184.5	5.9	1007	2	Q65XS3_ORYSA	Q65xs3 oryza sativ	976	182	5.8	678	2	Q7Q550_ANOGA	Q7q550 anopheles g
904	184.5	5.9	1046	2	Q5GQ97_CHICK	Q5gq97 gallus gall	977	182	5.8	1022	2	Q8HXV0_BOVIN	Q8hxxv0 bos taurus
905	184.5	5.9	1214	2	Q6JUN6_ORYSA	Q6jn6 oryza sativ	978	182	5.8	1029	2	Q8E6B2_BOVIN	Q8e6b2 bos taurus
906	184	5.9	187	2	Q6E4M5_PETMA	Q6e4m5 petromyzon	979	181.5	5.8	180	2	Q8BPJ0_MOUSE	Q8bpj0 mus musculus
907	184	5.9	192	2	Q2VGR6_PETMA	Q2vgj6 petromyzon	980	181.5	5.8	185	2	Q2VGR9_PETMA	Q2vgz9 petromyzon

981	181.5	5.8	191	2	Q2VH42_PETWA	Q2vh42	petromyzon	1054	178	5.7	298	2	Q32QX4_EPTST	Q32qx4	eptatretus
982	181.5	5.8	251	2	Q4G1K2_EPTST	Q4g1k2	eptatretus	1055	178	5.7	319	2	Q32QZ3_EPTBU	Q32qz3	eptatretus
983	181.5	5.8	259	2	Q4G1J8_EPTST	Q4g1j8	eptatretus	1056	178	5.7	364	2	Q66J59_XENLA	Q66j59	xenopus lae
984	181.5	5.8	298	2	Q32R41_EPTBU	Q32r41	eptatretus	1057	178	5.7	391	2	Q4RQ11_TETNG	Q4rq11	tetraodon n
985	181.5	5.8	357	1	PGS2_CHICK	P28675	gallus gall	1058	178	5.7	488	2	Q4RXQ5_TETNG	Q4rxq5	tetraodon n
986	181.5	5.8	599	2	Q7T3H6_BRARE	P72736	brachydanio	1059	178	5.7	522	1	LRTM1_HUMAN	Q86ue6	homo sapien
987	181.5	5.8	699	2	Q61PG3_CAERB	Q61pg3	caenorhabdi	1060	178	5.7	894	2	Q9BJD6_STRPU	Q9bjd6	strongyloce
988	181.5	5.8	2160	2	Q13328_MAGGR	Q13328	magnaporthe	1061	178	5.7	1049	1	TLR7_HUMAN	Q9nyk1	homo sapien
989	181.5	5.8	2160	2	Q13488_MAGGR	Q13488	magnaporthe	1062	178	5.7	1052	2	Q9Y4C4_HUMAN	Q9y4c4	homo sapien
990	181	5.8	192	2	Q2VGY4_PETWA	Q2vgy4	petromyzon	1063	178	5.7	1257	2	Q2VFN8_ANOGA	Q2vfn8	anopheles g
991	181	5.8	298	2	Q2YB69_EPTST	Q2y69	eptatretus	1064	177.5	5.7	187	2	Q2VH41_PETMA	Q2vh41	petromyzon
992	181	5.8	372	1	PGS1_HORSE	Q46403	equus cabal	1065	177.5	5.7	195	2	Q2VGD7_PETMA	Q2vgd7	petromyzon
993	181	5.8	569	2	Q7Q1F3_ANOGA	Q7q1f3	anopheles g	1066	177.5	5.7	215	2	Q2VGS6_PETMA	Q2vgs6	petromyzon
994	181	5.8	1013	2	Q8LQ10_ORISA	Q8lq10	oryza sativ	1067	177.5	5.7	275	2	Q4G1K5_EPTST	Q4g1k5	eptatretus
995	181	5.8	1333	2	Q7Q168_ANOGA	Q7q168	anopheles g	1068	177.5	5.7	796	2	Q4LDR7_PIG	Q4ldr7	sus scrofa
996	180.5	5.8	371	2	Q6GLQ6_XENLA	Q6glq6	xenopus lae	1069	177.5	5.7	796	2	Q59H19_PIG	Q59h19	sus scrofa
997	180.5	5.8	395	2	Q8BMW6_MOUSE	Q8bmw6	mus musculus	1070	177.5	5.7	809	2	Q4RMQ1_TETNG	Q4rmq1	tetraodon n
998	180.5	5.8	441	2	Q81170_DROVI	Q81170	drosofila	1071	177.5	5.7	1026	2	Q5SMW2_ORYSA	Q5smw2	oryza sativ
999	180.5	5.8	522	1	AMGO2_FONPY	Q5r7m3	pongo pygma	1072	177.5	5.7	1050	1	TLR7_MOUSE	P58681	mus musculus
1000	180.5	5.8	584	2	Q6PGX3_BRARE	Q6pgx3	brachydanio	1073	177.5	5.7	1050	2	Q548J0_MOUSE	Q548j0	m toll-like
1001	180.5	5.8	821	2	Q96PY3_HUMAN	Q96py3	homo sapien	1074	177.5	5.7	1360	2	Q7KTA0_DROME	Q7kta0	drosofila
1002	180.5	5.8	1443	2	Q9VJQ0_DROME	Q9vjq0	drosofila	1075	177.5	5.7	2300	1	CYAA_NEUTRA	Q01631	neurospora
1003	180.5	5.8	1460	2	Q5H261_XENTR	Q5hz61	xenopus tro	1076	177.5	5.7	2493	1	CYAA_NEUTRA	P49606	ustilago ma
1004	180	5.7	192	2	Q2VH29_PETWA	Q2vh29	petromyzon	1077	177.5	5.7	2493	2	Q4P3T1_USTMA	Q4p3t1	ustilago ma
1005	180	5.7	250	2	Q4G1M2_EPTBU	Q4g1m2	eptatretus	1078	177	5.6	187	2	Q6B4H5_PETMA	Q6b4h5	petromyzon
1006	180	5.7	369	1	PGS1_BOVIN	P21809	bos taurus	1079	177	5.6	192	2	Q2VGO0_PETMA	Q2vgo0	petromyzon
1007	180	5.7	522	1	LRTM1_PONPY	Q5r6b1	pongo pygma	1080	177	5.6	192	2	Q2VGR6_PETMA	Q2vgr6	petromyzon
1008	180	5.7	817	2	Q86P15_DROME	Q86p15	drosofila	1081	177	5.6	192	2	Q2VGM2_PETMA	Q2vgm2	petromyzon
1009	180	5.7	817	2	Q9VS84_DROME	Q9vs84	drosofila	1082	177	5.6	192	2	Q2VH26_PETMA	Q2vh26	petromyzon
1010	180	5.7	843	2	Q7ZTG5_CHICK	Q7ztg5	gallus gall	1083	177	5.6	192	2	Q2VH28_PETMA	Q2vh28	petromyzon
1011	180	5.7	869	2	Q4S0C1_TETNG	Q4s0c1	tetraodon n	1084	177	5.6	334	2	Q4S8U8_TETNG	Q4s8u8	tetraodon n
1012	179.5	5.7	185	2	Q2VGI7_PETWA	Q2vgi7	petromyzon	1085	177	5.6	343	1	LUM_COTJA	Q9d67	coturnix co
1013	179.5	5.7	187	2	Q6E4D6_PETWA	Q6e4d6	petromyzon	1086	177	5.6	347	2	Q58A48_BRARE	Q58a48	brachydanio
1014	179.5	5.7	195	2	Q2VGP4_PETWA	Q2vgp4	petromyzon	1087	177	5.6	662	1	LRC32_PONPY	Q7r101	pongo pygma
1015	179.5	5.7	585	2	Q61GX3_CAERB	Q61gx3	caenorhabdi	1088	177	5.6	666	2	Q7Q2W6_ANOGA	Q7q2w6	anopheles g
1016	179.5	5.7	799	2	Q3BBY2_MACMU	Q3bby2	macaca mula	1089	177	5.6	670	2	Q5FW85_MOUSE	Q5fw85	m adult mal
1017	179.5	5.7	820	2	Q5R3F8_HUMAN	Q5r3f8	homo sapien	1090	177	5.6	1370	2	Q58NA4_APTME	Q58na4	apis mellif
1018	179.5	5.7	820	2	LRI3_MOUSE	Q6plc6	mus musculus	1091	176.5	5.6	185	2	Q2VGE5_PETMA	Q2vge5	petromyzon
1019	179.5	5.7	4283	2	Q9ERV0_RAT	Q9erv0	rattus norv	1092	176.5	5.6	187	2	Q6E4M0_PETMA	Q6e4m0	petromyzon
1020	179	5.7	192	2	Q2VGC7_PETWA	Q2vgc7	petromyzon	1093	176.5	5.6	195	2	Q2VGT9_PETMA	Q2vgt9	petromyzon
1021	179	5.7	192	2	Q2VGH8_PETWA	Q2vgh8	petromyzon	1094	176.5	5.6	322	2	Q32R02_EPTBU	Q32r02	eptatretus
1022	179	5.7	192	2	Q2VH01_PETWA	Q2vh01	petromyzon	1095	176.5	5.6	520	2	Q5VR46_ORYSA	Q5vr46	oryza sativ
1023	179	5.7	194	2	Q2VH46_PETWA	Q2vh46	petromyzon	1096	176.5	5.6	522	1	AMGO2_HUMAN	Q86s12	homo sapien
1024	179	5.7	262	2	Q2YELL_EPTST	Q2yell	eptatretus	1097	176.5	5.6	522	2	Q4VBP6_HUMAN	Q4vbp6	homo sapien
1025	179	5.7	273	2	Q6E4B8_PETWA	Q6e4b8	petromyzon	1098	176.5	5.6	628	2	Q7PVZ6_ANOGA	Q7pvz6	anopheles g
1026	179	5.7	314	1	LRC52_MOUSE	Q5m8m9	mus musculus	1099	176.5	5.6	856	2	Q59H17_PIG	Q59h17	sus scrofa
1027	179	5.7	534	2	Q9VT89_DROME	Q9vt89	drosofila	1100	176.5	5.6	901	2	Q4SBD4_TETNG	Q4sbd4	tetraodon n
1028	179	5.7	700	2	Q9P244_HUMAN	Q9p244	homo sapien	1101	176.5	5.6	1495	1	LRC7_RAT	P70587	rattus norv
1029	179	5.7	742	2	Q9BJD4_STRPU	Q9bjd4	strongyloce	1102	176.5	5.6	1756	2	Q6AWK8_DROME	Q6awk8	drosofila
1030	179	5.7	751	2	Q2QP46_ORISA	Q2qp46	oryza sativ	1103	176	5.6	220	2	Q2VH09_PETMA	Q2vh09	petromyzon
1031	179	5.7	905	1	TLR3_MOUSE	Q99mb1	mus musculus	1104	176	5.6	249	2	Q4SUM4_TETNG	Q4sum4	tetraodon n
1032	179	5.7	905	2	Q499F3_MOUSE	Q499f3	mus musculus	1105	176	5.6	503	2	Q8LJ87_ORYSA	Q8lj87	oryza sativ
1033	179	5.7	969	2	Q4LBC9_ONCMY	Q4lbc9	oncorhynch	1106	176	5.6	623	2	Q5S521_DROME	Q5s521	drosofila
1034	179	5.7	1029	1	TLR9_SHEEP	Q5i2n4	ovis aries	1107	176	5.6	862	2	Q5GR02_CHICK	Q5gr02	gallus gall
1035	178.5	5.7	161	2	Q2VH51_PETWA	Q2vh51	petromyzon	1108	176	5.6	904	2	Q5TJ59_BOVIN	Q5tj59	bos taurus
1036	178.5	5.7	190	2	Q567L5_BRARE	Q567l5	brachydanio	1109	176	5.6	905	2	Q5TJ58_BOVIN	Q5tj58	bos taurus
1037	178.5	5.7	176	2	Q6E4D8_PETWA	Q6e4d8	petromyzon	1110	176	5.6	906	2	Q4SR20_TETNG	Q4sr20	tetraodon n
1038	178.5	5.7	348	2	Q5RI43_BRARE	Q5ri43	brachydanio	1111	176	5.6	1032	1	TLR9_CANFA	Q5i2m8	canis fami
1039	178.5	5.7	356	1	PGS2_COTJA	Q9deg8	coturnix co	1112	176	5.6	1257	2	Q9VK28_DROME	Q9vk28	drosofila
1040	178.5	5.7	443	2	Q67V77_ORYSA	Q67v77	oryza sativ	1113	176	5.6	1412	1	LAP2_HUMAN	Q96r11	homo sapien
1041	178.5	5.7	493	2	AMG01_HUMAN	Q86wk6	homo sapien	1114	175.5	5.6	167	2	Q2VGI8_PETMA	Q2vgi8	petromyzon
1042	178.5	5.7	587	2	Q4GGJ9_LEIMA	Q4ggj9	leishmania	1115	175.5	5.6	185	2	Q2VGN3_PETMA	Q2vgn3	petromyzon
1043	178.5	5.7	1024	1	POPC_RALSO	Q9rb2	ralstonia s	1116	175.5	5.6	251	2	Q2YE03_EPTST	Q2ye03	eptatretus
1044	178.5	5.7	1063	2	Q5Z666_ORYSA	Q5z666	oryza sativ	1117	175.5	5.6	272	2	Q4KEP14_9PETR	Q4kep14	ichthyomyzo
1045	178.5	5.7	1104	2	Q7XUH4_ORYSA	Q7xuh4	oryza sativ	1118	175.5	5.6	324	2	Q32R05_EPTBU	Q32r05	eptatretus
1046	178.5	5.7	1107	2	Q3MD20_ANAVT	Q3md20	anaeaba va	1119	175.5	5.6	384	2	Q4T0V4_TETNG	Q4t0v4	tetraodon n
1047	178.5	5.7	1310	1	GP125_MOUSE	Q7t36	mus musculus	1120	175.5	5.6	440	2	Q7TNM3_RAT	Q7tnm3	rattus norv
1048	178	5.7	187	2	Q6E4H4_PETWA	Q6e4h4	petromyzon	1121	175.5	5.6	492	1	AMG01_MOUSE	Q80z46	mus musculus
1049	178	5.7	192	2	Q2VH53_PETWA	Q2vh53	petromyzon	1122	175.5	5.6	841	2	Q2V898_BOSTR	Q2v898	boselaphus
1050	178	5.7	192	2	Q2VH56_PETWA	Q2vh56	petromyzon	1123	175.5	5.6	1017	2	Q5H718_FUGRU	Q5h718	fugu rubrip
1051	178	5.7	194	2	Q2VGE4_PETWA	Q2vge4	petromyzon	1124	175.5	5.6	1490	1	LRR7_MOUSE	Q80t67	mus musculus
1052	178	5.7	231	2	Q3TV01_MOUSE	Q3tv01	mus musculus	1125	175.5	5.6	1731	2	Q4S0D3_TETNG	Q4s0d3	tetraodon n
1053	178	5.7	296	2	Q32QX9_EPTST	Q32qx9	eptatretus	1126	175	5.6	168	2	Q2VHC0_PETMA	Q2vhc0	petromyzon

1127	175	5.6	192	2	Q2VGK6_PETMA	Q2v9k6 petromyzon	1200	172.5	5.5	378	2	Q5R294_DROSI	Q5r294 drosophila
1128	175	5.6	192	2	Q2VH74_PETMA	Q2vH74 petromyzon	1201	172.5	5.5	739	2	Q6ONV9_CAEBR	Q6onv9 caenorhabdi
1129	175	5.6	252	2	Q4GIJ2_EPTST	Q4giJ2 eptatretus	1202	172.5	5.5	823	2	Q68FM6_MOUSE	Q68fm6 mus musculus
1130	175	5.6	297	2	Q32QZ0_EPTBU	Q32qz0 eptatretus	1203	172.5	5.5	823	2	Q8CCW8_MOUSE	Q8ccw8 mus musculus
1131	175	5.6	323	2	Q32QZ0_EPTBU	Q32qz0 eptatretus	1204	172.5	5.5	1711	2	Q59DT7_DROME	Q59dt7 drosophila
1132	175	5.6	343	1	LUM_CHKCK	P51890 gallus gall	1205	172.5	5.5	1850	2	Q59DT8_DROME	Q59dt8 drosophila
1133	175	5.6	510	2	Q9BGY6_MACFA	Q9bgY6 macaca fasc	1206	172.5	5.5	1851	1	LAP4_DROME	Q7ky7 drosophila
1134	175	5.6	905	2	Q3TM31_MOUSE	Q3tm31 mus musculus	1207	172.5	5.5	4256	2	Q8MJF3_CANPA	Q8mjf3 canis famil
1135	175	5.6	941	2	Q5H722_FUGRU	Q5h722 fugu rubrip	1208	172	5.5	339	2	Q4SU68_TETNG	Q4su68 tetraodon n
1136	175	5.6	973	2	Q6KCC7_ONCWY	Q6kcc7 oncorhynch	1209	172	5.5	347	2	Q7ZUT1_BRARE	Q7zut1 brachydanio
1137	175	5.6	1137	2	Q7QHH1_ANOGA	Q7qhh1 anopheles g	1210	172	5.5	411	2	Q4S9P3_TETNG	Q4s9p3 tetraodon n
1138	174.5	5.6	130	2	Q6E4E5_PETMA	Q6e4e5 petromyzon	1211	172	5.5	577	2	Q8N3K5_HUMAN	Q8n3k5 homo sapien
1139	174.5	5.6	191	2	Q2VGI5_PETMA	Q2vgi5 petromyzon	1212	172	5.5	1134	2	Q6S510_ARATH	Q6s510 arabidopsis
1140	174.5	5.6	193	2	Q2VGDO_PETMA	Q2vgdo petromyzon	1213	172	5.5	1693	2	Q4INH4_GIBZE	Q4inh4 gibberella
1141	174.5	5.6	440	2	Q4J5V4_AZOV1	Q4j5v4 azotobacter	1214	171.5	5.5	171	2	Q2VGG0_PETMA	Q2vgg0 petromyzon
1142	174.5	5.6	512	2	Q9CQ76_MOUSE	Q9cq76 m 8 days em	1215	171.5	5.5	193	2	Q2VHD1_PETMA	Q2vhd1 petromyzon
1143	174.5	5.6	567	2	Q4SL10_TETNG	Q4sl10 tetraodon n	1216	171.5	5.5	195	2	Q2VH57_PETMA	Q2vh57 petromyzon
1144	174.5	5.6	602	1	LRC40_MOUSE	Q9cnc8 mus musculus	1217	171.5	5.5	378	2	Q9V900_DROME	Q9v900 drosophila
1145	174.5	5.6	605	1	LRC40_XENLA	Q6gpj5 xenopus lae	1218	171.5	5.5	605	1	LRC40_XENR	Q5m8g4 xenopus tro
1146	174.5	5.6	795	1	TLR6_MOUSE	Q9epw9 mus musculus	1219	171.5	5.5	683	1	LRC44_HUMAN	Q75427 homo sapien
1147	174.5	5.6	806	2	Q3UV88_MOUSE	Q3uv88 mus musculus	1220	171.5	5.5	791	2	Q2L8H0_LISMO	Q2l8h0 listeria mo
1148	174.5	5.6	1020	2	Q5ZED4_ORYSA	Q5zed4 oryza sativ	1221	171.5	5.5	858	1	LRC8D_RAT	Q2l8h0 listeria mo
1149	174.5	5.6	1060	2	Q6ZGM3_ORYSA	Q6zgm3 oryza sativ	1222	171.5	5.5	858	1	TLR5_HUMAN	Q60602 homo sapien
1150	174	5.6	194	2	Q2VH35_PETMA	Q2vh35 petromyzon	1223	171.5	5.5	858	2	Q32MI2_HUMAN	Q32mi2 homo sapien
1151	174	5.6	196	2	Q2VGF0_PETMA	Q2vgf0 petromyzon	1224	171.5	5.5	858	2	Q32MI3_HUMAN	Q32mi3 homo sapien
1152	174	5.6	299	2	Q32R28_EPTBU	Q32r28 eptatretus	1225	171.5	5.5	859	1	LRC8D_MOUSE	Q8bgr2 mus musculus
1153	174	5.6	490	2	Q4RYL5_TETNG	Q4ryl5 tetraodon n	1226	171.5	5.5	859	2	Q3TI70_MOUSE	Q3ti70 mus musculus
1154	174	5.6	535	2	Q8RX50_BRANI	Q8rx50 brassica ni	1227	171.5	5.5	859	2	Q3UVA9_MOUSE	Q3uva9 mus musculus
1155	174	5.6	544	2	Q7Q2W5_ANOGA	Q7q2w5 anopheles g	1228	171.5	5.5	1589	2	Q9IUU9_METAN	Q9uuu9 metarhizium
1156	174	5.6	651	2	Q4JQO2_XENLA	Q4jqo2 xenopus lae	1229	171	5.5	168	2	Q2VHF6_PETMA	Q2vhf6 petromyzon
1157	174	5.6	859	1	TLR5_MOUSE	Q9jlf7 mus musculus	1230	171	5.5	192	2	Q2VGI5_PETMA	Q2vgi5 petromyzon
1158	174	5.6	913	2	Q3KUR8_ONCWY	Q3kur8 oncorhynch	1231	171	5.5	194	2	Q2VGS3_PETMA	Q2vgs3 petromyzon
1159	174	5.6	951	1	LGR4_RAT	Q9z2h4 rattus norv	1232	171	5.5	299	2	Q3QZ7_EPTBU	Q3qz7 eptatretus
1160	173.5	5.5	161	2	Q2VH22_PETMA	Q2vh22 petromyzon	1233	171	5.5	354	2	Q3TSV1_MOUSE	Q3tsv1 mus musculus
1161	173.5	5.5	261	2	Q5M8T1_HUMAN	Q5m8t1 homo sapien	1234	171	5.5	360	1	PGS2_PIG	Q9xsd9 sus scrofa
1162	173.5	5.5	337	2	Q4RXJ0_TETNG	Q4rxj0 tetraodon n	1235	171	5.5	360	1	Q6DV11_GEGJA	Q6dv11 gekko japon
1163	173.5	5.5	353	2	Q64OB1_XENR	Q64ob1 xenopus tro	1236	171	5.5	469	2	Q3URB9_MOUSE	Q3urb9 mus musculus
1164	173.5	5.5	364	2	Q6GNX8_XENLA	Q6gnx8 xenopus lae	1237	171	5.5	643	2	Q502J4_BRARE	Q502j4 brachydanio
1165	173.5	5.5	421	1	OMD_HUMAN	Q99983 homo sapien	1238	171	5.5	833	1	TLR4_FELCA	P58727 felis silve
1166	173.5	5.5	421	2	Q5TBF4_HUMAN	Q5tbf4 homo sapien	1239	171	5.5	976	2	Q3TAN2_MOUSE	Q3tan2 mus musculus
1167	173.5	5.5	440	2	Q7TQ25_RAT	Q7tq25 rattus norv	1240	171	5.5	976	2	Q3V1N1_MOUSE	Q3v1n1 mus musculus
1168	173.5	5.5	537	1	LG14_MOUSE	Q8k1s1 mus musculus	1241	171	5.5	1317	2	Q5TUS9_ANOGA	Q5tus9 anopheles g
1169	173.5	5.5	537	2	Q3UYI9_MOUSE	Q3uyi9 mus musculus	1242	170.5	5.4	185	2	Q2VGH0_PETMA	Q2vgh0 petromyzon
1170	173.5	5.5	727	2	Q6GV21_BOVIN	Q6gv21 bos taurus	1243	170.5	5.4	246	2	Q6E4J1_PETMA	Q6e4j1 petromyzon
1171	173.5	5.5	806	2	Q7TPC5_MOUSE	Q7tpc5 mus musculus	1244	170.5	5.4	359	2	Q4R5D2_MACFA	Q4r5d2 macaca fasc
1172	173.5	5.5	826	1	TLR4_PAPAN	Q9tsp2 papio anubi	1245	170.5	5.4	373	1	ASPN_MOUSE	Q99mg4 mus musculus
1173	173.5	5.5	884	2	Q5H720_FUGRU	Q5h720 fugu rubrip	1246	170.5	5.4	741	2	Q8KTF7_LISMO	Q8ktf7 listeria mo
1174	173	5.5	168	2	Q2VGX8_PETMA	Q2vgx8 petromyzon	1247	170.5	5.4	761	2	Q3XNG0_9PROT	Q3xng0 magnetococc
1175	173	5.5	192	2	Q2VGG5_PETMA	Q2vgg5 petromyzon	1248	170.5	5.4	794	2	Q2L8H9_LISMO	Q2l8h9 listeria mo
1176	173	5.5	192	2	Q2VHAC_PETMA	Q2vha2 petromyzon	1249	170.5	5.4	1031	1	TLR9_FELCA	Q5i2m7 felis silve
1177	173	5.5	194	2	Q2VHC8_PETMA	Q2vhc8 petromyzon	1250	170.5	5.4	2145	1	CYAA_PODAN	Q01513 podospora a
1178	173	5.5	252	2	Q6G1I4_EPTST	Q6g1i4 eptatretus	1251	170	5.4	187	2	Q6E4D9_PETMA	Q6e4d9 petromyzon
1179	173	5.5	269	2	Q6E4C2_PETMA	Q6e4c2 petromyzon	1252	170	5.4	192	2	Q2VGG2_PETMA	Q2vgg2 petromyzon
1180	173	5.5	360	1	PGS2_HORSE	Q46542 equus caball	1253	170	5.4	192	2	Q2VGI5_PETMA	Q2vgi5 petromyzon
1181	173	5.5	470	2	Q9V354_DROME	Q9v354 drosophila	1254	170	5.4	192	2	Q2VGM4_PETMA	Q2vgm4 petromyzon
1182	173	5.5	539	2	Q5O3F6_BRARE	Q5o3f6 brachydanio	1255	170	5.4	192	2	Q2VH20_PETMA	Q2vh20 petromyzon
1183	173	5.5	664	2	Q5UT54_SALSA	Q5ut54 salmo salar	1256	170	5.4	364	1	LRC19_MOUSE	Q8bzt5 mus musculus
1184	173	5.5	853	2	Q8CB40_MOUSE	Q8cb40 mus musculus	1257	170	5.4	473	2	Q3TSO3_MOUSE	Q3tsq3 mus musculus
1185	173	5.5	892	2	Q466H0_METBA	Q466h0 methanosarc	1258	170	5.4	572	2	Q4QGJ6_LEIMA	Q4qgj6 leishmania
1186	173	5.5	925	1	GLHR_ATEL	P35409 anthopieura	1259	170	5.4	883	2	Q4VAM0_HUMAN	Q4vam0 homo sapien
1187	173	5.5	1459	2	Q7QOC5_ANOGA	Q7qoc5 anopheles g	1260	170	5.4	907	1	LGR5_HUMAN	Q75473 homo sapien
1188	173	5.5	1459	2	Q8WR64_ANOGA	Q8wr64 anopheles g	1261	170	5.4	907	2	Q4VAM2_HUMAN	Q4vam2 homo sapien
1189	172.5	5.5	161	2	Q2VGH1_PETMA	Q2vgh1 petromyzon	1262	170	5.4	1024	2	Q84IE6_RALSO	Q84ie6 ralstonia s
1190	172.5	5.5	161	2	Q2VHB2_PETMA	Q2vhb2 petromyzon	1263	170	5.4	1032	2	Q59ER8_HUMAN	Q59er8 homo sapien
1191	172.5	5.5	163	2	Q6E4E2_PETMA	Q6e4e2 petromyzon	1264	169.5	5.4	167	2	Q2VGL5_PETMA	Q2vgl5 petromyzon
1192	172.5	5.5	171	2	Q2VHC2_PETMA	Q2vhc2 petromyzon	1265	169.5	5.4	173	2	Q2VGD2_PETMA	Q2vgd2 petromyzon
1193	172.5	5.5	237	2	Q2YE13_EPTST	Q2ye13 eptatretus	1266	169.5	5.4	352	1	KERA_BOVIN	Q62702 bos taurus
1194	172.5	5.5	259	2	Q2YE22_EPTST	Q2ye22 eptatretus	1267	169.5	5.4	366	2	Q8BXO6_MOUSE	Q8bx06 mus musculus
1195	172.5	5.5	353	1	KERA_CHICK	Q42235 gallus gall	1268	169.5	5.4	463	2	Q2LYW7_DROPS	Q2lyw7 drosophila
1196	172.5	5.5	353	1	KERA_COTJA	Q9de66 coturnix co	1269	169.5	5.4	493	1	AMG01_RAT	Q80sd7 rattus norv
1197	172.5	5.5	359	1	PGS2_HUMAN	P07585 homo sapien	1270	169.5	5.4	651	2	Q4T8T9_TETNG	Q4t8t9 tetraodon n
1198	172.5	5.5	359	1	PGS2_PANTR	Q5riV9 pan troglod	1271	169.5	5.4	760	2	Q9TOK3_ARATH	Q9tok3 arabidopsis
1199	172.5	5.5	359	2	Q6FH10_HUMAN	Q6fh10 homo sapien	1272	169.5	5.4	876	2	Q67WE5_ORYSA	Q67we5 oryza sativ

1273	169.5	5.4	991	1	TLRL3_MOUSE	O6r5n8	mus musculus	1346	166.5	5.3	163	2	O6E4D4_PETMA	O6e4d4	petromyzon
1274	169.5	5.4	1271	1	FLII_MOUSE	Q9jj28	mus musculus	1347	166.5	5.3	185	2	O2VGJ9_PETMA	O2vgj9	petromyzon
1275	169	5.4	168	2	O2VGQ9_PETMA	O2vgq9	petromyzon	1348	166.5	5.3	350	2	O3KQ16_XENLA	O3kq16	xenopus lae
1276	169	5.4	217	2	O6WJ6_FELCA	O6wj6	felis silve	1349	166.5	5.3	370	2	O3ZBN5_BOVIN	O3zbn5	bos taurus
1277	169	5.4	273	2	O5XPY6 ICTALURUS p	O5xpy6	ictalurus p	1350	166.5	5.3	483	2	O5NE36_LISMO	O5ne36	listeria mo
1278	169	5.4	279	2	O58HK2_TRASC	O58hk2	trachemys s	1351	166.5	5.3	549	2	O9SVW8_ARATH	O9svw8	arabidopsis
1279	169	5.4	354	1	PGS2_MOUSE	P28G54	mus musculus	1352	166.5	5.3	582	2	O5R423_PONPY	O5r423	pongo pygma
1280	169	5.4	354	2	O3UKR1_MOUSE	O3ukr1	m 14 days p	1353	166.5	5.3	739	2	O84CF6_LISMO	O84cf6	listeria mo
1281	169	5.4	360	2	O6J0Y6_PAROL	O6j0y6	paralichthys	1354	166.5	5.3	741	2	O8KTF0_LISMO	O8ktf0	listeria mo
1282	169	5.4	757	2	O6NMS7_ORYSA	O6nms7	oryza sativ	1355	166.5	5.3	741	2	O8KTF9_LISMO	O8ktf9	listeria mo
1283	169	5.4	839	2	O9RX57_DEIRA	O9rx57	deinococcus	1356	166.5	5.3	743	2	O5SRV9_DROME	O5srv9	drosophila
1284	169	5.4	1175	2	O4RER3_TETNG	O4rer3	tetraodon n	1357	166.5	5.3	743	2	O8KTF2_LISMO	O8ktf2	listeria mo
1285	169	5.4	1298	2	O624K5_CABER	O624k5	caenorhabdi	1358	166.5	5.3	744	2	O8KH11_LISMO	O8kh11	listeria mo
1286	169	5.4	1658	2	O4PLE9_GIBIN	O4ple9	gibberella	1359	166.5	5.3	744	2	O8KI88_LISMO	O8ki88	listeria mo
1287	168.5	5.4	169	2	O2VH97_PETMA	O2vh97	petromyzon	1360	166.5	5.3	744	2	O8KTF3_LISMO	O8ktf3	listeria mo
1288	168.5	5.4	184	2	O2VGY2_PETMA	O2vgy2	petromyzon	1361	166.5	5.3	744	2	O8KTF5_LISMO	O8ktf5	listeria mo
1289	168.5	5.4	185	2	O2VGQ5_PETMA	O2vgq5	petromyzon	1362	166.5	5.3	744	2	O8KTF8_LISMO	O8ktf8	listeria mo
1290	168.5	5.4	246	2	O4KP10_LAMAP	O4kp10	lampetra ap	1363	166.5	5.3	746	2	O8KTF3_LISMO	O8ktf3	listeria mo
1291	168.5	5.4	255	2	O6WJ3_FELCA	O6wj3	felis silve	1364	166.5	5.3	792	2	O5NE37_LISMO	O5ne37	listeria mo
1292	168.5	5.4	333	2	O4SY28_TETNG	O4sy28	tetraodon n	1365	166.5	5.3	794	2	O2L8G9_LISMO	O2l8g9	listeria mo
1293	168.5	5.4	343	2	O50IS3_BRARE	O7sys8	brachydanio	1366	166.5	5.3	794	2	O2L8H1_LISMO	O2l8h1	listeria mo
1294	168.5	5.4	353	2	O7SYS8_XENLA	O7sys8	xenopus lae	1367	166.5	5.3	794	2	O2L8H2_LISMO	O2l8h2	listeria mo
1295	168.5	5.4	363	2	O8C9A7_MOUSE	O8c9a7	mus musculus	1368	166.5	5.3	794	2	O2L8H3_LISMO	O2l8h3	listeria mo
1296	168.5	5.4	366	2	O3UGP9_MOUSE	O3ugp9	mus musculus	1369	166.5	5.3	794	2	O2L8H4_LISMO	O2l8h4	listeria mo
1297	168.5	5.4	378	2	O5R264_DROSE	O5r364	drosophila	1370	166.5	5.3	794	2	O2L8H5_LISMO	O2l8h5	listeria mo
1298	168.5	5.4	619	2	O6K8K0_ORYSA	O6k8k0	oryza sativ	1371	166.5	5.3	794	2	O2L8H7_LISMO	O2l8h7	listeria mo
1299	168.5	5.4	685	2	O6T545_LISMO	O6t545	listeria mo	1372	166.5	5.3	797	2	O4EJ83_LISMO	O4ej83	listeria mo
1300	168.5	5.4	694	2	O61P91_CABER	O61p91	caenorhabdi	1373	166.5	5.3	800	1	INLA_LISMF	O723k6	listeria mo
1301	168.5	5.4	728	2	O6T546_LISMO	O6t546	listeria mo	1374	166.5	5.3	800	1	INLA_LISMO	P25146	listeria mo
1302	168.5	5.4	744	2	O8KTF6_LISMO	O8ktf6	listeria mo	1375	166.5	5.3	800	2	O4SGD5_LISMO	O4sgd5	listeria mo
1303	168.5	5.4	791	2	O2L8H6_LISMO	O2l8h6	listeria mo	1376	166.5	5.3	800	2	O4SGD6_LISMO	O4sgd6	listeria mo
1304	168.5	5.4	800	2	O4EQX8_LISMO	O4eqx8	listeria mo	1377	166.5	5.3	1012	2	O9SY16_ASTPE	O9sy16	asterina pe
1305	168.5	5.4	907	1	LGR5_MOUSE	O9zlp4	mus musculus	1378	166.5	5.3	1115	2	O60PY2_CABER	O65x09	oryza sativ
1306	168.5	5.4	1036	2	O9FN37_ARATH	O9fn37	arabidopsis	1379	166.5	5.3	1215	2	O60PY2_CABER	O60py2	caenorhabdi
1307	168.5	5.4	1360	2	O9ND11_DROME	O9nd11	drosophila	1380	166.5	5.3	1270	2	O7QHP7_ANOQA	O7qhp7	anopheles g
1308	168.5	5.4	1724	2	O4H4B6_BRARE	O4h4b6	brachydanio	1381	166.5	5.3	1280	2	O95Y17_ASTPE	O95y17	asterina pe
1309	168.5	5.4	3201	2	O2QBE0_9ALPH	O2qbe0	cercopithec	1382	166.5	5.3	3204	2	O6X248_9ALPH	O6x248	bovine herp
1310	168	5.4	351	2	O65YW8_XENLA	O65yw8	xenopus lae	1383	166	5.3	163	2	O6B4F8_PETMA	O6b4f8	petromyzon
1311	168	5.4	351	2	O32N68_XENLA	O32n68	xenopus lae	1384	166	5.3	170	2	O2VGK9_PETMA	O2vgk9	petromyzon
1312	168	5.4	402	2	O72U35_LEPIC	O72u35	leptospiira	1385	166	5.3	192	2	O2VGK1_PETMA	O2vgk1	petromyzon
1313	168	5.4	753	2	O9NRE6_HUMAN	O9nre6	homo sapien	1386	166	5.3	245	2	O4KP01_LAMAP	O4kp01	lampetra ap
1314	168	5.4	773	2	O5NRE35_LISMO	O5ne35	listeria mo	1387	166	5.3	393	2	O3UTG8_MOUSE	O3utg8	mus musculus
1315	168	5.4	951	1	LGRA_HUMAN	O9bxb1	homo sapien	1388	166	5.3	426	2	O72TC3_LEPIC	O72tc3	leptospiira
1316	168	5.4	977	2	O8GVW0_ORYSA	O8gvw0	oryza sativ	1389	166	5.3	768	2	O4SSE3_TETNG	O4sse3	tetraodon n
1317	168	5.4	1050	2	O2L4T3_CANFA	O2l4t3	canis fami	1390	166	5.3	806	2	O4SSE3_TETNG	O4sse3	tetraodon n
1318	167.5	5.3	147	2	O9TT00_PIG	O9tt00	sus scrofa	1391	166	5.3	835	1	TLR4_RAT	O6p690	rattus norv
1319	167.5	5.3	171	2	O2VHC1_PETMA	O2vhc1	petromyzon	1392	166	5.3	1030	1	TLR9_PIG	O51m3	sus scrofa
1320	167.5	5.3	185	2	O2VGV4_PETMA	O2vgv4	petromyzon	1393	166	5.3	1030	2	O865R8_PIG	O865r8	sus scrofa
1321	167.5	5.3	351	1	KERA_MOUSE	O35367	mus musculus	1394	166	5.3	1110	2	O7G768_ORYSA	O7g768	oryza sativ
1322	167.5	5.3	360	1	PGS2_SHEEP	O9ttc2	ovis aries	1395	166	5.3	1221	2	O9N523_CABEL	O9n523	caenorhabdi
1323	167.5	5.3	378	2	O72U36_LEPIC	O72u36	leptospiira	1396	166	5.3	2139	2	O4PDM0_USTMA	O4pdw0	ustilago ma
1324	167.5	5.3	396	2	O8C3D9_MOUSE	O8c3d9	mus musculus	1397	165.5	5.3	161	2	O2VGK0_PETMA	O2vgk0	petromyzon
1325	167.5	5.3	422	1	OMD_BOVIN	O77742	bos taurus	1398	165.5	5.3	169	2	O2VHG0_PETMA	O2vhu0	petromyzon
1326	167.5	5.3	694	2	O4RYL2_TETNG	O4ryl2	tetraodon n	1399	165.5	5.3	195	2	O2VGU2_PETMA	O2vgu2	petromyzon
1327	167.5	5.3	907	2	O3V1L2_MOUSE	O3vl12	mus musculus	1400	165.5	5.3	327	2	O2VHG2_PETMA	O2vhu2	petromyzon
1328	167.5	5.3	917	2	O75GM9_ORYSA	O75gm9	oryza sativ	1401	165.5	5.3	360	1	PGS2_BOVIN	O5rh5	brachydanio
1329	167.5	5.3	1174	2	O7XS37_ORYSA	O7xs37	oryza sativ	1402	165.5	5.3	360	1	PGS2_BOVIN	P21793	bos taurus
1330	167	5.3	168	2	O2VGH8_PETMA	O2vgh8	petromyzon	1403	165.5	5.3	360	1	PGS2_CANFA	O29393	canis fami
1331	167	5.3	262	2	O2VGH8_EPTST	O2ve18	eptatretus	1404	165.5	5.3	360	2	O3MHN1_BOVIN	O3mhn1	bos taurus
1332	167	5.3	537	2	O6P2A4_RAT	O6p2a4	rattus norv	1405	165.5	5.3	641	2	O5H716_FUGRU	O5h716	fugu rubrip
1333	167	5.3	582	2	O6AYT5_RAT	O6ayt5	rattus norv	1406	165.5	5.3	1005	2	O3L273_SPAAU	O3l273	sparus aura
1334	167	5.3	633	2	O8F3F6_LEPIN	O8f3f6	leptospiira	1407	165.5	5.3	1063	2	O3L274_SPAAU	O3l274	sparus aura
1335	167	5.3	743	2	O84CF7_LISMO	O84cf7	listeria mo	1408	165.5	5.3	1101	2	O59H95_HUMAN	O59h95	homo sapien
1336	167	5.3	744	2	O8KTF4_LISMO	O8ktf4	listeria mo	1409	165.5	5.3	1256	1	FLII_DROME	O24020	drosophila
1337	167	5.3	794	2	O6YW99_ORYSA	O6yw99	oryza sativ	1410	165.5	5.3	1269	1	FLII_HUMAN	O31045	homo sapien
1338	167	5.3	838	1	TLR4_CRIGR	O9w92	cricketulus	1411	165.5	5.3	1269	1	FLII_HUMAN	O5r449	pongo pygma
1339	167	5.3	886	2	O469S7_METRA	O469s7	methanosarc	1412	165	5.3	196	2	O5R4G9_PONPY	O5r4g9	pongo pygma
1340	167	5.3	939	2	O4SZU0_TETNG	O4szu0	tetraodon n	1413	165	5.3	283	2	O4RX02_TETNG	O4rx02	tetraodon n
1341	167	5.3	1112	2	O41397_LYCPM	O41397	lycopersico	1414	165	5.3	436	2	O5R6F8_PONPY	O5r6f8	pongo pygma
1342	167	5.3	1112	2	O41398_LYCPM	O41398	lycopersico	1415	165	5.3	902	2	O7RYP2_XENLA	O7ryp2	neurospora
1343	167	5.3	1112	2	O4G2W2_LYCPM	O4g2w2	lycopersico	1416	165	5.3	955	2	O32NJ0_XENLA	O32nj0	xenopus lae
1344	167	5.3	1263	2	O4SID1_TETNG	O4sid1	tetraodon n	1417	165	5.3	994	2	O9C637_ARATH	O9c637	arabidopsis
1345	167	5.3	1845	2	O5QNQ9_MOUSE	O5qng9	mus musculus	1418	165	5.3	1135	2	O7XS12_ORYSA	O7xs12	oryza sativ

1419	165	5.3	1154	2	Q7QHH4	ANOGA	Q7qhh4	anopheles g
1420	164.5	5.2	171	2	Q2VHG5	PETMA	Q2vgh5	petromyzon
1421	164.5	5.2	185	2	Q4VH97	PETMA	Q4vhu7	petromyzon
1422	164.5	5.2	235	2	Q4G1H9	EPTST	Q4gh9	eptaretus
1423	164.5	5.2	468	2	Q44V99	9BURK	Q44v99	burkholderi
1424	164.5	5.2	468	2	Q4LVE2	9BURK	Q4lve2	burkholderi
1425	164.5	5.2	582	1	SHOC2	HUMAN	Q9uq13	homo sapien
1426	164.5	5.2	582	2	Q5VZS9	HUMAN	Q5vzs9	homo sapien
1427	164.5	5.2	582	2	Q5RAV5	PONPY	Q5rav5	pongo pygma
1428	164.5	5.2	611	2	Q2RBL3	ORYSA	Q2rbl3	oryza sativ
1429	164.5	5.2	734	2	Q5R7N1	PONPY	Q5r7n1	pongo pygma
1430	164.5	5.2	805	2	Q658W7	HUMAN	Q658w7	homo sapien
1431	164.5	5.2	819	2	Q659A9	HUMAN	Q659a9	homo sapien
1432	164.5	5.2	858	1	LRC8D	HUMAN	Q7llw4	homo sapien
1433	164.5	5.2	1421	2	Q2XXU4	DROYA	Q2xxu4	drosofila
1434	164.5	5.2	1426	2	Q2XXU5	DROYA	Q2xxu5	drosofila
1435	164	5.2	257	1	LRR3C	MOUSE	P59034	mus musculus
1436	164	5.2	257	2	Q543Z4	MOUSE	Q543z4	mus musculus
1437	164	5.2	426	2	Q8F2I3	LEPINA	Q8f2i3	leptospira
1438	164	5.2	441	2	Q399Q6	BURS3	Q399q6	burkholderi
1439	164	5.2	515	2	Q60MT7	CAEBR	Q60mt7	caenorhabdi
1440	164	5.2	559	2	Q60UG7	CAEBR	Q60ug7	caenorhabdi
1441	164	5.2	570	2	Q8L3T8	ORYSA	Q8l3t8	oryza sativ
1442	164	5.2	611	2	Q7TQ62	MOUSE	Q7tq62	mus musculus
1443	164	5.2	696	1	SLIKI	HUMAN	Q96px8	homo sapien
1444	164	5.2	696	1	SLIK1	MOUSE	Q810c1	mus musculus
1445	164	5.2	696	1	SLIK1	PONPY	Q5rac4	pongo pygma
1446	164	5.2	760	2	Q69Z70	MOUSE	Q69z70	mus musculus
1447	164	5.2	805	2	Q7QFF0	ANOGA	Q7qff0	anopheles g
1448	164	5.2	807	2	Q2M124	DROPS	Q2m124	drosofila
1449	164	5.2	828	1	LGR6	HUMAN	Q9hbx8	homo sapien
1450	164	5.2	833	2	Q7Q8I8	ANOGA	Q7q8i8	anopheles g
1451	164	5.2	839	2	Q8MIQ2	RABIT	Q8miq2	oryctolagus
1452	164	5.2	870	2	Q6PCD4	HUMAN	Q6pcd4	homo sapien
1453	164	5.2	904	1	TLR3	HUMAN	Q15455	homo sapien
1454	164	5.2	904	2	Q4VAL2	HUMAN	Q00468	homo sapien
1455	164	5.2	904	2	Q6E4E0	PETMA	Q00468	homo sapien
1456	164	5.2	1032	2	Q865B9	CANFA	Q6e4e0	petromyzon
1457	164	5.2	1395	2	Q7SC01	NEUCR	Q6e4h7	petromyzon
1458	164	5.2	1913	2	Q5SVA2	HUMAN	Q2vgf3	petromyzon
1459	164	5.2	2045	1	AGRN	HUMAN	Q2vgx2	petromyzon
1460	164	5.2	2045	2	Q6F0E1	HUMAN	Q502f2	brachydanio
1461	163.5	5.2	163	2	Q6E4E0	PETMA	Q9de04	oreochromis
1462	163.5	5.2	166	2	Q6E4I0	PETMA	Q5r5r1	pongo pygma
1463	163.5	5.2	180	2	Q6E4H7	PETMA	Q539z4	homo sapien
1464	163.5	5.2	185	2	Q2VGF3	PETMA	Q48809	arabidopsis
1465	163.5	5.2	195	2	Q2VGX2	PETMA	Q2vh67	petromyzon
1466	163.5	5.2	362	2	Q502F2	ERARE	Q2vh86	petromyzon
1467	163.5	5.2	370	2	Q9DB04	ORENI	Q2vgt3	petromyzon
1468	163.5	5.2	582	2	Q5RSR1	PONPY	Q2vgw9	petromyzon
1469	163.5	5.2	671	2	Q53GZ4	HUMAN	Q2vgw9	petromyzon
1470	163.5	5.2	786	2	Q48809	ARATH	Q9de03	oreochromis
1471	163	5.2	158	2	Q2VH67	PETMA	Q4rb6	tetraodon n
1472	163	5.2	170	2	Q2VH86	PETMA	Q6zh85	oryza sativ
1473	163	5.2	172	2	Q2VGT3	PETMA	Q8r378	mus musculus
1474	163	5.2	192	2	Q2VGE0	PETMA	Q88520	mus musculus
1475	163	5.2	194	2	Q2VGM9	PETMA	Q3ujh6	mus musculus
1476	163	5.2	359	2	Q9DS03	ORENI	Q6pn3	mus musculus
1477	163	5.2	452	2	Q4RB6	TETNG	Q9bjd5	strongyloce
1478	163	5.2	501	2	Q6ZH85	ORYSA	Q76ct9	paralichthy
1479	163	5.2	524	2	Q8R378	MOUSE	Q76ct9	paralichthy
1480	163	5.2	582	1	SHOC2	MOUSE	Q9biw9	caenorhabdi
1481	163	5.2	582	2	Q3UJH6	MOUSE	Q80u72	mus musculus
1482	163	5.2	929	2	Q6P9N3	MOUSE	Q2vhe8	petromyzon
1483	163	5.2	933	2	Q9BDU5	STRPUL	Q2vgt1	petromyzon
1484	163	5.2	961	2	Q76CT7	PAROL	Q9v428	drosofila
1485	163	5.2	961	2	Q76CT9	PAROL	Q5xih1	rattus norv
1486	163	5.2	1221	2	Q9BIW9	CAEBL		
1487	163	5.2	1612	1	LAP4	MOUSE		
1488	162.5	5.2	161	2	Q2VHE8	PETMA		
1489	162.5	5.2	192	2	Q2VGT1	PETMA		
1490	162.5	5.2	283	2	Q9V428	DROME		
1491	162.5	5.2	375	2	Q5XIH1	RAT		

ALIGNMENTS

RESULT 1

Q6UKL5	HUMAN	PRELIMINARY; PRT; 598 AA.
AC	Q6UKL5	
DT	05-JUL-2004	integrated into UniProtKB/TrEMBL.
DT	05-JUL-2004	sequence version 1.
DT	07-FEB-2006	entry version 10.
DE	CSRV314.	
GN	ORFNames=UNQ314;	
OS	Homo sapiens (Human).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;	
OC	Homo.	
OX	NCBI_TaxID=9606;	
RN	[1]	
RP	NCLEOTIDE SEQUENCE.	
RX	MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;	
RA	Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,	
RA	Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,	
RA	Eaton D., Foster J.S., Grimaldi C., Gu O., Hass P.E., Heldens S.,	
RA	Huang A., Kim H.S., Klinevski L., Jin Y., Johnson S., Lee J.,	
RA	Lewis L., Liao D., Mark M.R., Robbie E., Sanchez C., Schoenfeld J.,	
RA	Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,	
RA	Vandlen R.L., Watanabe C., Wieand D., Woods K., Xie M.-H.,	
RA	Yansura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,	
RA	Wood W.I., Godowski P.J., Gray A.M.;	
RT	"The secreted protein discovery initiative (SPDI), a large-scale	
RT	effort to identify novel human secreted and transmembrane proteins: a	
RT	bioinformatics assessment."	
RL	Genome Res. 13:2265-2270 (2003).	
CC	Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms	
CC	Distributed under the Creative Commons Attribution-NoDerivs License	
CC	-----	
DR	EMBL; AY58298; AAQ88665.1; -; mRNA.	
DR	InterPro; IPR006210; EGF.	
DR	InterPro; IPR000742; EGF_3.	
DR	InterPro; IPR006209; EGF_like.	
DR	InterPro; IPR013032; EGF_like_reg.	
DR	InterPro; IPR003961; FN_III.	
DR	InterPro; IPR001611; LRR.	
DR	InterPro; IPR000483; LRR_C.	
DR	InterPro; IPR000372; LRR_Cys_N.	
DR	InterPro; IPR003591; LRR_typ.	
DR	Pfam; PF00008; EGF_1.	
DR	Pfam; PF00041; fn3_1.	
DR	Pfam; PF00360; LRR_1; 3.	
DR	Pfam; PF01463; LRRCT; 1.	
DR	Pfam; PF01462; LRRNT; 1.	
DR	PRINTS; PR00019; LEURICRPT.	
DR	SMART; SM00181; EGF; 1.	
DR	SMART; SM00082; LRRCT; 1.	
DR	SMART; SM00013; LRRNT; 1.	
DR	PROSITE; PS00022; EGF_1; 1.	
DR	PROSITE; PS01186; EGF_2; 1.	
DR	PROSITE; PS50026; EGF_3; 1.	
DR	PROSITE; PS50853; FN3; 1.	
DR	PROSITE; PS50853; FN3; 1.	
DR	SEQUENCE 598 AA; 63030 MW; C596CEBE963AA86C CRC64;	
DR	SEQUENCE 598 AA; 63030 MW; C596CEBE963AA86C CRC64;	

Query Match	100.0%	Score 3135;	DB 2;	Length 598;
Best Local Similarity	100.0%;	Pred. No. 1.2e-171;	Indels 0;	Gaps 0;
Matches 598;	Conservative 0;	Mismatches 0;		
QY	1	MCSRVP	LLP	LLP
DB	1	MCSRVP	LLP	LLP
QY	61	ENGI	TMLD	ASSF
DB	61	ENGI	TMLD	ASSF
QY	121	ALRL	AGLGLQ	LDGLFS
DB	121	ALRL	AGLGLQ	LDGLFS
QY	181	RPED	LAGLAA	QELD
DB	181	RPED	LAGLAA	QELD
QY	241	SVTL	LASPEE	TRCH
DB	241	SVTL	LASPEE	TRCH
QY	301	APT	LSPT	APATEA
DB	301	APT	LSPT	APATEA
QY	361	FTGL	YCES	OGGTRP
DB	361	FTGL	YCES	OGGTRP
QY	421	LYRN	LSGDKR	LV
DB	421	LYRN	LSGDKR	LV
QY	481	PPAV	HSNHP	VTQARE
DB	481	PPAV	HSNHP	VTQARE
QY	541	GPCA	GPLE	GVKVP
DB	541	GPCA	GPLE	GVKVP

RESULT 2

Q6UXL4 HUMAN PRELIMINARY; PRT: 673 AA.

AC Q6UXL4;

DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.

DT 07-FEB-2006, entry version 1.

DT CSRV314 (Slit-like 2).

DE Name=SLITL2; ORFNames=UNQ314;

GN Homo sapiens (Human).

OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;

OC Homo.

OX NCBI_TaxID=9606;

RN [1]

RX MEDLINE=22987296; PubMed=12975309; DOI=10.1101/gr.1293003;

RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,

RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,

RA Eaton D., Foster J.S., Grimaldi C., Gu Q., Hase P.E., Heldens S.,

RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,

RA Lewis L., Liao D., Mark M.R., Robbie E., Sanchez C., Schoenfeld J.,

RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,

RA Vandlen R.L., Watanabe C., Wiedand D., Woods K., Xie M.-H.,

RA Yansura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,

RA Wood W.I., Godowski P.J., Gray A.M.;

RT "The secreted protein discovery initiative (SPDI), a large-scale

RT effort to identify novel human secreted and transmembrane proteins: a

Db	61	ENGITMLDAGSFAGLQGLDLSQNIASLPSGVQFQPLANLSNLDLTANRLHEITNETF	120
Qy	91	-----LRLPRLLLDLSHNS	105
Db	121	RGLRLRLYLKGNRIHQPCAFDTLDRLLLEKLQDNELRALPLRLPRLLLDLSHNS	180
Qy	106	LLALEPGILDTANVEALRLAGLQGLDGLFSRLNLHDLVDNSQLERVPPVIRGLRG	165
Db	181	LLALEPGILDTANVEALRLAGLQGLDGLFSRLNLHDLVDNSQLERVPPVIRGLRG	240
Qy	166	LTRLRAGNTRIAQLRPEDLAGLAAQLDGLVNSLSQALPGDLSGLFPRLRLAAARNPF	225
Db	241	LTRLRAGNTRIAQLRPEDLAGLAAQLDGLVNSLSQALPGDLSGLFPRLRLAAARNPF	300
Qy	226	NCVCPLSWFGPWRVRESHVTLASPEETRCHFFPKNAGRLLELDYADFGCPATTTATVPT	285
Db	301	NCVCPLSWFGPWRVRESHVTLASPEETRCHFFPKNAGRLLELDYADFGCPATTTATVPT	360
Qy	286	TRPVVREPTALSSSLAPTWSLTAPATEAPSPSTAPPTVGVPPQDCPPSTCLNGGTC	345
Db	361	TRPVVREPTALSSSLAPTWSLTAPATEAPSPSTAPPTVGVPPQDCPPSTCLNGGTC	420
Qy	346	HLGTRHHLACLCPGFTGLYCESQMGQTRSPSTVTPRPRSLTLGIEPVSPSLRVGL	405
Db	421	HLGTRHHLACLCPGFTGLYCESQMGQTRSPSTVTPRPRSLTLGIEPVSPSLRVGL	480
Qy	406	QRYLOGSSVQLRSRLTYRNLSGDPKRLVTLRLPASLAETVTLQRPNATVSVCMPLGP	465
Db	481	QRYLOGSSVQLRSRLTYRNLSGDPKRLVTLRLPASLAETVTLQRPNATVSVCMPLGP	540
Qy	466	GRVPEGEACGEAHTPPAVSHNHAPVTOAREGNLPLLIAPALAAVLLAALAAVGAAYCVR	525
Db	541	GRVPEGEACGEAHTPPAVSHNHAPVTOAREGNLPLLIAPALAAVLLAALAAVGAAYCVR	600
Qy	526	RGRAMAAADKQGVQPGAGPLEBEGVKVPLEPGPKATEGGGEALPSGSECEVPLMGFP	585
Db	601	RGRAMAAADKQGVQPGAGPLEBEGVKVPLEPGPKATEGGGEALPSGSECEVPLMGFP	660
Qy	586	PGLSQPLHAKPYI 598	
Db	661	PGLSQPLHAKPYI 673	
RESULT 3			
Q6EMK4 HUMAN			
ID	Q6EMK4	HUMAN	PRELIMINARY; PRT; 673 AA.
AC	Q6EMK4		
DT	16-AUG-2004		integrated into UniProtKB/TrEMBL.
DT	16-AUG-2004		sequence version 1.
DT	07-FEB-2006		entry version 11.
DE	Vasorin.		
GN	Name=SLIT2;		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;		
OC	Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	NUCLEOTIDE SEQUENCE.		
RX	PubMed:15247411; DOI=10.1073/pnas.0404117101;		
RA	Ikedo Y., Imai Y., Kumagai H., Nohara T., Morikawa Y., Hiseoka T.,		
RA	Manabe I., Maemura K., Nakaoka T., Imamura T., Miyazono K., Komuro I.,		
RA	Nagai R., Kitamura T.;		
RT	"Vasorin, a transforming growth factor [beta]-binding protein		
RT	expressed in vascular smooth muscle cells, modulates the arterial		
RT	response to injury in vivo."		
RL	Proc. Natl. Acad. Sci. U.S.A. 101:10732-10737(2004).		
CC	-----		
CC	Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms		
CC	Distributed under the Creative Commons Attribution-NoDerivs License		
CC	-----		
CC	EMBL; AY166584; AAO27704.1; -; mRNA.		

DR	Ensembl; ENSG00000168140; Homo sapiens.	
DR	HGNC; HGNC:18517; SLITL2.	
DR	InterPro; IPR006210; EGF.	
DR	InterPro; IPR000742; EGF 3.	
DR	InterPro; IPR006209; EGF_like.	
DR	InterPro; IPR013032; EGF_like_reg.	
DR	InterPro; IPR003961; FN_III.	
DR	InterPro; IPR001611; LRR.	
DR	InterPro; IPR000483; LRR C.	
DR	InterPro; IPR000372; LRR_cys N.	
DR	InterPro; IPR003885; LRR_cyst.	
DR	InterPro; IPR003591; LRR_typ.	
DR	Pfam; PF00008; EGF; 1.	
DR	Pfam; PF00041; fn3; 1.	
DR	Pfam; PF00560; LRR 1; 6.	
DR	Pfam; PF01463; LRRCT; 1.	
DR	Pfam; PF01462; LRRNT; 1.	
DR	PRINTS; PR00019; LEURICHRPT.	
DR	SMART; SM00181; EGF; 1.	
DR	SMART; SM00369; LRR_TYP; 2.	
DR	SMART; SM00082; LRRCT; 1.	
DR	SMART; SM00013; LRRNT; 1.	
DR	PROSITE; PS00022; EGF 1; 1.	
DR	PROSITE; PS01186; EGF_2; 1.	
DR	PROSITE; PS00026; EGF_3; 1.	
DR	PROSITE; PS00853; FN3; 1.	
SQ	SEQUENCE 673 AA; 71713 MW; 891E149652DEA286 CRC64;	
Query Match		
Best Local Similarity 98.2%; Score 3078.5; DB 2; Length 673;		
Matches 596; Conservative 0; Mismatches 2; Indels 75; Gaps 1;		
QY	1	MCSRVPLLLPLLLLLALGPGVGCGSCCQSPQTVFCTARQGTTPRDPVPPDTVGLYVF 60
DB	1	MCSRVPLLLPLLLLLALGPGVGCGSCCQSPQTVFCTARQGTTPRDPVPPDTVGLYVF 60
QY	61	ENGITWLDASSFAGLPGIQLLDLSQNIAS----- 90
DB	61	ENGITWLDAGSFAGLPGIQLLDLSQNIASLPSGVFPQLANLSNLDLTANRLHEITNETF 120
QY	91	-----LRLPRLLLLDLSHNS 105
DB	121	RGLRLRLRYLGNRIHQPGAFDTLDRLLLEKLQDNELRALPPURLPRLLLLDLSHNS 180
QY	106	LLALEPGILDTANVEALRLAGLQGLDGLFSRLNLHDLVDVSNQLERVPPVIRGLRG 165
DB	181	LLALEPGILDTANVEALRLAGLQGLDGLFSRLNLHDLVDVSNQLERVPPVIRGLRG 240
QY	166	LTRLRAGNTRIAQLRPEDLAGLAAQLQELDVNSLSLQALPGDLSGLFPRRLRLAAARNPF 225
DB	241	LTRLRAGNTRIAQLRPEDLAGLAAQLQELDVNSLSLQALPGDLSGLFPRRLRLAAARNPF 300
QY	226	NCVCPLSWFGPWRVRESHVTLASPEETRCHFFPKNAGRLLELDYADFGCPATTTATVPT 285
DB	301	NCVCPLSWFGPWRVRESHVTLASPEETRCHFFPKNAGRLLELDYADFGCPATTTATVPT 360
QY	286	TRPVVREPTALSSSLAPTWSLTAPATEAPSPSTAPPTVGPVPQDCPPSTCLNGGTC 345
DB	361	TRPVVREPTALSSSLAPTWSLTAPATEAPSPSTAPPTVGPVPQDCPPSTCLNGGTC 420
QY	346	HLGTRHHLACLCEPGFTGLYCESQMGQTRPSPTVTPRPRSLTLGIEPVSPSLRVGL 405
DB	421	HLGTRHHLACLCEPGFTGLYCESQMGQTRPSPTVTPRPRSLTLGIEPVSPSLRVGL 480
QY	406	QRYLOGSSVQLRSRLTYRNLSGDPKRLVTLRLPASLAETVTLQRPNATVSVCMPLGP 465
DB	481	QRYLOGSSVQLRSRLTYRNLSGDPKRLVTLRLPASLAETVTLQRPNATVSVCMPLGP 540
QY	466	GRVPEGEACGEAHTPPAVHSHNHPVTOAREGNLPLLIAPALAAVLLAALAAVGAAYCVR 525
DB	541	GRVPEGEACGEAHTPPAVHSHNHPVTOAREGNLPLLIAPALAAVLLAALAAVGAAYCVR 600
QY	526	RGRAMAAADKQGVQPGAGPLEBEGVKVPLEPGPKATEGGGEALPSGSECEVPLMGFP 585

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Db 601 RGRMAAAQDKGVGPAGPLGVKPLPGPKATEGGALPSGSECEVPLMGPPG 660
QY 586 PGLQSPFLHAKPYI 598
Db 661 PGLQSPFLHAKPYI 673

RESULT 4
Q96CX1_HUMAN
ID Q96CX1_HUMAN PRELIMINARY; PRT; 601 AA.
AC Q96CX1;
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT 01-DEC-2001, sequence version 1.
DT 07-FEB-2006, entry version 25.
DE SLTL2 protein (Fragment).
GN Name=SLTL2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausberg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore D., Max S.T., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Young A.C., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Driguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences."
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=Lung;
RC TISSUE=Lung;
RG NIH MQC Project;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
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CC -----
CC HMBL; BC013767; AAH13767.1; -; mRNA.
DR HSP; Q9BZR6; 1P8T.
DR Ensembl; ENSG00000168140; Homo sapiens.
DR InterPro; IPR006210; EGF.
DR InterPro; IPR000742; EGF_3.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR013032; EGF_like_reg.
DR InterPro; IPR003961; FN III.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR000483; LRR_C.
DR InterPro; IPR003885; LRR_cyst.
DR InterPro; IPR003591; LRR_typ.
DR Pfam; PF00008; EGF; 1.
DR Pfam; PF00041; fn3; 1.
DR Pfam; PF00560; LRR_1; 6.
DR Pfam; PF01463; LRRCT; 1.
DR PRINTS; PR00019; LEURICHRPT.
DR SMART; SM00181; EGF; 1.
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DR SMART; SM00369; LRR_TYP; 2.
DR SMART; SM00082; LRRCT; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS00026; EGF_3; 1.
DR PROSITE; PS0853; FN3; 1.
KW EGF-like domain; Leucine-rich repeat.
FT NON_TER 1
SQ SEQUENCE 601 AA; 64179 MW; 4964077778D9ABD2 CRC64;

Query Match 86.0%; Score 2697.5; DB 2; Length 601;
Best Local Similarity 87.4%; Pred. No. 1.5e-146;
Matches 525; Conservative 0; Mismatches 1; Indels 75; Gaps 1;

QY 73 AGLPGLQLLDLSQNIAS----- 90
Db 1 AGLPGLQLLDLSQNIASLPGVFQPLANLSNLDLTANRLHEITNETRGRRLRLRYLG 60
QY 91 -----LRLPRLLLDLSHNSLLALEPGILDTA 117
Db 61 KNIRHIQPGAFDTLRLLEKLQDNELRALPPLRLPRLLLLDLSHNSLLALEPGILDTA 120
QY 118 NVEALRLAGLQQLDEGLFSLRLNHLDDVSDNQLRVPVIRGLRGLTRLRAGNTRI 177
Db 121 NVEALRLAGLQQLDEGLFSLRLNHLDDVSDNQLRVPVIRGLRGLTRLRAGNTRI 180
QY 178 AQLRPEDLAGLAALQELDVSNLSLOALPGDLSGLFPLRLLLAAARNPNCVPLSWFGPW 237
Db 181 AQLRPEDLAGLAALQELDVSNLSLOALPGDLSGLFPLRLLLAAARNPNCVPLSWFGPW 240
QY 238 VRESHVTLASPEETRCHPPKPNAGRLLELDYADFGCPATTTTATVPTTRPVVREPTALS 297
Db 241 VRESHVTLASPEETRCHPPKPNAGRLLELDYADFGCPATTTTATVPTTRPVVREPTALS 300
QY 298 SSLAPTWLSPTAPATEAPSPSTAPTPTVGPVQPOQDCPPSTCLNGTCHLGRHHLAACL 357
Db 301 SSLAPTWLSPTAPATEAPSPSTAPTPTVGPVQPOQDCPPSTCLNGTCHLGRHHLAACL 360
QY 358 PGFTGLYCESQMGQTRSPPTVTPRPSRLTGLIEPVSPSLRVLQRYLQSSVQLR 417
Db 361 PGFTGLYCESQMGQTRSPPTVTPRPSRLTGLIEPVSPSLRVLQRYLQSSVQLR 420
QY 418 SLRLTYRNLSGDPKRLVTLRLPASLAETVTLRPNATYSVCVMPPLGPRVPEGEACGE 477
Db 421 SLRLTYRNLSGDPKRLVTLRLPASLAETVTLRPNATYSVCVMPPLGPRVPEGEACGE 480
QY 478 AHTPPAVHSHNAPVTQAREGNLPLIAPALAAVLLAALAAVGAAYCVRGRMAAAADK 537
Db 481 AHTPPAVHSHNAPVTQAREGNLPLIAPALAAVLLAALAAVGAAYCVRGRMAAAADK 540
QY 538 GQVGPAGPLEGVKVPLEPGPKATEGGALPSGSECEVPLMGPPGGLQSPFLHAKPY 597
Db 541 GQVGPAGPLEGVKVPLEPGPKATEGGALPSGSECEVPLMGPPGGLQSPFLHAKPY 600
QY 598 1 598
Db 601 1 601

RESULT 5
Q8BJJ0_MOUSE
ID Q8BJJ0_MOUSE PRELIMINARY; PRT; 673 AA.
AC Q8BJJ0;
DT 01-MAR-2003, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2003, sequence version 1.
DT 07-FEB-2006, entry version 21.
DE 9 days embryo whole body cDNA, RIKEN full-length enriched library,
DE clone:D03006D07 product:hypothetical prokaryotic membrane lipoprotein
DE lipid attachment site/cysteine-rich flanking region, N-
DE terminal/leucine-rich repeat/EGF-like domain/leucine-rich repeat,
DE typical subtype/leucine-rich repeat, outliners/cysteine-rich flanking
DE region, C-terminal/leucine-rich region/Fibronectin type III domain
DE containing protein, full insert sequence.
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GN Names-Slit12;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eumetazoa; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=9927253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Methods Enzymol. 303:19-44(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX PubMed=16141072; DOI=10.1126/science.1112014;
RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
RA Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
RA Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
RA Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,
RA Ambesi-Impombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
RA Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
RA Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
RA Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
RA di Bernardo D., Down T., Engstrom P., Fagioli M., Faulkner G.,
RA Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
RA Georgi-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
RA Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
RA Hill D., Huminecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
RA Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
RA Kitano H., Kollas G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
RA Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
RA Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
RA Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
RA Mottagui-Tabar S., Mulder N., Nakano N., Nakachi H., Ng P.,
RA Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
RA Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavese G., Pesole G.,
RA Petrosky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
RA Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
RA Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
RA Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
RA Sperling S., Stupka E., Sugtara K., Sultana R., Takenaka Y., Taki K.,
RA Tammoja K., Tan S.B., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
RA Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
RA Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
RA Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
RA Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
RA Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
RA Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
RA Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,
RA Kawashio T., Okada M., Plessey C., Shibata K., Shiraki T., Suzuki S.,
RA Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
RA Hayashizaki Y.;
RT "The transcriptional landscape of the mammalian genome.";
RL Science 309:1559-1563(2005).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX PubMed=16141073; DOI=10.1126/science.1112009;
RG RIKEN Genome Exploration Research Group, and Genome Science Group
(Genome Network Core Team) and the FANTOM Consortium;
RT "Antisense Transcription in the Mammalian Transcriptome.";
RL Science 309:1564-1566(2005).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=22354683; PubMed=1246681; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., Mckenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Perle G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita K.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayashizaki Y.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shingawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bona M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schonbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [7]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=2030913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Iehi Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Wataniki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuda S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multiplexed sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [8]
RP NUCLEOTIDE SEQUENCE.

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RC STRAIN=C57BL/6J; TISSUE=Whole body;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ono M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh K., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akai S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
CC -----
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CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AK083684; BAC38992.1; -; mRNA.
DR HSSP; P00740; 1EDM.
DR Ensembl; ENSMUSG00000039646; Mus musculus.
DR MGI; MGI:2177651; Slit12.
DR InterPro; IPR006210; EGF.
DR InterPro; IPR000742; EGF 3.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR013032; EGF-like_reg.
DR InterPro; IPR003961; FNIII.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR000483; LRR C.
DR InterPro; IPR000372; LRR_cys_N.
DR InterPro; IPR003885; LRR_cysC.
DR InterPro; IPR003591; LRR_Typ.
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DR Pfam; PF00041; fn3; 1.
DR Pfam; PF00560; LRR 1; 6.
DR Pfam; PF01463; LRRCT; 1.
DR Pfam; PF01462; LRRNT; 1.
DR PRINTS; PR00019; LEURICRPT.
DR SMART; SM00181; EGF; 1.
DR SMART; SM00060; FN3; 1.
DR SMART; SM00369; LRR_Typ; 3.
DR SMART; SM00082; LRRCT; 1.
DR SMART; SM00013; LRRNT; 1.

Query Match 79.5%; Score 2491; DB 2; Length 673;
Best Local Similarity 73.5%; Pred. No. 1.2e-134;
Matches 491; Conservative 25; Mismatches 74; Indels 78; Gaps 3;

QY 6 PLLLPALLALGPGVCGCGCQSQPTVFCFARQGTTPVRDVPDVTGLVFNIGIT 65
DB 9 PLL--LALLLGGVCGCGCQSQPTVFCFARQGTTPVRDVPDVTGLVFNIGIT 66
QY 66 MLDASSFAGLPGQLLDSQNIAS----- 90
DB 67 TLDVGCFAGLPGQLLDSQNIAS----- 90
QY 91 -----LRLPRLLLDLSHNSLLE 110
DB 127 LERLYLGNRIHQGAFDALDRLELKLDPNELRVLPPLHLPRLLLDLSHNSIPALE 186
QY 111 PGILDANVALRALAGLQGLDGLFSRLNLHLDVDSNQLERVPPVIRGLGLTRLR 170
DB 187 AGILDANVALRALAGLQGLDGLFSRLNLHLDVDSNQLEHWPVSVQGLGLTRLR 246
QY 171 LAGNTRIAQRPEDLAGLAQLDVSNSLQALPGDLGSLFRLRLRLAAARNPFCVCP 230
DB 247 LAGNTRIAQRPEDLAGLQALQELDVNSLSLQALPSDLSLFPRLRLRLAAARNPFCVCP 306
QY 231 LSWFGPWVRSHVTLASPEETRCHFPKNAAGRLLELDYADFGCPATTTTATPTTPPV 290
DB 307 LSWFGPWVRSHVTLASPEETRCHFPKNAAGRLLELDYADFGCPATTTTATPTTPV 366
QY 291 REPTALSSSLAPTWSLPTAPATEAPSPPTAPPTVPQPDQCPPTCLNGGTCHLGTR 350
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DB 367 REPTLSTSSQAPTWPSHTPTTQASTVLSTAPPTWPAQPQDPCPASICLNGGSCRLGAR 426
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DB 427 HHWECLCEGFTGLICVCSOMGQTRPSPPTVTPRPRSLTGLIEPVSPTSLRVLQRYLQ 486
QY 411 GSSVOLRLRLTYRNLSDGDKRLVTLRLPASLAETVTLQLRPNATYSVCVMPGLPGRVPE 470
DB 487 GNTVQRLRLTYRNLSDGDKRLVTLRLPASLAETVTLQLRPNATYSVCVMPGLPGRVPE 546
QY 471 GEEACGEAHTPPAVNSHAPVTOAREGNLPLLIAPALAAVLLAALAAVAAAYCVRGRAM 530
DB 547 GEEACGEANTSOAVRSNHAPVTOAREGNLPLLIAPALAAVLLAALAAVAAAYCVRARA - 605
QY 531 AAAADKQGVGCGAGPLEGKVPLEPGPKATEGGEGALPGSCEVEPMLGPGPGLQS 590
DB 606 TSTAQDKGVGCGTGTGLEGVKAPLEPGKATEGGEGALPGSCEVEPMLGPGPGLQS 665
QY 591 PLHAKPYI 598
DB 666 VLPKHYI 673

RESULT 6
Q8R2G5_MOUSE PRELIMINARY; PRT; 673 AA.
AC Q8R2G5;
DT 01-JUN-2002, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2002, sequence version 1.
DT 07-FEB-2006, entry version 27.
DE Slit-like 2 protein precursor (15 days embryo head cDNA, RIKEN full-
DE length enriched library, clone:4022415F23 product:Slit-like 2
DE (Drosophila), full insert sequence).
GN Name=Slit2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6;
RA Schrewe H., Kutejova E.;
RT "Structure and expression analysis of the mouse Slit-like 2 (Slit2)
RT gene.";
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Kidney;
RX MEDLINE-22388257; PubMed-12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
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RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Small D.E.,
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RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Kidney;
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- RA Director MGC Project;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
RN [4]
- RC STRAIN=C57BL/6J; TISSUE=Head;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Methods Enzymol. 303:19-44(1999).
RN [5]
- RC STRAIN=C57BL/6J; TISSUE=Head;
RX PubMed=16141072; DOI=10.1126/science.1112014;
RA Oyama R., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
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RA Iida J., Inamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
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RA Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
RA Hayashizaki Y.;
RL "The transcriptional landscape of the mammalian genome.";
RL Science 309:1559-1563(2005).
RN [6]
- RC STRAIN=C57BL/6J; TISSUE=Head;
RX PubMed=16141073; DOI=10.1126/science.1112009;
RG RIKEN Genome Exploration Research Group, and Genome Science Group
(Genome Network Core Team) and the FANTOM Consortium;
RT "Antisense Transcription in the Mammalian Transcriptome.";
RL Science 309:1564-1566(2005).
RN [7]
- RC STRAIN=C57BL/6J; TISSUE=Head;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
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RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
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RL Nature 420:563-573(2002).
RN [8]
- RC STRAIN=C57BL/6J; TISSUE=Head;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
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RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [9]
- RC STRAIN=C57BL/6J; TISSUE=Head;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
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RN [10]
- RC STRAIN=C57BL/6J; TISSUE=Head;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
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sequencing pipeline with 384 multicapillary sequencer.";
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RN [11]
- RC STRAIN=C57BL/6J; TISSUE=Head;
RA Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,
RA Hori F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S.,
RA Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N.,

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OC Muroidea; Muridae; Murinae; Mus.
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RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RY Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Methods Enzymol. 303:19-44(1999).
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RY Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N., Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K., Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M., Davis M.J., Wilmink L.G., Adinin V., Allen J.E., Ambesi-Impombato A., Apweiler R., Aturaliya R.N., Bailey T.L., Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M., Chiu K.P., Choudhary V., Christofoels A., Clutterbuck D.R., Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G., Di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G., Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M., Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E., Gustigich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N., Hill D., Humintech L., Iacono M., Ikeo K., Iwama A., Ishikawa T., Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H., Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K., Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J., Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L., Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K., Mottagui-Tabar S., Mulder N., Nakano N., Nakachi H., Ng P., Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O., Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavese G., Pesole G., Petrovsky N., Piazza S., Reed J.F., Ring B.Z., Ringwald M., Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C., Schombach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y., Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B., Sperling S., Stupka E., Sugtara K., Sultana R., Takenaka Y., Taki K., Tamajo K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A., Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K., Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C., Grimmond S.M., Tesseadale R.D., Liu E.T., Brusic V., Quackenbush J., Raymond C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y., Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T., Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N., Kawashima T., Kojima M., Kondo S., Konno K., Nakano K., Ninomiya N., Nishio T., Okada M., Plessey C., Shibata K., Shiraki T., Suzuki S., Tagami M., Waki K., Wataniki A., Okamura-Oho Y., Suzuki H., Kawai J., Hayashizaki Y.
RT "The transcriptional landscape of the mammalian genome.";
RL Science 309:1559-1563(2005).
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RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX PubMed=16141073; DOI=10.1126/science.1112009;
RY RIKEN Genome Exploration Research Group, and Genome Science Group (Genome Network Core Team) and the FANTOM Consortium;
RT "Antisense transcription in the Mammalian Transcriptome.";
RL Science 309:1564-1566(2005).
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RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
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RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs";
RL Nature 420:563-573 (2002).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
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RA Hayashizaki Y.,
RT "Functional annotation of a full-length mouse cDNA collection";
RL Nature 409:685-690 (2001).
RN [6]
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RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes";
RL Genome Res. 10:1617-1630 (2000).
RN [7]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
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RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer";
RL Genome Res. 10:1757-1771 (2000).
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RC STRAIN=C57BL/6J; TISSUE=Whole body;
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RA Muramatsu M., Hayashizaki Y.,
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
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EMBL: AK012169; BAB28075.1; -; mRNA.
DR HSSP; P00740; 1EDM.
DR Ensembl; ENSMUSG00000039646; Mus musculus.
DR MGI; MGI:2177651; Slit12.
DR InterPro; IPR006210; EGF.
DR InterPro; IPR000742; EGF_3.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR013032; EGF_like_reg.
DR InterPro; IPR003961; FN III.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR000483; LRR_C.
DR InterPro; IPR000372; LRR_cys_N.
DR InterPro; IPR003885; LRR_cyst.
DR InterPro; IPR003591; LRR_tyr.
DR Pfam; PF00008; EGF_1.
DR Pfam; PF00041; fn3_1.
DR Pfam; PF00560; LRR_1; 6.
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DR Pfam; PF01462; LRRNT; 1.
DR PRINTS; PR00019; LEURICRPT.
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DR SMART; SM00013; LRRNT; 1.
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Matches 490; Conservative 25; Mismatches 75; Indels 78; Gaps 3;
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DB 9 PLL--LLLVLLGSGVQGCPCSCQCNQNPQVFTARQGTTPRDPVPPDTVGLYVFENGIT 66
QY 66 MLDASSFAGLPGQLLDLSQNIAS----- 90
DB 67 TLDVGCFCAGLPGQLLDLSQNIATSLPGGIFQPLVNLNLDLTANKLHEISNETFRGLRR 126
QY 91 -----LRLPRLLLDLSHNSLALAE 110
DB 127 LERLVYGNRIIRHIOFGAFDALDRLELKLDPNEURVLPLHLPRLLLDLSHNSLPALE 186
QY 111 PGILDTANVEALRLAGLGLQQLDEGLFSLRLNLDHLDVSDNQLERVPVIRGLGLTRLR 170
DB 187 AGILDTANVEALRLAGLGLRLQDEGLFGRLNLDHLDVVDNQLHMPFSVIQGLGLTRLR 246
QY 171 LAGNTRIAQLRPEDLAGLAALQELDVSNLSLQALPGDLISGLFPRRLLLAAARNPNCVCP 230
DB 247 LAGNTRIAQLRPEDLAGLALQELDVSNLSLQALPSLSSLPFLRLLLAAARNPNCVCP 306
QY 231 LSWFGPWVRESHVTLASPEETCRCHPKNAGRLLLLELDVADFGCPATTTTATVTPRPV 290
DB 307 LSWFGPWVRENHVTLASPEETCRCHPKNAGRLLLLDLDVADFGCPVTTTATVPTIRSTI 366
QY 291 REPTALSSSLAPTWSLPTAPATEAPSPSTAPPTVGPVQPDQCPSPSTCLNGTCHLGR 350

Q3MK9_BRARE
ID Q3MK9_BRARE PRELIMINARY; PRT; 688 AA.
AC Q3MK9;
DT 25-OCT-2005, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, sequence version 1.
DE Slit-like 2 protein.
GN Names:slit2;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AB;
RX PubMed=1612671; DOI=10.1016/j.bbrc.2005.08.071;
RA Chen L., Yao J.H., Zhang S.H., Wang L., Song H.D., Xue J.L.;
RT "Slit-like 2, a novel zebrafish slit homologue that might involve in
zebrafish central neural and vascular morphogenesis.";
RL Biochem. Biophys. Res. Commun. 336:364-371(2005).
CC
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CC Distributed under the Creative Commons Attribution-NoDerivs License
CC
CC
CC EMBL; AY838878; AAW57297.1; -, mRNA.
DR ZFIN; ZDB-GENE-050522-43; slitl2.
DR InterPro; IPR000742; EGF_3.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR013032; EGF-like_reg.
DR InterPro; IPR003961; FN III.
DR InterPro; IPR000119; Hist_DNA_bd_bac.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR000483; LRR_C.
DR InterPro; IPR000372; LRR_cys_N.
DR InterPro; IPR003885; LRR_cysE.
DR InterPro; IPR003591; LRR_typ.
DR Pfam; PF00008; EGF_1.
DR Pfam; PF00560; LRR_1; 7.
DR Pfam; PF01462; LRRNT; 1.
DR PRINTS; PR00019; LEURICHRPT.
DR SMART; SM00369; LRR_TYP; 2.
DR SMART; SM00082; LRRCT; 1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS50026; EGF_3; 1.
DR PROSITE; PS50853; FN3; 1.
DR PROSITE; PS00045; HISTONE LIKE; UNKNOWN_1.
SQ SEQUENCE 688 AA; 75284 Mw; 4E197E063AF3608C CRC64;

Query Match 31.0%; Score 972.5; DB 2; Length 688;
Best Local Similarity 36.3%; Pred. No. 1.6e-47;
Matches 239; Conservative 77; Mismatches 222; Indels 121; Gaps 15;

QY 6 PLLPLLLALLGPGVQGCSPGCCQSQPQTVFCTARQGTVPDPDPTVGLVFNENGIT 65
DB 6 PLSHLILLQLCCCLSSRCHDCTCLPSNNIFCVQRNLVMPRLPSTGKQLYVFNQKIN 65
QY 66 MLDASSFAGLPGIQLDLSONQIA----- 89
DB 66 ILQQQDFVELGELEMLDLSONSLEIPDGVPFSLSLNHLNLDSSNITHSKDSFGLVN 125
QY 90 -----SLRPLRLLLDLSNLSLLE 110
DB 126 LERLYLSNIIQNIHPAEPGLENLLELKLQGNQISVLPAQLQLPRLHLDLSSYNIPPLV 185
QY 111 PGLTDANVENALRAGLQQLDEGLFSLRLNHLHDLDVSDNQLRVPVIRGLRGLTRLR 170
DB 186 AOLQTPHLESKIAGLGLTSDEELGSLVNLHLVDVSNQNLVDIQPTLKSNGGLRLN 245
QY 171 LAGNTRIAQLRPEDLAGLAALOEGLDVSNLISLQALPGDLGLFRLRLLLAAARNPNCVCP 230
DB 246 LTGNP-LGSLKHEDFQVNLNLELDLSNLNLQGFPEGFNLFKLEKLTAAENPFNCLCP 304

QY 231 LSWFGPWVRESHVTLASPEETRCHFPKNAKGRLLLELDYADFCGPATTTTATVPTTRPVV 290
DB 305 LAWFPALWKDVRVELLRTETTRCHFPFINSKGLKLEHKDFCPTTTTILTSAGTSSTT 364
QY 291 REPTALSSSLAPTWSLPTAPATEAPSPSTAPPTVGPVPOP-----OD-----CP 335
DB 365 SKPKNSSTQLGTYTHIVPPAP---PSDISSADADNFPVQTTAFPPSRIMEDSSEGEIMCP 420
QY 336 PSTCLNGGTCHLGRHHLACLCPGFTGYCSQMGQGTTRPSPTP-----VTPRPPRS 388
DB 421 PNICLNGGTICFKSNGVIVCLCPSPSMGNYCEIQ-NEAMLPPSPRVSLETIATVQGN-- 477
QY 389 LTGLIEFPVPTSLRVGLQRYLOGSSVQLRSRLTYENLSGPKDLVTLRLPASLAEYTVT 448
DB 478 -TISHHITSTSLDLHRYIQ-TRPHIGIRLTYSNLSPDRRRLQQLSVPPSYPEYTLR 535
QY 449 QLRPNATYSVCMPLQGRVPEGEAEACGEAHT---PPAVHSNHAPVTQAREGNLPLLIAP 505
DB 536 GLQPNSTYSCASPLGE-PHASVSACMEARTAGIPSSSHEPSVDRTEPSSSLTIPIV-- 592
QY 506 ALAAVLLAALAAVGAAYCVRRGRAMAAAOQKQGVGAGPLEGLGVKVPLEPG---PK 561
DB 593 AVAVVMVAIIAT-VVVISRRRRPKAPVMDLHE----TSPLEMEGVKTNPENGLTHPK 646

RESULT 10
Q503G2 BRARE
ID Q503G2 BRARE PRELIMINARY; PRT; 643 AA.
AC Q503G2;
DT 07-JUN-2005, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 5.
DE Slit-like 2.
GN Names:slit2;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Singapore local strain; TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Sapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Hellon E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Singapore local strain; TISSUE=Embryo;
RG NIH MGC Project;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
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CC
CC EMBL; BC095341; AAH95341.1; -, mRNA.

Ensembl, ENSDARG0000002890; Danio rerio.
ZFIN; ZDB-GENE-050522-43; slt12.
DR InterPro; IPR000742; EGF 3.
DR InterPro; IPR013032; EGF_like_reg.
DR InterPro; IPR003961; FN III.
DR InterPro; IPR001119; Hist_DNA_bd_bac.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR000483; LRR_C.
DR InterPro; IPR003885; LRR_cyst.
DR InterPro; IPR003591; LRR_typ.
DR Pfam; PF00008; EGF 1.
DR Pfam; PF00560; LRR 1; 7.
DR PRINTS; PR00019; LEURICHRPT.
DR SMART; SM00369; LRR_TYP; 2.
DR SMART; SM00082; LRRCT; 1.
DR PROSITE; PS00022; EGF 1; UNKNOWN_1.
DR PROSITE; PS50026; EGF 3; 1.
DR PROSITE; PS50835; FN3; 1.
DR PROSITE; PS00045; HISTONE LIKE; UNKNOWN 1.
SQ SEQUENCE 643 AA; 70201 MW; 964BE8792A7C642 CRC64;

Query Match 29.6%; Score 927.5; DB 2; Length 643;
Best Local Similarity 41.0%; Pred. No. 5.6e-45;
Matches 218; Conservative 75; Mismatches 198; Indels 41; Gaps 14;

Qy 57 LYVFENGITWLDASSFAGLPGQLDLSONQTA---SLRLPRLLLDLSHNSLLALEPGI 113
Db 84 LYLYSNIIQNTHPAEPGLEHLEKLGQNLQSVLPALQPLRLLHLDSYNSIPPLVAQD 143

Qy 114 LDATNVEALRLAGLGLQQDEGLFSRLRNHLVDSDNQLERVPPVIRGLGLTRLRLAG 173
Db 144 LQTPHLESUKIAGLGTLDELGLGSLINLHVLDVSQNLVDIQPTLKSMGGLNMLTG 203

Qy 174 NTRIAQRPEDLAGLAALOELDVNSLSLOALFGDLSGLFPRLRLAAARNPNVCVPSLW 233
Db 204 NP-LGSLKHEDFNVLNLELDLSNLQGPFEGFNLPFKLEKLTAENPNCLCPJAW 262

Qy 234 FGPVWRSHVTLASPETRCHPPKNAGRLLELDYADFGCCPATTTTATVTPRPVREP 293
Db 263 FPWLKDVRVELLRTETRCHPPINSKGKLEKLBHKDFGCPTTIETLSAGTSSTSKP 322

Qy 294 TALSSSIAPTWLSPTAPATEAFSPSTAPP-----TVGPVPQPQD-----CPSTCLNG 342
Db 323 TNSSTQSQTTHIVPPAPLSDISSADNFNVYTQTTAFPSRIEMDESSEGGIMCPNNICUNG 382

Qy 343 GTCHLTRHHACLCEGFTGLYCESOMSGTRPSPTP-----VTPRPRESLTGI EP 395
Db 383 GTCLFNSGVIVCLCPPSMGLSCYELQ-NEAMLPSPRSVLETATTQPN---TISHH 438

Qy 396 VSPTSRVGLQRYLOGSSVOLSRILTYRLNSGPKRLVTLRLPASLAETYVTQLRPNAT 455
Db 439 ITSTSISLDLHYIQ-TRPHIRGIRLYTNLSGPDRLQLSVPPSYEYLRLGLQPNST 497

Qy 456 YSVCVMPLGRVPEGEAECAEHT---PPAVHSNHAPVTQAREGNILLPIALAAVLL 512
Db 498 YSVCASPLGE-PVHASVSACMEARTAGIPSSHEPSVDTEPSSSLTPTIW--AVAVMV 554

Qy 513 AALAAGVAAVCYVRGRAMAAAADKQVGFGAGPLEGVKVLEPBG---PK 561
Db 555 VAIIAT-VVISRRRPKAPVDMLHE----TSPLEMGVKTNPENGLTHPK 601

RESULT 11
Q4SQ68 TETNG PRELIMINARY; PRT; 962 AA.
AC Q4SQ68
DT 19-JUL-2005, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 4.
DE Chromosome 19 SCAF14535, whole genome shotgun sequence.
GN ORfNames=GSTENG00014497001;
OC Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

[illegible]

RESULT 12

Q50LG9	HUMAN	PRELIMINARY; PRT; 513 AA.
AC	Q50LG9;	
DT	07-JUN-2005,	integrated into UniProtKB/TrEMBL.
DT	07-JUN-2005,	sequence version 1.
DT	21-FEB-2006,	entry version 7.
DE	Hypothetical protein LRRC24.	
GN	Name=LRRC24;	
OS	Homo sapiens (Human).	
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;	
OC	Homo.	
OX	NCBI_TaxID=9606;	
OX	[1]	
RN	NUCLEOTIDE SEQUENCE.	
RP	TISSUE=Brain;	
RC	TISSUE=Brain;	
RP	Shimizu N., Asakawa S., Shimizu A., Yamazaki S., Ishikawa S.K.;	
RT	"Novel gene containing leucine rich repeat on human chromosome 8.";	
RL	Submitted (APR-2004) to the EMBL/Genbank/DBJ databases.	
[2]		
RN	NUCLEOTIDE SEQUENCE.	
RP	TISSUE=Brain;	
RC	TISSUE=Brain;	
RP	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;	
RX	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,	
RA	Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,	
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,	
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,	
RA	Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,	
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,	
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,	
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,	
RA	Bosak S.A., McSwain P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,	
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,	
RA	Vallalon D.K., Munz D.M., Sodergren E.J., Lu X., Gibbs R.A.,	
RA	Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,	
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,	
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,	
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,	
RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,	
RA	Schmerch A., Schein J.E., Jones S.J.W., Marra M.A.;	
RT	"Generation and initial analysis of more than 15,000 full-length human	
RL	and mouse cDNA sequences.";	
RL	[Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002)].	
RN	[3]	

RP	NUCLEOTIDE SEQUENCE.
RC	TISSUE=Brain;
RG	NIH MGC Project;
RL	Submitted (DSC-2005) to the EMBL/GenBank/DBDJ databases.
CC	-!- SUBCELLULAR LOCATION: Membrane; single-pass type I membrane protein (By similarity).
CC	-----
CC	Copyrighted by the Uniprot Consortium, see http://www.uniprot.org/terms
CC	Distributed under the Creative Commons Attribution-NoDerivs License
CC	-----
DR	EMBL; AB78281; BAD9781.1; -; mRNA.
DR	EMBL; BC111067; AA111068.1; -; mRNA.
DR	Ensembl; ENSG00000188270; Homo sapiens.
DR	InterPro; IPR003599; Ig-like.
DR	InterPro; IPR007110; Ig-like.
DR	InterPro; IPR003598; Ig_C2.
DR	InterPro; IPR001611; LRR.
DR	InterPro; IPR000483; LRR_C.
DR	InterPro; IPR000372; LRR_Cys_N.
DR	InterPro; IPR003591; LRR_typ.
DR	Pfam; PF00560; LRR_1; 5.
DR	Pfam; PFO1463; LRRT; 1.
DR	PRINTS; PR00019; LEURICHRPT.
DR	SMART; SM00409; IG; 1.
DR	SMART; SM00408; IGG2; 1.
DR	SMART; SM00369; LRR_TYD; 3.
DR	SMART; SM00082; LRRT; 1.
DR	SMART; SM00013; LRRT; 1.
DR	PROSITE; PS50835; IG_LIKE; 1.
KW	Hypothetical protein; Immunoglobulin domain; Leucine-rich repeat;
KW	Repeat.
SQ	SEQUENCE 513 AA; 55199 MW; 3770FA80D979C1DE CRC64;
	Query Match 11.8%; Score 368.5; DB 2; Length 513;
	Best Local Similarity 26.4%; Pred. No. 5.2e-13;
	Matches 170; Conservative 63; Mismatches 217; Indels 195; Gaps 28;
Qy	1 MCSRVPLLLPLLILLALPGVGQCPCSCQSQPQTVECTAQGTTPRDPVPPDTVGLYVF 60
Db	1 MALRAPALLPULLLL-LPLRAAGCPAACRC-YATVCEGAURLRVPLIGIPPGTQTFLQ 58
Qy	61 ENGITMLDASSFAGLPGLQLDLISQNOIASURL-----PRLLLDLSHNSLALEPG-I 113
Db	59 DNNIARLEPGALAPLAARLYLHNNSLRALEAGAPRAQPRLLELATLSNRLCLRSQAF 118
Qy	114 LDATANVALRIAGLGLOOLDEGLFSRLRNHLDDVDNQLERVPVPIRGLTRLRLAG 173
Db	119 VGLAQLRVLYLAGNLQRLLDFTFLHPRLQLELHQENSIE-----159
Qy	174 NTRIAQLRPDLAGLAALQELDVSNLSIQALPGDSLGFPRRLRLAAARNPENCVCPLSW 233
Db	160 -----LLEDQALGSLALLDUSRNQLGTISRALQPLASLQVRLITEPNWCDCALHW 214
Qy	234 FGPVVRESHVTLASPEETR--CHFPKKNAGRLLELDYADFGCPATTTTATVTPTRPVVR 291
Db	215 LGAWIKEGGQRULTSRDKIMCAEPRLALQSLLDVSHSLIC-----IPPSVHV-- 264
Qy	292 EPITALSSSLAPTWLSPATAEAPSPSTAPPVGVPPQODCPP--STCLNGTGTCHLTG 349
Db	265 QPLELTANLGED-LRVACQASGYPOP----LVTWKVPQPREGRPAQAQLEGGL--LGL 317
Qy	350 RHLACLCPGEF-----TGLY-CESQMGG-----TRSP-TPTVTRP 385
Db	318 GGHSASTGGGMFLSNITLAHGKYECESNAGGAARVFRLLVNASRQQPQAPQPPP 377
Qy	386 PRSLTLGIEVPVPTSLRVGLQRYLQGSSVOLRSURLTYRNLGNLSDPKRLVTLRPLASLAEY 445
Db	378 PAARPASSEP-----387
Qy	446 TVTQLRNATYSVCVMPLGPGRVPEGEEAGEAHTPPAVHSNHAPVTOAREGNLPLLIAP 505
Db	388 ----REAG-SMAFRLG-----VAQT-----AIAA 409

RN	and	Pro	[3]
RL			
RN			

DR LinkHub; Q6PIG9; -
DR InterPro; IPR003961; FN III.
DR InterPro; IPR013098; I-set.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig c2.
DR InterPro; IPR001611; Lg.
DR InterPro; IPR00483; LRR_C.
DR InterPro; IPR003591; LRR_Typ.
DR Pfam; PF00041; fn3; 1.
DR Pfam; PF07679; I-set; 1.
DR Pfam; PF00560; LRR_1; 6.

QY		8	LLPLLLLLALPGVGOGPSGCQC---	SQPQTVFTCARGGTTVPDRDPPDTTGLCYVFNGI	64
Db		1	MAPPLLLILLASGAAACP	CVCQNCLSSLTCAHRLGLFVPKVDRTVELRLADNFI	60
QY		65	TWLDASSFAGLPGLQLDLSONQIASL----	RLPRLLDLLSHNSLLALEPGLL-DTA	117
Db		61	QALGPDPFRNMITGLVDLTLRSNAITRIGARAFGDLES	LSRLSHLDGNRLVELGTGSLRGVP	120
QY		118	NVEALRLAGLGLQQIDEGFLSR--LRNLHDLVDSONQLSERVP-	PVIRGHLRGLTRLBLAGNT	175
Db		121	NLOHLILSGNQLGRIPACAFDDFLESTEDDLSYNNLRQVFWAGIGAMPALHTLNLDHNL	180	
QY		176	RIAQLRPDDLGLAALQBELDVSNLSLOALPGDLSGLFPRLR----	LIAAARNPEN	226
Db		181	-IDALPPGAFAQOLGQLSKDLTJSNRLATPAD--	PLFSRGDRDAESPAPLVLSFGSNPLH	237
QY		227	CVCPLSWFGPMWRSHVTLAGSEETR-CHFFPKPNAGRLLLELDYADFGPCATTTTATVPT	285	
Db		238	CNCELLMLR-----	RLAREDDLETCAS PGLAGRYFWAVEGEFSC-----	278
QY		286	TRPVREPTALSSSIAPTWSLTARAT---EAPSPPSTAPPTVGVPOQ-----	PODCPP	336
Db		279	-----EPPLIARHTQRLMWLEGQCATURCRALGDPAPTMHWVGPDRLVLGNSSRARAPF	332	
QY		337	STCLNGGTCGLTRHHACLCLC--	PRGFCTGLYCE-----SOMGOCTSPSTPPTVTPR	384
Db		333	NGTLEIGVTGADGAGGYTCIANTPAGEARTARVELRVIALPHCGNSSAEGRPGPSPDIAAS	392	
QY		385	PPRSL-----	TLGIEP---VSPTSRLVGORYLOGGSVQ-LRSRLTYRNLSGPDFKLVTLL	436
Db		393	ARTAAEBGETLSEFAVQVTEVTATSGVSWGPGRPADPEWMFMFOIQYN--	SSEDETLIYR	450

Qy 437 RLPSLALEYVTVQLRPNPATYSVCVMNPLGPRVPGESEA-----CGEAHTPPAVHSHAPV 499
Dd :|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:
Db 451 IVPASHHFLKHLVPGADYDLCLIALSPAAGPSDLTATRLLGCAHFSTLPASPCLHALQ 510
Qy 492 TQAREGNLPLLIAPALAAVLAAALAAVGAAVYCVRRGMAAAAAODKGQVPGAGPLEEG 551
Dd :|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:
Db 511 AHVLGGTLTV-----AVGGVLVAALLVFTVALLV-RRG-----AGNRGLPLKUSH 555
Qy 552 VKVPLEPQPXAT 563
Dd :|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:
Db 556 VQSQTNGGPSPT 567

RESULT 14
LRFN4_MOUSE STANDARD; PRT: 636 AA.
AC Q8OXU8; O8K3C4;
DT 29-MAR-2005, integrated into UniProtKB/Swiss-Prot.
DT 01-JUN-2003, sequence version 1.
DT 07-MAR-2006, entry version 25.
DE Leucine-rich repeat and fibronectin type-III domain-containing protein
DE 4 precursor.
OS Mus musculus (Mouse).
GN Name=Lrln4;
NCBI_TaxID=10090;
[1]
NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RP STRAIN=C57BL/6J; TISSUE=Head;
RX PubMed=16141072; DOI=10.1126/science.1112014;
RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
RA Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
RA Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
RA Davis M.B., Wilming L.G., Aidinis V., Allen J.E.,
RA Ambesi-Impombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
RA Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
RA Chiu K.P., Chowdhury V., Christoffels A., Clutterbuck D.R.,
RA Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
RA di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G.,
RA Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
RA Georgii-Hemming P., Gingeras T.R., Gojboori T., Green R.E.,
RA Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
RA Hill D., Huminski L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
RA Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
RA Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
RA Kurochkin I.V., Larreau L.F., Lazarevic D., Lipovich L., Liu J.,
RA Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
RA Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
RA Motaghi-Tabar S., Mulder N., Nakano N., Nakachi H., Ng P.,
RA Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
RA Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavese G., Pesole G.,
RA Petrovsky N., Piazza S., Reed J.C., Reid J.F., Ring B.Z., Ringwald M.,
RA Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
RA Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
RA Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
RA Sperling S., Stupka E., Sugura K., Sulana R., Takenaka Y., Taki K.,
RA Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
RA Ueda H.R., van Nimwegen E., Verardo R., Wei C.I., Yang K.,
RA Yamashita H., Zdobych E., Zhu S., Zimmer A., Hide W., Bult C.,
RA Grimmond S.M., Teasdale R.D., Liu E.T., Brusica V., Quackenbush J.,
RA Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
RA Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
RA Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
RA Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,
RA Nishio T., Okada M., Plešský C., Shibata K., Shiraki T., Suzuki S.,
RA Tagami M., Waki K., Watabiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
RA Hayashizaki Y.;
RT "The transcriptional landscape of the mammalian genome."
RL Science 309:1559-1563 (2005).
RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RP

FT	CARBOHYD	25	25	N-linked (GlcNAc . . .) (Potential).
FT	CARBOHYD	70	70	N-linked (GlcNAc . . .) (Potential).
FT	CARBOHYD	324	324	N-linked (GlcNAc . . .) (Potential).
FT	CARBOHYD	333	333	N-linked (GlcNAc . . .) (Potential).
FT	CARBOHYD	376	376	N-linked (GlcNAc . . .) (Potential).
FT	CARBOHYD	440	440	N-linked (GlcNAc . . .) (Potential).
FT	DISULFID	302	351	By similarity.
FT	CONFLICT	503	503	T -> N (in Ref. 2; AAH23156).
SQ	SEQUENCE	636	AA; 67252	MW; 1ER86B96CB88BA91 CRC64;
Query Match				
Best Local Similarity				
Matches 170; Conservative 62; Mismatches 276; Indels 116; Gaps 25;				
QY	8	LPILLILLALGCVGCGSCGC	---	SQPTVFCTARQGTTPRDPVPTGLGVFENG1 64
Db	1	MAPILLILLASGAACPLFCVQNLSESLTCAHRLGLFFPNVDRTRVELRADNFI	60	
QY	65	TMLDASSFAGLPGQLQLDLSNQIASL	-----	LRPLRLLLDLSHNSLAL-EPGILDTA 117
Db	61	QALGPPDFRNTGLVDLTLSRNAITRIGARSGDLESRLSLDGNRLVELGSSSLRGFV	120	
QY	118	NVEALRLAGLQQLDEGLFSR-LRNLHLDVSDNQLRVP-PVIRGLRGLRFLRAGNT	175	
Db	121	NLQHLILSGNLGRIGAPGAFDDFLDSLEDLVSYNNLRQVPWAGIGSMPALHTLNLHNL	180	
QY	176	RTAQLRPDLAGLALQELDVSNLSLQALPGDLSGLFPRLR	-----	LLAAARNPN 226
Db	181	-IDALPPGVFAQLSLSRLDLSLTNRLATPD--PULFSRGRDAEASPSPLVLSFSGNPLH	237	
QY	227	CVCPLSMFGPVRRESHVTLASPETR-CHFPKPNAGRLLELDYDFGCPATTTATVPT	285	
Db	238	CNCELLWLR	-----	RLRPDDLTCASPPTLAGRYFWAYPEGEFSC----- 278
QY	286	TRPVVREPTALSSSLAPTMSLPATP	---	EAPSPSTAPPTVPVPQPD----- 333
Db	279	-----EPPLIARHTQRLVLEQRATLRALGDPVPTMHWVG----	PDDRVLVGNSSRA 328	
QY	334	-CPPTSLNGCTCHLGRHILACL--PEGFTGLYCESQ-	-----	GQCTRPSPTP 380
Db	329	WAPFNGTLEIGTVGADGAGAYTCIATNPAGEATARVELRVLALPHGNTSAEGRCFQPSD	388	
QY	381	VTPRPRLS----	TLGTEP----	VSPTSRLRGLQRYLQGSVQ-LRSLRLTYRNLSPDKR 432
Db	389	IAASARTAAGEGTLESEPAVQTEVTATSLVSWGLGRPADPVMFQIQYN--SSEDET	446	
QY	433	LVTLRPLASLAETVTLRNRNATYVVCVMPILGRCRVPGESEA-----	CGEAHTPPAVHSN 487	
Db	447	LIVRIVPASSHHFLKHLVPGADYDLCLLALSPAAGFSDLTATRLLGCAHFSTLPATPLC	506	
QY	488	HAPVQAREGNPLLIAPALAAVLLAAVGAAYCVRGRMAAAQDKGVQPGAGPL	547	
Db	507	HALQAHVLGGLTV----	AVGVLLVAALLVFTVALLV-RGRG-----	AGNGRLPL 551
QY	548	ELEGVKVLEPGPKATCGGGEALP	571	
Db	552	KLSHVQ-----	SQTNGTSPMP 568	

RESULT 15

ID	Q3TQ8_MOUSE	PRELIMINARY; PRT; 636	AA.
AC	Q3TQ8_MOUSE		
DT	11-OCT-2005	integrated into UniProtKB/TrEMBL.	
DT	11-OCT-2005	sequence version 1.	
DT	07-MAR-2006	entry version 8.	
DE	4 days neonate male adipose cDNA, RIKEN full-length enriched library,		
DE	clone:B4302124 product:leucine rich repeat and fibronectin type III		
DE	domain containing 4, full insert sequence.		
GN	Name=brfn4; (Mouse).		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;		

OC	Muroidea; Muridae; Murinae; Mus.
OX	NCBI_TaxID=10090;
RN	[1]
RP	NUCLEOTIDE SEQUENCE.
RC	STRAIN=C57BL/6J; TISSUE=Adipose;
RX	MEDLINE=92279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA	Carninci P., Kasukawa T., Lenhard B., Wells C., Kodzius R., Zhao M.A., Maeda N., Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Zhao M.A., Maeda N., Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M., Davis M.J., Wilming L.G., Aidinis V., Allen J.E., Ambesi-Impombato A., Anweiler R., Aturaliya R.N., Bailey T.L., Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M., Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R., Crome M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G., Di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G., Fletcher C.F., Fukushima T., Furuno M., Putaki S., Gariboldi M., Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E., Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N., Hill D., Huminecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T., Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H., Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K., Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J., Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L., Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K., Mottagui-Tabar S., Mulder N., Nakano N., Nakachi H., Ng P., Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O., Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavoni G., Pesole G., Petkovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M., Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C., Schonbach C., Sekiguchi K., Semple C.A., Sessa L., Sheng Y., Shibata Y., Shimada K., Silva D., Sinclair B., Sinsch R., Sperling S., Stupka E., Sugiura K., Sultana R., Takenaka Y., Taki K., Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A., Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K., Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C., Grimmond S.M., Tesdale R.D., Liu E.T., Brusic V., Quackenbush J., Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y., Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T., Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N., Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N., Nishio T., Okada M., Plessey C., Shibata K., Shiraki T., Suzuki S., Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J., Hayashizaki Y.;
RT	"The transcriptional landscape of the mammalian genome.";
RL	Science 309:1559-1563(2005).
RN	[3]
RP	NUCLEOTIDE SEQUENCE.
RC	STRAIN=C57BL/6J; TISSUE=Adipose;
RX	PubMed=16141073; DOI=10.1126/science.1112009;
RG	RIKEN Genome Exploration Research Group, and Genome Science Group (Genome Network Core Team) and the PANTOM Consortium;
RT	"Antisense Transcription in the Mammalian Transcriptome.";
RL	Science 309:1564-1566(2005).
RN	[4]
RP	NUCLEOTIDE SEQUENCE.
RC	STRAIN=C57BL/6J; TISSUE=Adipose;
RX	MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA	Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S., Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H., Yagi K., Tomaru Y., Hasegawa Y., Nogami D.A., Schonbach C., Gojobori T., Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J., Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W., Blake J.A., Brad D., Brusica V., Chothia C., Corbani L.E., Cousins S., Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S., Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J., Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,

